

Gln	Ala	Thr	Val	Gln	Thr	Asp	Lys	Val	Asp	Gly	Lys	Leu	Phe	Ala	Leu	625	630	635	640
Ala	Pro	Lys	Ala	Leu	Tyr	Glu	Thr	Ser	Trp	Gln	Lys	Ile	Thr	Ile	Pro	645	650	655	
Ala	Asn	Ser	Ser	Lys	Gln	Val	Thr	Ile	Pro	Ile	Asp	Val	Ser	Gln	Phe	660	665	670	
Ser	Lys	Asp	Leu	Leu	Ala	Pro	Met	Lys	Asn	Gly	Tyr	Phe	Leu	Glu	Gly	675	680	685	
Phe	Val	Arg	Phe	Lys	Gln	Asp	Pro	Thr	Lys	Glu	Glu	Leu	Met	Ser	Ile	690	695	700	
Pro	Tyr	Ile	Gly	Phe	Arg	Gly	Asp	Phe	Gly	Asn	Leu	Ser	Ala	Leu	Glu	705	710	715	720
Lys	Pro	Ile	Tyr	Asp	Ser	Lys	Asp	Gly	Ser	Ser	Tyr	Tyr	His	Glu	Ala	725	730	735	
Asn	Ser	Asp	Ala	Lys	Asp	Gln	Leu	Asp	Gly	Asp	Gly	Leu	Gln	Phe	Tyr	740	745	750	
Ala	Leu	Lys	Asn	Asn	Phe	Thr	Ala	Leu	Thr	Thr	Glu	Ser	Asn	Pro	Trp	755	760	765	
Thr	Ile	Ile	Lys	Ala	Val	Lys	Glu	Gly	Val	Glu	Asn	Ile	Glu	Asp	Ile	770	775	780	
Glu	Ser	Ser	Glu	Ile	Thr	Glu	Thr	Ile	Phe	Ala	Gly	Thr	Phe	Ala	Lys	785	790	795	800
Gln	Asp	Asp	Asp	Ser	His	Tyr	Tyr	Ile	His	Arg	His	Ala	Asn	Gly	Lys	805	810	815	
Pro	Tyr	Ala	Ala	Ile	Ser	Pro	Asn	Gly	Asp	Gly	Asn	Arg	Asp	Tyr	Val	820	825	830	
Gln	Phe	Gln	Gly	Thr	Phe	Leu	Arg	Asn	Ala	Lys	Asn	Leu	Val	Ala	Glu	835	840	845	
Val	Leu	Asp	Lys	Glu	Gly	Asn	Val	Val	Trp	Thr	Ser	Glu	Val	Thr	Glu	850	855	860	
Gln	Val	Val	Lys	Asn	Tyr	Asn	Asn	Asp	Leu	Ala	Ser	Thr	Leu	Gly	Ser	865	870	875	880
Thr	Arg	Phe	Glu	Lys	Thr	Arg	Trp	Asp	Gly	Lys	Asp	Lys	Asp	Gly	Lys	885	890	895	
Val	Val	Ala	Asn	Gly	Thr	Tyr	Thr	Tyr	Arg	Val	Arg	Tyr	Thr	Pro	Ile	900	905	910	
Ser	Ser	Gly	Ala	Lys	Glu	Gln	His	Thr	Asp	Phe	Asp	Val	Ile	Val	Asp	915	920	925	
Asn	Thr	Thr	Pro	Glu	Val	Ala	Thr	Ser	Ala	Thr	Phe	Ser	Thr	Glu	Asp	930	935	940	
Arg	Arg	Leu	Thr	Leu	Ala	Ser	Lys	Pro	Lys	Thr	Ser	Gln	Pro	Val	Tyr	945	950	955	960
Arg	Glu	Arg	Ile	Ala	Tyr	Thr	Tyr	Met	Asp	Glu	Asp	Leu	Pro	Thr	Thr	965	970	975	
Glu	Tyr	Ile	Ser	Pro	Asn	Glu	Asp	Gly	Thr	Phe	Thr	Leu	Pro	Glu	Glu	980	985	990	
Ala	Glu	Thr	Met	Glu	Gly	Ala	Thr	Val	Pro	Leu	Lys	Met	Ser	Asp	Phe	995	1000	1005	
Thr	Tyr	Val	Val	Glu	Asp	Met	Ala	Gly	Asn	Ile	Thr	Tyr	Thr	Pro		1010	1015	1020	
Val	Thr	Lys	Leu	Leu	Glu	Gly	His	Ser	Asn	Lys	Pro	Glu	Gln	Asp		1025	1030	1035	
Gly	Ser	Asp	Gln	Ala	Pro	Asp	Lys	Lys	Pro	Glu	Thr	Lys	Pro	Glu		1040	1045	1050	
Gln	Asp	Gly	Ser	Gly	Gln	Ala	Pro	Asp	Lys	Lys	Pro	Glu	Thr	Lys		1055	1060	1065	
Pro	Glu	Gln	Asp	Gly	Ser	Gly	Gln	Thr	Pro	Asp	Lys	Lys	Pro	Glu					

1070	1075	1080
Thr Lys Pro Glu Gln Asp Gly	Ser Gly Gln Thr Pro	Asp Lys Lys
1085	1090	1095
Pro Glu Thr Lys Pro Glu Lys	Asp Ser Ser Gly Gln	Thr Pro Gly
1100	1105	1110
Lys Thr Pro Gln Lys Gly Gln	Pro Ser Arg Thr Leu	Glu Lys Arg
1115	1120	1125
Ser Ser Lys Arg Ala Leu Ala	Thr Lys Ala Ser Thr	Lys Asp Gln
1130	1135	1140
Leu Pro Thr Thr Asn Asp Lys	Asp Thr Asn Arg Leu	His Leu Leu
1145	1150	1155
Lys Leu Val Met Thr Thr Phe	Phe Leu Gly Leu Val	Ala His Ile
1160	1165	1170
Phe Lys Thr Lys Arg Thr Glu	Asp	
1175	1180	

		675					680				685				
Leu	Thr	Ser	Leu	Asn	Phe	Ile	Asp	Leu	Ser	Gln	Asn	Asn	Leu	Ala	Leu
	690					695					700				
Leu	Pro	Lys	Thr	Ile	Glu	Lys	Leu	Arg	Ala	Leu	Ser	Thr	Ile	Val	Ala
705					710					715					720
Ser	Arg	Asn	His	Ile	Thr	Arg	Ile	Asp	Asn	Ile	Ser	Phe	Lys	Asn	Leu
				725					730					735	
Pro	Lys	Leu	Ser	Val	Leu	Asp	Leu	Ser	Thr	Asn	Glu	Ile	Ser	Asn	Leu
			740					745					750		
Pro	Asn	Gly	Ile	Phe	Lys	Gln	Asn	Asn	Gln	Leu	Thr	Lys	Leu	Asp	Phe
		755					760					765			
Phe	Asn	Asn	Leu	Leu	Thr	Gln	Val	Glu	Glu	Ser	Val	Phe	Pro	Asp	Val
	770					775					780				
Glu	Thr	Leu	Asn	Leu	Asp	Val	Lys	Phe	Asn	Gln	Ile	Lys	Ser	Val	Ser
785					790					795					800
Pro	Lys	Val	Arg	Ala	Leu	Ile	Gly	Gln	His	Lys	Leu	Thr	Pro	Gln	Lys
				805					810					815	
His	Ile	Ala	Lys	Leu	Glu	Ala	Ser	Leu	Asp	Gly	Glu	Lys	Ile	Lys	Tyr
			820					825					830		
His	Gln	Ala	Phe	Ser	Leu	Leu	Asp	Leu	Tyr	Tyr	Trp	Glu	Gln	Lys	Thr
		835					840					845			
Asn	Ser	Ala	Ile	Asp	Lys	Glu	Leu	Val	Ser	Val	Glu	Glu	Tyr	Gln	Gln
	850					855					860				
Leu	Leu	Gln	Glu	Lys	Gly	Ser	Asp	Thr	Val	Ser	Leu	Leu	Asn	Asp	Met
865					870						875				880
Gln	Val	Asp	Trp	Ser	Ile	Val	Ile	Gln	Leu	Gln	Lys	Lys	Ala	Ser	Asn
				885					890					895	
Gly	Gln	Tyr	Val	Thr	Val	Asp	Glu	Lys	Leu	Leu	Ser	Asn	Asp	Pro	Lys
			900				905						910		
Asp	Asp	Leu	Thr	Gly	Glu	Phe	Ser	Leu	Lys	Asp	Pro	Gly	Thr	Tyr	Arg
		915					920					925			
Ile	Arg	Lys	Ala	Leu	Ile	Thr	Lys	Lys	Phe	Ala	Thr	Gln	Lys	Glu	His
	930					935					940				
Ile	Tyr	Leu	Thr	Ser	Asn	Asp	Ile	Leu	Val	Ala	Lys	Gly	Pro	His	Ser
945					950					955					960
His	Gln	Lys	Asp	Leu	Val	Glu	Asn	Gly	Leu	Arg	Ala	Leu	Asn	Gln	Lys
				965					970					975	
Gln	Leu	Arg	Asp	Gly	Ile	Tyr	Tyr	Leu	Asn	Ala	Ser	Met	Leu	Lys	Thr
			980					985					990		
Asp	Leu	Ala	Ser	Glu	Ser	Met	Ser	Asn	Lys	Ala	Ile	Asn	His	Arg	Val
		995					1000					1005			
Thr	Leu	Val	Val	Lys	Lys	Gly	Val	Ser	Tyr	Leu	Glu	Val	Glu	Phe	
	1010					1015					1020				
Arg	Gly	Ile	Lys	Val	Gly	Lys	Met	Leu							

Ser	Leu	Thr	Thr	Glu	Lys	Ala	Lys	Val	Val	Lys	Glu	Thr	Asn	Asn	
1130						1135					1140				
Pro	Gln	Glu	Asn	Ser	His	Leu	Thr	Ser	Thr	Asp	Gln	Leu	Lys	Gly	
1145						1150					1155				
Pro	Gln	Asn	Arg	Gln	Gln	Glu	Lys	Thr	Pro	Thr	Ser	Pro	Pro	Ser	
1160						1165					1170				
Ala	Ala	Thr	Gly	Ile	Ala	Asn	Leu	Thr	Asp	Leu	Leu	Ala	Lys	Lys	
1175						1180					1185				
Ala	Thr	Gly	Gln	Ser	Thr	Gln	Glu	Thr	Ser	Lys	Thr	Asp	Asp	Thr	
1190						1195					1200				
Asp	Lys	Ala	Glu	Lys	Leu	Lys	Gln	Leu	Val	Arg	Asp	His	Gln	Thr	
1205						1210					1215				
Ser	Ile	Glu	Gly	Lys	Thr	Ala	Lys	Asp	Thr	Lys	Thr	Lys	Lys	Ser	
1220						1225					1230				
Asp	Lys	Lys	His	Arg	Ser	Asn	Gln	Gln	Ser	Asn	Gly	Glu	Glu	Ser	
1235						1240					1245				
Ser	Ser	Arg	Tyr	His	Leu	Ile	Ala	Gly	Leu	Ser	Ser	Phe	Met	Ile	
1250						1255					1260				
Val	Ala	Leu	Gly	Phe	Ile	Ile	Gly	Arg	Lys	Thr	Leu	Phe	Lys		
1265						1270					1275				

<210> SEQ ID NO 3

<211> LENGTH: 1827

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 3

atgtctaaaa	ttattggtat	tgacttaggt	acaacaaact	cagcagtagc	agttcttgaa	60
gggactgaat	caaaaatcat	tgctaacc	gaaggcaatc	gtacaactcc	ttcagtagta	120
tcattcaaaa	atggtgaaat	tatcgtgggt	gatgctgcaa	aacgtcaagc	agtgacaaac	180
ccagaaacag	taatctctat	taaatctaaa	atgggaactt	ctgaaaaagt	ttctgcaaat	240
ggtaaagaat	atactcctca	agaaatttca	gcaatgattc	ttcaatacct	taaaggttat	300
gctgaagact	atcttggaga	aaaagtagaa	aaagcagtta	ttactgttcc	agcttacttc	360
aacgatgcac	aacgtcaggc	aactaaagac	gctggtaaaa	ttgcaggtct	tgaagtagaa	420
cgtatcgtta	acgaaccaac	agcagccgca	cttgcttatg	gtatggataa	gactgacaag	480
gatgaaaaaa	tcttagtttt	tgaccttggg	ggtggatcaa	ttgacgtatc	aatccttgaa	540
ttaggtgatg	gtgtcttcga	cgttcttgca	acagcaggtg	ataacaaact	tggtgggtgac	600
gactttgacc	aaaaaattat	tgatttctta	gtggctgaat	ttaagaaaga	aaatggcatt	660
gacttatcac	aagataagat	ggcacttcaa	cgcttgaaag	atgctgctga	aaaagctaaa	720
aaagatcttt	cagggtgtgac	acaaacacaa	atttcattac	cgttcatcac	tgctggttct	780
gccggtcctc	ttcacttgga	gatgagctta	tctcgtgcta	aatttgacga	tctcactcgc	840
gaccttgtag	aacgtacgaa	aactccagtt	cgtcaagccc	tttcagatgc	aggattgtca	900
ttgtcagaaa	ttgatgaagt	tatccttggt	ggtggatcaa	ctcgtatccc	agcagttgtc	960
gaagctgtaa	aagctgaaac	tggtaaagaa	ccaaataaat	ctgtaaacc	tgatgaagtg	1020
gttgctatgg	gtgctgctat	ccaaggtggg	gttatcactg	gggatgtgaa	agacgttgtc	1080
cttccttgacg	taacaccatt	gtcacttggg	attgaaacaa	tgggtggtgt	cttcactaaa	1140
ttgatcgacc	gcaatacaac	tatccaaca	tctaaatcac	aagtcttctc	aacagcagca	1200
gacaaccaac	cagctgttga	tatccatggt	cttcaagggtg	aacgccaat	ggcagcagat	1260
aacaagactc	ttggtcgctt	ccaattgact	gatatcccag	ctgcacctcg	tggaatccca	1320
caaattgaag	taacatttga	tatcgataaa	aacggtattg	tttctgtaaa	agctaaagac	1380
cttggtacgc	aaaaggaaca	acacatcggt	atcaaatcaa	acgacggact	ttctgaagaa	1440
gaaattgatc	gcatgatgaa	agacgctgaa	gctaattgccg	aagccgatgc	gaaacgtaaa	1500
gaagaagttg	accttaaaaa	cgaagttgac	caagctatct	ttgctactga	aaaaacaatc	1560
aaagaaactg	aaggtaaagg	ctttgataca	gaacgcgatg	cagcgcaatc	agctcttgac	1620
gagttaaaaa	ctgcgcaaga	atctggcaac	cttgacgaca	tgaaagctaa	acttgaagca	1680
ttaaatagaa	aagcgcaagc	tttggctggt	aaaatgtacg	agcaagctgc	agcagctcaa	1740
caagcagcac	aaggtgcaga	aggtgcacaa	gctaattgatt	cagcaataaa	tgatgatggt	1800
gtagatggcg	aatttacaga	aaagtaa				1827

<210> SEQ ID NO 4

<211> LENGTH: 608

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 4

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Met Ser Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Ala Val
1      5      10      15
Ala Val Leu Glu Gly Thr Glu Ser Lys Ile Ile Ala Asn Pro Glu Gly
20      25      30
Asn Arg Thr Thr Pro Ser Val Val Ser Phe Lys Asn Gly Glu Ile Ile
35      40      45
Val Gly Asp Ala Ala Lys Arg Gln Ala Val Thr Asn Pro Glu Thr Val
50      55      60
Ile Ser Ile Lys Ser Lys Met Gly Thr Ser Glu Lys Val Ser Ala Asn
65      70      75      80
Gly Lys Glu Tyr Thr Pro Gln Glu Ile Ser Ala Met Ile Leu Gln Tyr
85      90      95
Leu Lys Gly Tyr Ala Glu Asp Tyr Leu Gly Glu Lys Val Glu Lys Ala
100     105     110
Val Ile Thr Val Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln Ala Thr
115     120     125
Lys Asp Ala Gly Lys Ile Ala Gly Leu Glu Val Glu Arg Ile Val Asn
130     135     140
Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Met Asp Lys Thr Asp Lys
145     150     155     160
Asp Glu Lys Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe Asp Val
165     170     175
Ser Ile Leu Glu Leu Gly Asp Gly Val Phe Asp Val Leu Ala Thr Ala
180     185     190
Gly Asp Asn Lys Leu Gly Gly Asp Asp Phe Asp Gln Lys Ile Ile Asp
195     200     205
Phe Leu Val Ala Glu Phe Lys Lys Glu Asn Gly Ile Asp Leu Ser Gln
210     215     220
Asp Lys Met Ala Leu Gln Arg Leu Lys Asp Ala Ala Glu Lys Ala Lys
225     230     235     240
Lys Asp Leu Ser Gly Val Thr Gln Thr Gln Ile Ser Leu Pro Phe Ile
245     250     255
Thr Ala Gly Ser Ala Gly Pro Leu His Leu Glu Met Ser Leu Ser Arg
260     265     270
Ala Lys Phe Asp Asp Leu Thr Arg Asp Leu Val Glu Arg Thr Lys Thr
275     280     285
Pro Val Arg Gln Ala Leu Ser Asp Ala Gly Leu Ser Leu Ser Glu Ile
290     295     300
Asp Glu Val Ile Leu Val Gly Gly Ser Thr Arg Ile Pro Ala Val Val
305     310     315     320
Glu Ala Val Lys Ala Glu Thr Gly Lys Glu Pro Asn Lys Ser Val Asn
325     330     335
Pro Asp Glu Val Val Ala Met Gly Ala Ala Ile Gln Gly Gly Val Ile
340     345     350
Thr Gly Asp Val Lys Asp Val Val Leu Leu Asp Val Thr Pro Leu Ser
355     360     365
Leu Gly Ile Glu Thr Met Gly Gly Val Phe Thr Lys Leu Ile Asp Arg
370     375     380
Asn Thr Thr Ile Pro Thr Ser Lys Ser Gln Val Phe Ser Thr Ala Ala
385     390     395     400
Asp Asn Gln Pro Ala Val Asp Ile His Val Leu Gln Gly Glu Arg Pro
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				405					410					415			
Met	Ala	Ala	Asp	Asn	Lys	Thr	Leu	Gly	Arg	Phe	Gln	Leu	Thr	Asp	Ile		
			420					425					430				
Pro	Ala	Ala	Pro	Arg	Gly	Ile	Pro	Gln	Ile	Glu	Val	Thr	Phe	Asp	Ile		
		435					440					445					
Asp	Lys	Asn	Gly	Ile	Val	Ser	Val	Lys	Ala	Lys	Asp	Leu	Gly	Thr	Gln		
	450				455						460						
Lys	Glu	Gln	His	Ile	Val	Ile	Lys	Ser	Asn	Asp	Gly	Leu	Ser	Glu	Glu		
465				470					475					480			
Glu	Ile	Asp	Arg	Met	Met	Lys	Asp	Ala	Glu	Ala	Asn	Ala	Glu	Ala	Asp		
			485					490					495				
Ala	Lys	Arg	Lys	Glu	Glu	Val	Asp	Leu	Lys	Asn	Glu	Val	Asp	Gln	Ala		
		500						505					510				
Ile	Phe	Ala	Thr	Glu	Lys	Thr	Ile	Lys	Glu	Thr	Glu	Gly	Lys	Gly	Phe		
	515					520						525					
Asp	Thr	Glu	Arg	Asp	Ala	Ala	Gln	Ser	Ala	Leu	Asp	Glu	Leu	Lys	Ala		
	530				535						540						
Ala	Gln	Glu	Ser	Gly	Asn	Leu	Asp	Asp	Met	Lys	Ala	Lys	Leu	Glu	Ala		
545				550					555					560			
Leu	Asn	Glu	Lys	Ala	Gln	Ala	Leu	Ala	Val	Lys	Met	Tyr	Glu	Gln	Ala		
			565					570					575				
Ala	Ala	Ala	Gln	Gln	Ala	Ala	Gln	Gly	Ala	Glu	Gly	Ala	Gln	Ala	Asn		
		580					585					590					
Asp	Ser	Ala	Asn	Asn	Asp	Asp	Val	Val	Asp	Gly	Glu	Phe	Thr	Glu	Lys		
	595					600						605					

<210> SEQ ID NO 5

<211> LENGTH: 1275

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 5

atgaaaattg	gaaaaaaaaat	agttttaatg	ttcacagcta	tttgtttaac	aactgtcttg	60
gcattagggtg	tctatctaac	tagtgcttat	accttctcaa	caggagaatt	atcaaagacc	120
tttaaagatt	tttcgacatc	ttcaaacaaa	agtgatgcc	ttaaacaaac	aagagctttt	180
tctatcttgt	tgatgggtgt	tgatacaggc	tcttcagagc	gtgcctccaa	gtgggaagga	240
aacagtgatt	cgatgatttt	ggttacggtt	aatccaaaga	ccaagaaaac	aactatgact	300
agtttagaac	gagatacctt	aaccacgtta	tctggaccca	aaaataatga	aatgaatggg	360
ggtgaagcta	agcttaacgc	tgcttatgca	gcagggtggcg	ctcagatggc	tattatgacc	420
gtgcaagatc	ttttgaatat	caccattgat	aactatgttc	aaattaatat	gcaaggcctt	480
attgatcttg	tgaatgcagt	tggagggatt	acagttacaa	atgagtttga	ttttcctatc	540
tcgattgctg	aaaacgaacc	tgaatatcaa	gctactgttg	cgcttggaa	acacaaaatt	600
aacggtgaac	aagcttttgt	ttatgctcgt	atgcgttatg	atgatcctga	gggagattat	660
ggtcgacaaa	agcgtcaacg	tgaagtcatt	caaaaggat	tgaaaaaaat	ccttgctctt	720
gatagcatta	gctcttatcg	gaagatttta	tctgctgtaa	gtagtaatat	gcaaacgaat	780
atcgaaatct	cttctcgcac	tatccctagt	ctattaggtt	atcgtgacgc	acttagaact	840
attaagactt	atcaactaaa	aggagaagat	gccactttat	cagatgggtg	atcataccaa	900
attgttacct	ctaatacattt	gtagaaatc	caaaatcgta	tccgaacaga	attaggactt	960
cataagggtta	atcaattaaa	aacaaatgct	actgtttatg	aaaatttgta	tgggtcaact	1020
aagtctcaga	cagtaaacaa	caactatgac	tcttcaggcc	aggctccatc	ttattctgat	1080
agtcatagct	cttacgctaa	ttattcaagt	ggagtagata	ccggccagag	tgctagtaca	1140
gaccaggact	ctactgcttc	aagccatagg	ccagctacgc	cgtcttcttc	atcagatgct	1200
ttagcagctg	atgagtctag	ctcatcaggg	tctggatcat	tagttcctcc	tgctaataatc	1260
aaccctcaga	cctaa					1275

<210> SEQ ID NO 6

<211> LENGTH: 424

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 6

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Met Lys Ile Gly Lys Lys Ile Val Leu Met Phe Thr Ala Ile Val Leu
1           5           10           15
Thr Thr Val Leu Ala Leu Gly Val Tyr Leu Thr Ser Ala Tyr Thr Phe
20           25           30
Ser Thr Gly Glu Leu Ser Lys Thr Phe Lys Asp Phe Ser Thr Ser Ser
35           40           45
Asn Lys Ser Asp Ala Ile Lys Gln Thr Arg Ala Phe Ser Ile Leu Leu
50           55           60
Met Gly Val Asp Thr Gly Ser Ser Glu Arg Ala Ser Lys Trp Glu Gly
65           70           75           80
Asn Ser Asp Ser Met Ile Leu Val Thr Val Asn Pro Lys Thr Lys Lys
85           90           95
Thr Thr Met Thr Ser Leu Glu Arg Asp Thr Leu Thr Thr Leu Ser Gly
100          105          110
Pro Lys Asn Asn Glu Met Asn Gly Val Glu Ala Lys Leu Asn Ala Ala
115          120          125
Tyr Ala Ala Gly Gly Ala Gln Met Ala Ile Met Thr Val Gln Asp Leu
130          135          140
Leu Asn Ile Thr Ile Asp Asn Tyr Val Gln Ile Asn Met Gln Gly Leu
145          150          155          160
Ile Asp Leu Val Asn Ala Val Gly Gly Ile Thr Val Thr Asn Glu Phe
165          170          175
Asp Phe Pro Ile Ser Ile Ala Glu Asn Glu Pro Glu Tyr Gln Ala Thr
180          185          190
Val Ala Pro Gly Thr His Lys Ile Asn Gly Glu Gln Ala Leu Val Tyr
195          200          205
Ala Arg Met Arg Tyr Asp Asp Pro Glu Gly Asp Tyr Gly Arg Gln Lys
210          215          220
Arg Gln Arg Glu Val Ile Gln Lys Val Leu Lys Lys Ile Leu Ala Leu
225          230          235          240
Asp Ser Ile Ser Ser Tyr Arg Lys Ile Leu Ser Ala Val Ser Ser Asn
245          250          255
Met Gln Thr Asn Ile Glu Ile Ser Ser Arg Thr Ile Pro Ser Leu Leu
260          265          270
Gly Tyr Arg Asp Ala Leu Arg Thr Ile Lys Thr Tyr Gln Leu Lys Gly
275          280          285
Glu Asp Ala Thr Leu Ser Asp Gly Gly Ser Tyr Gln Ile Val Thr Ser
290          295          300
Asn His Leu Leu Glu Ile Gln Asn Arg Ile Arg Thr Glu Leu Gly Leu
305          310          315          320
His Lys Val Asn Gln Leu Lys Thr Asn Ala Thr Val Tyr Glu Asn Leu
325          330          335
Tyr Gly Ser Thr Lys Ser Gln Thr Val Asn Asn Asn Tyr Asp Ser Ser
340          345          350
Gly Gln Ala Pro Ser Tyr Ser Asp Ser His Ser Ser Tyr Ala Asn Tyr
355          360          365
Ser Ser Gly Val Asp Thr Gly Gln Ser Ala Ser Thr Asp Gln Asp Ser
370          375          380
Thr Ala Ser Ser His Arg Pro Ala Thr Pro Ser Ser Ser Ser Asp Ala
385          390          395          400
Leu Ala Ala Asp Glu Ser Ser Ser Ser Gly Ser Gly Ser Leu Val Pro
405          410          415
Pro Ala Asn Ile Asn Pro Gln Thr
420
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<210> SEQ ID NO 7
<211> LENGTH: 2166
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 7
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cttagcctta ttatccttgt tattattatt ggtgggtcttt tgtttacctt ctacattagc      120
agtgtccga aactgtcaga agcccagtta aaatcaacaa actctagctt ggtttatgac      180
ggtaataaca atctgattgc tgatttgggt tctgaaaagc gtgaaaatgt aacagctgat      240
agtatcccta ttaatctagt taatgctatt acctcaattg aagataaacg tttctttaac      300
catcgtggag tagatcttta tcgtattttt ggtgctgcct ttcataatct aacgagtcag      360
accactcaag ggggggtcaac gcttgatcag caactcatta aactagccta tttttctact      420
aatgaatctg atcaaacctt aaaacgtaag gctcaagaag tttggcttgc tcttcaaagt      480
gagcgaaaaat atactaaaca agaaatcctg actttttaca tcaacaaagt atatatgggt      540
aatggcaact atgggtatgct gacagccgct aagtcttatt atggcaagga tcttaaggat      600
ttatcttatg cccaactagc cctattggct ggaatccctc aagctcctag tcaatatgat      660
ccttaccttc atcctgaagc tgctcaaaat cgccgtaacg tcgtgttgca acagatgtac      720
atggaaaaaac atctgacgaa agcagaatat gaaactgcc a tcgcaactcc cgtcgtgtaa      780
ggtctacaat cactccaaca gcgctcaact tatccaaaat atatggataa ttatctaaaa      840
caagttattg aagaagtcaa aaaagaaacg aataaagata tttttaccgc tggtttaaaa      900
gtttatacca atattatccc cgatgcgcag cagactcttt ataatattta tcattctggt      960
gattatgttt actatccaga ccaagatttc caagttgctt caacgattgt tgatgtgaca     1020
aatggtcattg ttattgctca gcttggcgga cgtaatcaag atgaaaatgt ttcatttggg     1080
actaaccaag ctgttttaac tgatcgtgac tgggggttcta ccatgaagcc aatcacagcc     1140
tatgctcctg ctattgaatc tgggtgtttat acttctactg ctcagtcgac taatgactca     1200
gtctattatt ggcttggaa cactacccaa ttgtttaact gggaccttag atataacgga     1260
tggatgacaa tccaagctgc tattatgcta tcgcgaaatg tcccagcagt ccgagcactg     1320
gaagccgcag gacttgacta tgctcgatct ttcttaagca gtttaggtat taactatccc     1380
gaaatgcact actcaaacgc tatctcaagt aataacagta gctcagataa aaaatatggt     1440
gcaagtagtg aaaaaatggc cgctgcatac gctgcttttg caaatggtgg tatttatcat     1500
aaaccaaggt atgtcaataa agtggaaatt agtgatggta caagtaaaac ttttgatgaa     1560
aaagggaaaac gtgccatgaa agaaaccacg gcctatatga tgacagatat gtaaaaaact     1620
gttctcactt atggtacagg tactgctgct gccattcctg gtggtgacga agctggtaaa     1680
acaggggactt ctaactacac tgatgaggaa ctagtataaa ttggtgaaaa atacggcctt     1740
tatccagatt atggttggtac attagcgcca gacgaaaaat ttggtggcct tactaagcgc     1800
tacgccatgg ctgtttggac aggttacaaa aaccgcttga cccaggtata cggatcaagt     1860
ctagagattg catctgacgt ttatcgtagc atgatgactt acttaacaaa tggttacagt     1920
gaagattgga cgatgcaaaa tggctctttat cgcagtgggt gattcctcta cttaagcgga     1980
acctatgcga gcaacaccga ctataactaat tcggtttaca acaatcttta cagcaataac     2040
acgacaacag cttctagcca aacgacttca gatgatacta gtagtagcaa tgatacaagt     2100
aattcaacca atacagacaa caatggcagt catccatcta ccatgataa aaagacaact     2160
cattaa                                           2166

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<210> SEQ ID NO 8
<211> LENGTH: 721
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 8
Met Ile Thr Ile Lys Asn Pro Lys Ile Leu Lys Trp Leu Lys Tyr Val
1          5          10          15
Leu Ser Ala Ile Leu Ser Leu Ile Ile Leu Val Ile Ile Ile Gly Gly
20          25          30
Leu Leu Phe Thr Phe Tyr Ile Ser Ser Ala Pro Lys Leu Ser Glu Ala
35          40          45
Gln Leu Lys Ser Thr Asn Ser Ser Leu Val Tyr Asp Gly Asn Asn Asn
50          55          60
Leu Ile Ala Asp Leu Gly Ser Glu Lys Arg Glu Asn Val Thr Ala Asp

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65					70					75				80	
Ser	Ile	Pro	Ile	Asn	Leu	Val	Asn	Ala	Ile	Thr	Ser	Ile	Glu	Asp	Lys
				85					90					95	
Arg	Phe	Phe	Asn	His	Arg	Gly	Val	Asp	Leu	Tyr	Arg	Ile	Phe	Gly	Ala
			100					105					110		
Ala	Phe	His	Asn	Leu	Thr	Ser	Gln	Thr	Thr	Gln	Gly	Gly	Ser	Thr	Leu
		115					120					125			
Asp	Gln	Gln	Leu	Ile	Lys	Leu	Ala	Tyr	Phe	Ser	Thr	Asn	Glu	Ser	Asp
	130					135					140				
Gln	Thr	Leu	Lys	Arg	Lys	Ala	Gln	Glu	Val	Trp	Leu	Ala	Leu	Gln	Met
145					150					155					160
Glu	Arg	Lys	Tyr	Thr	Lys	Gln	Glu	Ile	Leu	Thr	Phe	Tyr	Ile	Asn	Lys
				165					170					175	
Val	Tyr	Met	Gly	Asn	Gly	Asn	Tyr	Gly	Met	Leu	Thr	Ala	Ala	Lys	Ser
			180					185					190		
Tyr	Tyr	Gly	Lys	Asp	Leu	Lys	Asp	Leu	Ser	Tyr	Ala	Gln	Leu	Ala	Leu
	195						200					205			
Leu	Ala	Gly	Ile	Pro	Gln	Ala	Pro	Ser	Gln	Tyr	Asp	Pro	Tyr	Leu	His
	210					215					220				
Pro	Glu	Ala	Ala	Gln	Asn	Arg	Arg	Asn	Val	Val	Leu	Gln	Gln	Met	Tyr
225					230					235					240
Met	Glu	Lys	His	Leu	Thr	Lys	Ala	Glu	Tyr	Glu	Thr	Ala	Ile	Ala	Thr
				245					250					255	
Pro	Val	Ala	Glu	Gly	Leu	Gln	Ser	Leu	Gln	Gln	Arg	Ser	Thr	Tyr	Pro
			260					265					270		
Lys	Tyr	Met	Asp	Asn	Tyr	Leu	Lys	Gln	Val	Ile	Glu	Glu	Val	Lys	Lys
	275						280					285			
Glu	Thr	Asn	Lys	Asp	Ile	Phe	Thr	Ala	Gly	Leu	Lys	Val	Tyr	Thr	Asn
	290					295					300				
Ile	Ile	Pro	Asp	Ala	Gln	Gln	Thr	Leu	Tyr	Asn	Ile	Tyr	His	Ser	Gly
305					310					315					320
Asp	Tyr	Val	Tyr	Tyr	Pro	Asp	Gln	Asp	Phe	Gln	Val	Ala	Ser	Thr	Ile
				325					330					335	
Val	Asp	Val	Thr	Asn	Gly	His	Val	Ile	Ala	Gln	Leu	Gly	Gly	Arg	Asn
			340					345					350		
Gln	Asp	Glu	Asn	Val	Ser	Phe	Gly	Thr	Asn	Gln	Ala	Val	Leu	Thr	Asp
	355						360					365			
Arg	Asp	Trp	Gly	Ser	Thr	Met	Lys	Pro	Ile	Thr	Ala	Tyr	Ala	Pro	Ala
	370					375					380				
Ile	Glu	Ser	Gly	Val	Tyr	Thr	Ser	Thr	Ala	Gln	Ser	Thr	Asn	Asp	Ser
385					390					395					400
Val	Tyr	Tyr	Trp	Pro	Gly	Thr	Thr	Thr	Gln	Leu	Phe	Asn	Trp	Asp	Leu
				405					410					415	
Arg	Tyr	Asn	Gly	Trp	Met	Thr	Ile	Gln	Ala	Ala	Ile	Met	Leu	Ser	Arg
			420					425					430		
Asn	Val	Pro	Ala	Val	Arg	Ala	Leu	Glu	Ala	Ala	Gly	Leu	Asp	Tyr	Ala
	435						440					445			
Arg	Ser	Phe	Leu	Ser	Ser	Leu	Gly	Ile	Asn	Tyr	Pro	Glu	Met	His	Tyr
	450					455					460				
Ser	Asn	Ala	Ile	Ser	Ser	Asn	Asn	Ser	Ser	Ser	Asp	Lys	Lys	Tyr	Gly
465					470					475					480
Ala	Ser	Ser	Glu	Lys	Met	Ala	Ala	Ala	Tyr	Ala	Ala	Phe	Ala	Asn	Gly
				485					490					495	
Gly	Ile	Tyr	His	Lys	Pro	Arg	Tyr	Val	Asn	Lys	Val	Glu	Phe	Ser	Asp
			500					505					510		
Gly	Thr	Ser	Lys	Thr	Phe	Asp	Glu	Lys	Gly	Lys	Arg	Ala	Met	Lys	Glu
			515				520						525		

Thr	Thr	Ala	Tyr	Met	Met	Thr	Asp	Met	Leu	Lys	Thr	Val	Leu	Thr	Tyr
530						535					540				
Gly	Thr	Gly	Thr	Ala	Ala	Ala	Ile	Pro	Gly	Val	Ala	Gln	Ala	Gly	Lys
545					550					555					560
Thr	Gly	Thr	Ser	Asn	Tyr	Thr	Asp	Glu	Glu	Leu	Ala	Lys	Ile	Gly	Glu
				565					570					575	
Lys	Tyr	Gly	Leu	Tyr	Pro	Asp	Tyr	Val	Gly	Thr	Leu	Ala	Pro	Asp	Glu
			580					585					590		
Asn	Phe	Val	Gly	Phe	Thr	Lys	Arg	Tyr	Ala	Met	Ala	Val	Trp	Thr	Gly
	595						600					605			
Tyr	Lys	Asn	Arg	Leu	Thr	Pro	Val	Tyr	Gly	Ser	Ser	Leu	Glu	Ile	Ala
	610					615					620				
Ser	Asp	Val	Tyr	Arg	Ser	Met	Met	Thr	Tyr	Leu	Thr	Asn	Gly	Tyr	Ser
625					630					635					640
Glu	Asp	Trp	Thr	Met	Pro	Asn	Gly	Leu	Tyr	Arg	Ser	Gly	Gly	Phe	Leu
				645				650						655	
Tyr	Leu	Ser	Gly	Thr	Tyr	Ala	Ser	Asn	Thr	Asp	Tyr	Thr	Asn	Ser	Val
			660					665					670		
Tyr	Asn	Asn	Leu	Tyr	Ser	Asn	Asn	Thr	Thr	Thr	Ala	Ser	Ser	Gln	Thr
	675					680					685				
Thr	Ser	Asp	Asp	Thr	Ser	Ser	Ser	Asn	Asp	Thr	Ser	Asn	Ser	Thr	Asn
	690					695				700					
Thr	Asp	Asn	Asn	Gly	Ser	His	Pro	Ser	Thr	Asp	Asp	Lys	Lys	Thr	Thr
705					710					715					720
His															

<210> SEQ ID NO 9

<211> LENGTH: 1470

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 9

gtgtcagaag	aaagcaaaga	agtcgaagta	acaaaagaat	cgcaaacatt	ggggcttaat	60
gaagccaagt	caatgacaat	tggtgaagct	gtacgcaaac	agtcagagat	aaaagcaggt	120
gttactaagg	atgatagtat	tttagataag	tacattaagc	aacaccgtga	cgaagtttct	180
tctcaaaaag	ttgatgctaa	gtatacacag	cttgatacac	ctagtttaga	taactttatc	240
aaaaaacaaa	gagaagcatt	gagtaaagcc	ggctctgttg	atgacgaacc	tgtgtctgcg	300
gagtctgctg	agcaagatag	cacttttggt	gaagaagtag	ctgaagactt	agctccaatg	360
gagactactg	cgggtggtaac	tgggattccg	gtggaagcga	cagtcacctg	gtagatctta	420
gatccatcag	agaggggtcat	tccagaacca	cagatgacca	aggaagaacc	aaaaagagat	480
cagtttcttt	ctgaagatag	ccaccatcca	gccaaacaaa	acacgaaaaa	aggttggtta	540
atagctttat	ttctgctatt	attggccatt	cttgagcttg	tatttggttg	gaaccatttc	600
ttgagacaag	acagtggtaa	aacaactcaa	acagcaagta	aacagacaaa	gacctctttg	660
cagaccgaca	gtgctaaaaa	agcaacgcgc	ttgaaggctg	ctgctaaagc	tttcgaaaaa	720
ctatatggta	ctttttatac	agatgccaca	aagagcaaat	taaaaaatag	tgcctttgct	780
actttgccag	atttagaagc	tgccttgaaa	gctttggaag	gctctgctta	ctatgataag	840
gcgaaagcaa	aagtcgattc	ccttaagaaa	gctattgctg	ctattacagc	ggttaacggg	900
aaatttggtt	ccgatgttgt	tgtagatggg	gaaaagggtt	cggctgaagt	caaggctgat	960
gctaattttg	atgatattat	aagtgcaccc	ttgacaatag	gaaatgcaaa	tcttgatgct	1020
gtcttgacag	caagcatcac	agaaggctcg	cagcaactag	ccagcaaggc	tgaggccgct	1080
aaagcagcta	atgagcaagc	agtccaggat	caagcagctc	aaggacaaa	tacatcagta	1140
gcaccatctg	gctatggctt	gacaagttaa	gatcctgcaa	gcttacaacg	gcatttatca	1200
cgtgtacctt	acaatcaaga	tgttattgct	gacagagcta	acccatcttg	ggcatttaac	1260
ccaggagttc	ttgaaaaaat	tgtagcaacc	tcacaagcta	gaggttatat	ttcagggaac	1320
caatatattt	tagagccggg	taatattatt	aattggcaatg	gttactataa	tatgtttaag	1380
cctgatggca	cttatctgtt	ctctattaat	tgtgaagacg	gttattttgt	aggaaatggc	1440
aaagggttat	ctgatgcttt	agattactga				1470

<210> SEQ ID NO 10
 <211> LENGTH: 489
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 10

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Leu	Gly	Leu	Asn	Glu	Ala	Lys	Ser	Met	Thr	Ile	Gly	Glu	Ala	Val	Arg	20	25	30	
Lys	Gln	Ser	Glu	Ile	Lys	Ala	Gly	Val	Thr	Lys	Asp	Asp	Ser	Ile	Leu	35	40	45	
Asp	Lys	Tyr	Ile	Lys	Gln	His	Arg	Asp	Glu	Val	Ser	Ser	Gln	Lys	Phe	50	55	60	
Asp	Ala	Lys	Tyr	Thr	Glu	Leu	Asp	Thr	Ala	Ser	Leu	Asp	Asn	Phe	Ile	65	70	75	80
Lys	Lys	Gln	Arg	Glu	Ala	Leu	Ser	Lys	Ala	Gly	Leu	Val	Asp	Asp	Glu	85	90	95	
Pro	Val	Ser	Ala	Glu	Ser	Ala	Glu	Gln	Asp	Ser	Thr	Leu	Val	Glu	Glu	100	105	110	
Val	Ala	Glu	Asp	Leu	Ala	Pro	Met	Glu	Thr	Thr	Ala	Val	Val	Thr	Gly	115	120	125	
Ile	Pro	Val	Glu	Ala	Thr	Val	Pro	Val	Leu	Asp	Leu	Asp	Pro	Ser	Glu	130	135	140	
Arg	Val	Ile	Pro	Glu	Pro	Gln	Met	Thr	Lys	Glu	Glu	Pro	Lys	Arg	Asp	145	150	155	160
Gln	Phe	Leu	Ser	Glu	Asp	Ser	His	His	Pro	Ala	Lys	Gln	Asn	Thr	Lys	165	170	175	
Lys	Gly	Trp	Leu	Ile	Ala	Leu	Phe	Leu	Leu	Leu	Leu	Ala	Ile	Leu	Ala	180	185	190	
Val	Val	Phe	Gly	Trp	Asn	His	Phe	Leu	Arg	Gln	Asp	Ser	Gly	Lys	Thr	195	200	205	
Thr	Gln	Thr	Ala	Ser	Lys	Gln	Thr	Lys	Thr	Ser	Leu	Gln	Thr	Asp	Ser	210	215	220	
Ala	Lys	Lys	Ala	Thr	Arg	Leu	Lys	Ala	Ala	Ala	Lys	Ala	Phe	Glu	Lys	225	230	235	240
Leu	Tyr	Gly	Thr	Phe	Tyr	Thr	Asp	Ala	Thr	Lys	Ser	Lys	Leu	Lys	Asn	245	250	255	
Ser	Ala	Phe	Ala	Thr	Leu	Pro	Asp	Leu	Glu	Ala	Ala	Leu	Lys	Ala	Leu	260	265	270	
Glu	Gly	Ser	Ala	Tyr	Tyr	Asp	Lys	Ala	Lys	Ala	Lys	Val	Asp	Ser	Leu	275	280	285	
Lys	Lys	Ala	Ile	Ala	Ala	Ile	Thr	Ala	Val	Asn	Gly	Lys	Phe	Val	Ser	290	295	300	
Asp	Val	Val	Val	Asp	Gly	Glu	Lys	Val	Ser	Ala	Glu	Val	Lys	Ala	Asp	305	310	315	320
Ala	Asn	Phe	Asp	Asp	Leu	Ser	Ser	Ala	Thr	Leu	Thr	Ile	Gly	Asn	Ala	325	330	335	
Asn	Leu	Asp	Ala	Val	Leu	Gln	Ala	Ser	Ile	Thr	Glu	Gly	Arg	Gln	Gln	340	345	350	
Leu	Ala	Ser	Lys	Ala	Glu	Ala	Ala	Lys	Ala	Ala	Asn	Glu	Gln	Ala	Val	355	360	365	
Gln	Asp	Gln	Ala	Ala	Gln	Gly	Gln	Ser	Thr	Ser	Val	Ala	Pro	Ser	Gly	370	375	380	
Tyr	Gly	Leu	Thr	Ser	Tyr	Asp	Pro	Ala	Ser	Leu	Gln	Arg	His	Leu	Ser	385	390	395	400
Arg	Val	Pro	Tyr	Asn	Gln	Asp	Val	Ile	Ala	Asp	Arg	Ala	Asn	Pro	Ser	405	410	415	

Trp	Ala	Phe	Asn	Pro	Gly	Val	Leu	Glu	Lys	Ile	Val	Ala	Thr	Ser	Gln
			420					425					430		
Ala	Arg	Gly	Tyr	Ile	Ser	Gly	Asn	Gln	Tyr	Ile	Leu	Glu	Pro	Val	Asn
		435					440					445			
Ile	Ile	Asn	Gly	Asn	Gly	Tyr	Tyr	Asn	Met	Phe	Lys	Pro	Asp	Gly	Thr
	450					455					460				
Tyr	Leu	Phe	Ser	Ile	Asn	Cys	Lys	Thr	Gly	Tyr	Phe	Val	Gly	Asn	Gly
465					470					475					480
Lys	Gly	Tyr	Ala	Asp	Ala	Leu	Asp	Tyr							
				485											

<210> SEQ ID NO 11

<211> LENGTH: 861

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 11

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attagtttat	gtctggcctt	tttattgcta	aatattatta	tccctaagtc	aaattcacgt	120
ttgaaaaaga	gtgattttct	gaaaaaagaa	caagtagcta	tccaatatgt	tgctatagga	180
gattcattga	cagaaggagt	aggtgatcta	actcatcaag	gtggttttgt	tcctttgtta	240
acgaatgata	tcagtgaata	ttttaaggct	aatgttaatc	atcaaaatta	cggcgtatct	300
ggtgatacca	gtcaacaaat	tcttgatagg	atgataaaac	aaaagcagat	acagttatct	360
ttaaaaaaag	cagatataat	gacgttaacc	gttggtggta	atgatgttat	ggcagttatt	420
cggaagaatt	tagcggattt	gcaagtttct	agttttagaa	agccagctcg	tcagtatcaa	480
aaacgattaa	gacagattat	cgagttagcc	agaaaagata	ataaagatct	tcctatTTTT	540
attttaggca	tctataatcc	gttttatttg	aattttccag	aactaactga	tatgcaaaaa	600
gtgattgatg	actggaatac	caaaaactaag	gagggtgttg	gagaatacga	tcgtgtgtac	660
tttgtgccaa	taaatgacct	cttgtataaa	gggataaatg	gacaagaagg	aattgttcac	720
tcttcaggag	atcaaaactac	aattgtcaat	gatgccttgt	ttactgggga	ccattttcac	780
ccaaataata	ctggctatca	aatcatgtca	aatgcagtaa	tggagaaaat	taaaaagcat	840
gaaaaaaaaa	tcaaacctta	a				861

<210> SEQ ID NO 12

<211> LENGTH: 286

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 12

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Phe	Phe	Phe	Val	Ile	Ser	Leu	Cys	Leu	Ala	Phe	Leu	Leu	Leu	Asn	Ile
			20					25					30		
Ile	Ile	Pro	Lys	Ser	Asn	Ser	Arg	Leu	Lys	Lys	Ser	Asp	Phe	Leu	Lys
		35				40					45				
Lys	Glu	Gln	Val	Ala	Ile	Gln	Tyr	Val	Ala	Ile	Gly	Asp	Ser	Leu	Thr
	50				55					60					
Glu	Gly	Val	Gly	Asp	Leu	Thr	His	Gln	Gly	Gly	Phe	Val	Pro	Leu	Leu
65					70				75					80	
Thr	Asn	Asp	Leu	Ser	Glu	Tyr	Phe	Lys	Ala	Asn	Val	Asn	His	Gln	Asn
			85					90					95		
Tyr	Gly	Val	Ser	Gly	Asp	Thr	Ser	Gln	Gln	Ile	Leu	Asp	Arg	Met	Ile
		100					105					110			
Lys	Gln	Lys	Gln	Ile	Gln	Leu	Ser	Leu	Lys	Lys	Ala	Asp	Ile	Met	Thr
	115					120					125				
Leu	Thr	Val	Gly	Gly	Asn	Asp	Val	Met	Ala	Val	Ile	Arg	Lys	Asn	Leu
	130				135						140				
Ala	Asp	Leu	Gln	Val	Ser	Ser	Phe	Arg	Lys	Pro	Ala	Arg	Gln	Tyr	Gln
145					150					155					160

Lys	Arg	Leu	Arg	Gln	Ile	Ile	Glu	Leu	Ala	Arg	Lys	Asp	Asn	Lys	Asp	
				165					170					175		
Leu	Pro	Ile	Phe	Ile	Leu	Gly	Ile	Tyr	Asn	Pro	Phe	Tyr	Leu	Asn	Phe	
			180					185					190			
Pro	Glu	Leu	Thr	Asp	Met	Gln	Lys	Val	Ile	Asp	Asp	Trp	Asn	Thr	Lys	
		195					200					205				
Thr	Lys	Glu	Val	Val	Gly	Glu	Tyr	Asp	Arg	Val	Tyr	Phe	Val	Pro	Ile	
	210					215					220					
Asn	Asp	Leu	Leu	Tyr	Lys	Gly	Ile	Asn	Gly	Gln	Glu	Gly	Ile	Val	His	
225					230				235					240		
Ser	Ser	Gly	Asp	Gln	Thr	Thr	Ile	Val	Asn	Asp	Ala	Leu	Phe	Thr	Gly	
			245					250						255		
Asp	His	Phe	His	Pro	Asn	Asn	Thr	Gly	Tyr	Gln	Ile	Met	Ser	Asn	Ala	
		260						265					270			
Val	Met	Glu	Lys	Ile	Lys	Lys	His	Glu	Lys	Lys	Ile	Lys	Pro			
		275				280						285				

<210> SEQ ID NO 13

<211> LENGTH: 696

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 13

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actgggtggg	cagatggtga	tctttcagaa	aaagggacac	aacaagcgat	tgatgcaggt	120
aaattgatca	aagaagcagg	tattgaattt	gaccttgctt	tcacttcagt	attgacacgt	180
gctatcaaaa	caactaacct	tgcccttgaa	aatgcaggct	aattgtgggt	tccaactgaa	240
aaatcatggc	gcttgaacga	gcgtcactat	ggtgctttga	ctggcaaaaa	caaagctgaa	300
gctgcagaac	aattttgtga	tgaacaagtt	catatctggc	gtcgttcata	cgacgtgttg	360
ccgccagcta	tggctaaaaga	tgatgagtat	tcagcacaca	aagaccgtcg	ttatgctgat	420
cttgacccag	cccttattcc	agatgctgaa	aacttaaaag	tcactcttga	acgcgcaatg	480
ccttactggg	aagaaaaaat	tgctccagct	cttcttgacg	gtaaaaaacgt	ctttgttggc	540
gcacatggta	actcaatccg	cgctcttggt	aaacacatta	aaggtctttc	agatgacgaa	600
atcatggatg	tggaaattcc	aaacttccca	ccacttggtt	ttgaattaga	tgaaaaactt	660
aacattgtta	aagaatacta	ccttggtggt	gaataa			696

<210> SEQ ID NO 14

<211> LENGTH: 231

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 14

Met	Val	Lys	Leu	Val	Phe	Ala	Arg	His	Gly	Glu	Ser	Glu	Trp	Asn	Lys	
1				5					10					15		
Ala	Asn	Leu	Phe	Thr	Gly	Trp	Ala	Asp	Val	Asp	Leu	Ser	Glu	Lys	Gly	
			20					25					30			
Thr	Gln	Gln	Ala	Ile	Asp	Ala	Gly	Lys	Leu	Ile	Lys	Glu	Ala	Gly	Ile	
		35					40					45				
Glu	Phe	Asp	Leu	Ala	Phe	Thr	Ser	Val	Leu	Thr	Arg	Ala	Ile	Lys	Thr	
	50					55					60					
Thr	Asn	Leu	Ala	Leu	Glu	Asn	Ala	Gly	Gln	Leu	Trp	Val	Pro	Thr	Glu	
65					70				75					80		
Lys	Ser	Trp	Arg	Leu	Asn	Glu	Arg	His	Tyr	Gly	Ala	Leu	Thr	Gly	Lys	
			85					90						95		
Asn	Lys	Ala	Glu	Ala	Ala	Glu	Gln	Phe	Cys	Asp	Glu	Gln	Val	His	Ile	
		100						105					110			
Trp	Arg	Arg	Ser	Tyr	Asp	Val	Leu	Pro	Pro	Ala	Met	Ala	Lys	Asp	Asp	
		115					120					125				
Glu	Tyr	Ser	Ala	His	Lys	Asp	Arg	Arg	Tyr	Ala	Asp	Leu	Asp	Pro	Ala	

130	135	140
Leu Ile Pro Asp Ala Glu Asn Leu Lys Val Thr Leu Glu Arg Ala Met		
145	150	155
Pro Tyr Trp Glu Glu Lys Ile Ala Pro Ala Leu Leu Asp Gly Lys Asn		160
	165	170
Val Phe Val Gly Ala His Gly Asn Ser Ile Arg Ala Leu Val Lys His		175
	180	185
Ile Lys Gly Leu Ser Asp Asp Glu Ile Met Asp Val Glu Ile Pro Asn		190
	195	200
Phe Pro Pro Leu Val Phe Glu Leu Asp Glu Lys Leu Asn Ile Val Lys		205
	210	220
Glu Tyr Tyr Leu Gly Gly Glu		
225	230	

<210> SEQ ID NO 15

<211> LENGTH: 1056

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 15

atgaaaaact	caaataaact	cattgctagt	gttgtgacat	tggcctcagt	gatggcttta	60
gcagcttgct	aatcaactaa	tgacaatact	aaggttattt	cgatgaaagg	tgatacaatt	120
agcgtagtg	atttttacia	tgaaacaaaa	aacacagaag	tatcgcaaaa	agcgatgcta	180
aatctggtaa	ttagtcgtgt	ttttgaagct	caatatgggtg	ataaggtttc	aaaaaaagaa	240
gttgaaaagg	cgtatcataa	aacagctgaa	cagtatggcg	cttcattctc	tgctgctttg	300
gcacaatcaa	gcttgacacc	tgagactttt	aagcgtcaga	tccgctcttc	aaaattagta	360
gaatatgcgg	ttaaagaagc	agctaaaaaa	gaattgacaa	cacaagaata	taagaaagca	420
tatgaatctt	atactccaac	aatggcagtc	gaaatgatta	ctttagataa	tgaagagaca	480
gctaaatcag	tcttagagga	actaaaagcc	gaaggcgag	actttacagc	tattgctaaa	540
gaaaaacaaa	caacacctga	gaaaaaagt	acctataaat	ttgattcagg	tgcgacaaat	600
gtaccgactg	atgtcgtaaa	agcggcttca	agtttgaatg	agggtggcat	atcagacgtt	660
atctcggttt	tagatccaac	ttcttatcaa	aagaagtttt	acattgttaa	gggtactaaa	720
aaagcagaaa	aaaaatcaga	ttggcaagaa	tataagaaac	gtttgaaagc	tatcattata	780
gctgaaaaat	caaaaagatat	gaatttccaa	aacaagggtta	ttgcaaatgc	attggataaa	840
gctaattgtaa	aaattaaaga	caaagctttt	gctaataattt	tggcgcaata	tgcaaatctt	900
gggtcaaaaaa	ctaaagctgc	aagtgaaagt	tcaacaacca	gcgaatcatc	aaaagctgca	960
gaagagaacc	catcagaatc	agagcaaaaca	cagacatcat	cagctgaaga	accaactgag	1020
actgaggctc	agacgcaaga	gccagctgca	caataa			1056

<210> SEQ ID NO 16

<211> LENGTH: 351

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 16

Met Lys Asn Ser Asn Lys Leu Ile Ala Ser Val Val Thr Leu Ala Ser	
1	15
Val Met Ala Leu Ala Ala Cys Gln Ser Thr Asn Asp Asn Thr Lys Val	
20	30
Ile Ser Met Lys Gly Asp Thr Ile Ser Val Ser Asp Phe Tyr Asn Glu	
35	45
Thr Lys Asn Thr Glu Val Ser Gln Lys Ala Met Leu Asn Leu Val Ile	
50	60
Ser Arg Val Phe Glu Ala Gln Tyr Gly Asp Lys Val Ser Lys Lys Glu	
65	80
Val Glu Lys Ala Tyr His Lys Thr Ala Glu Gln Tyr Gly Ala Ser Phe	
85	95
Ser Ala Ala Leu Ala Gln Ser Ser Leu Thr Pro Glu Thr Phe Lys Arg	
100	110

Gln	Ile	Arg	Ser	Ser	Lys	Leu	Val	Glu	Tyr	Ala	Val	Lys	Glu	Ala	Ala		
		115					120					125					
Lys	Lys	Glu	Leu	Thr	Thr	Gln	Glu	Tyr	Lys	Lys	Ala	Tyr	Glu	Ser	Tyr		
		130				135					140						
Thr	Pro	Thr	Met	Ala	Val	Glu	Met	Ile	Thr	Leu	Asp	Asn	Glu	Glu	Thr		
					150					155					160		
Ala	Lys	Ser	Val	Leu	Glu	Glu	Leu	Lys	Ala	Glu	Gly	Ala	Asp	Phe	Thr		
				165					170					175			
Ala	Ile	Ala	Lys	Glu	Lys	Thr	Thr	Thr	Pro	Glu	Lys	Lys	Val	Thr	Tyr		
			180					185					190				
Lys	Phe	Asp	Ser	Gly	Ala	Thr	Asn	Val	Pro	Thr	Asp	Val	Val	Lys	Ala		
		195				200					205						
Ala	Ser	Ser	Leu	Asn	Glu	Gly	Gly	Ile	Ser	Asp	Val	Ile	Ser	Val	Leu		
		210			215						220						
Asp	Pro	Thr	Ser	Tyr	Gln	Lys	Lys	Phe	Tyr	Ile	Val	Lys	Val	Thr	Lys		
				230					235						240		
Lys	Ala	Glu	Lys	Lys	Ser	Asp	Trp	Gln	Glu	Tyr	Lys	Lys	Arg	Leu	Lys		
			245					250						255			
Ala	Ile	Ile	Ile	Ala	Glu	Lys	Ser	Lys	Asp	Met	Asn	Phe	Gln	Asn	Lys		
			260					265					270				
Val	Ile	Ala	Asn	Ala	Leu	Asp	Lys	Ala	Asn	Val	Lys	Ile	Lys	Asp	Lys		
		275				280					285						
Ala	Phe	Ala	Asn	Ile	Leu	Ala	Gln	Tyr	Ala	Asn	Leu	Gly	Gln	Lys	Thr		
		290			295						300						
Lys	Ala	Ala	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Glu	Ser	Ser	Lys	Ala	Ala		
				310					315					320			
Glu	Glu	Asn	Pro	Ser	Glu	Ser	Glu	Gln	Thr	Gln	Thr	Ser	Ser	Ala	Glu		
			325					330						335			
Glu	Pro	Thr	Glu	Thr	Glu	Ala	Gln	Thr	Gln	Glu	Pro	Ala	Ala	Gln			
			340					345						350			

<210> SEQ ID NO 17

<211> LENGTH: 1275

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 17

ttgaaaaaat	taaatgttat	tcttgttggt	ttattaagca	ttctgatgtt	gagtttagct	60
attgtgttta	ttaatcgttg	gaaactaaac	gaagatagtc	agcgtatagt	tttggctgaa	120
aagaaaaaaa	acacgtcaga	tttagtgatc	aaagctgtaa	aacatattaa	aaaagatcaa	180
aaagactatt	attatTTTTT	cccgataaaa	caagcagatg	atttttttgt	agataattta	240
cctgtttcat	tatacaaaaa	aaagaattca	gataaagaat	tgatttttagt	aaggcctaaa	300
ctgcaatctt	ctcacctaag	atcagttaac	actttgacta	tttctaaaat	agtttatcag	360
aaaaaatttt	ttcatTTTggc	taaaaaatca	gaaaaagtta	taagtacata	tcacgttaca	420
gacgacttga	aaccgtttca	ggtaaaggat	ctagtatcag	gacatttaga	aagaatacaa	480
gaagaagtgtg	aaaaaaaaata	tccagatgct	ggttttaata	gcgataagta	taatggctta	540
aaagaatcta	attctttatt	aagcgatggc	tttgaggtaa	aatcgggaaa	ccttatTTTT	600
gataaaaaagc	taacgatacc	tttgacgaca	ttatttgatg	ttattaatcc	agatttttta	660
gcaaatagcg	atagagctgc	gtatgataat	tataggacct	acaaagaaca	gcatcccaaa	720
aaactagttg	cattaacggt	tgatgatggt	ccagatccga	cgacgactcc	tcaagtttta	780
gatatttttg	caaaatacca	ggctaaggga	actttcttta	tgatagggttc	aaaggttgtg	840
aataatgaaa	accttactaa	acgtgttagc	gacgctggcc	atgaaattgc	taatcatact	900
tgggatcatc	ctaacttgac	taatctttca	gtcagcgaga	ttcaacatca	agttaatatg	960
acgaaccagg	ctattgaaaa	agcttggtggc	aagaaacctc	gctattttacg	ccctccatac	1020
ggagctacaa	atgcaactgt	tcagcaatcc	tcaggattaa	cacaaatgct	ttggacgggt	1080
gatacaagag	attgggaaaa	tcatagcact	gatggcatta	tgactaatgt	caaaaaccaa	1140
ttgcaaccgg	gaggagtgtg	tttaatgcat	gatattcatc	aaacaactat	caatgctttg	1200
ccgacagtta	tggaaatatct	aaaagcagaa	ggatacgaat	gtgtgactgt	atcagaactc	1260

tatgcgcatc agtaa

1275

<210> SEQ ID NO 18

<211> LENGTH: 424

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 18

Met	Lys	Lys	Leu	Asn	Val	Ile	Leu	Val	Gly	Leu	Leu	Ser	Ile	Leu	Met
1				5					10					15	
Leu	Ser	Leu	Ala	Ile	Val	Phe	Ile	Asn	Arg	Trp	Lys	Leu	Asn	Glu	Asp
			20					25					30		
Ser	Gln	Arg	Ile	Val	Leu	Ala	Glu	Lys	Lys	Lys	Asn	Thr	Ser	Asp	Leu
		35					40					45			
Val	Ile	Lys	Ala	Val	Lys	His	Ile	Lys	Lys	Asp	Gln	Lys	Asp	Tyr	Tyr
	50					55					60				
Tyr	Phe	Ser	Pro	Ile	Lys	Gln	Ala	Asp	Asp	Phe	Phe	Val	Asp	Asn	Leu
65					70					75					80
Pro	Val	Ser	Leu	Tyr	Lys	Lys	Lys	Asn	Ser	Asp	Lys	Glu	Leu	Ile	Leu
				85					90					95	
Val	Arg	Pro	Lys	Leu	Gln	Ser	Ser	His	Leu	Arg	Ser	Val	Asn	Thr	Leu
			100					105					110		
Thr	Ile	Ser	Lys	Ile	Val	Tyr	Gln	Lys	Lys	Phe	Phe	His	Leu	Ala	Lys
		115					120					125			
Lys	Ser	Glu	Lys	Val	Ile	Ser	Thr	Tyr	His	Val	Thr	Asp	Asp	Leu	Lys
	130					135					140				
Pro	Phe	Gln	Val	Lys	Asp	Leu	Val	Ser	Gly	His	Leu	Glu	Arg	Ile	Gln
145					150					155					160
Glu	Glu	Val	Glu	Lys	Lys	Tyr	Pro	Asp	Ala	Gly	Phe	Asn	Ser	Asp	Lys
				165					170					175	
Tyr	Asn	Gly	Leu	Lys	Glu	Ser	Asn	Ser	Leu	Leu	Ser	Asp	Gly	Phe	Glu
		180					185					190			
Val	Lys	Ser	Gly	Asn	Leu	Ile	Phe	Asp	Lys	Lys	Leu	Thr	Ile	Pro	Leu
	195						200					205			
Thr	Thr	Leu	Phe	Asp	Val	Ile	Asn	Pro	Asp	Phe	Leu	Ala	Asn	Ser	Asp
	210					215					220				
Arg	Ala	Ala	Tyr	Asp	Asn	Tyr	Arg	Thr	Tyr	Lys	Glu	Gln	His	Pro	Lys
225					230					235					240
Lys	Leu	Val	Ala	Leu	Thr	Phe	Asp	Asp	Gly	Pro	Asp	Pro	Thr	Thr	Thr
			245						250					255	
Pro	Gln	Val	Leu	Asp	Ile	Leu	Ala	Lys	Tyr	Gln	Ala	Lys	Gly	Thr	Phe
		260					265						270		
Phe	Met	Ile	Gly	Ser	Lys	Val	Val	Asn	Asn	Glu	Asn	Leu	Thr	Lys	Arg
	275					280						285			
Val	Ser	Asp	Ala	Gly	His	Glu	Ile	Ala	Asn	His	Thr	Trp	Asp	His	Pro
	290					295					300				
Asn	Leu	Thr	Asn	Leu	Ser	Val	Ser	Glu	Ile	Gln	His	Gln	Val	Asn	Met
305					310					315					320
Thr	Asn	Gln	Ala	Ile	Glu	Lys	Ala	Cys	Gly	Lys	Lys	Pro	Arg	Tyr	Leu
			325						330					335	
Arg	Pro	Pro	Tyr	Gly	Ala	Thr	Asn	Ala	Thr	Val	Gln	Gln	Ser	Ser	Gly
		340					345						350		
Leu	Thr	Gln	Met	Leu	Trp	Thr	Val	Asp	Thr	Arg	Asp	Trp	Glu	Asn	His
	355						360					365			
Ser	Thr	Asp	Gly	Ile	Met	Thr	Asn	Val	Lys	Asn	Gln	Leu	Gln	Pro	Gly
	370					375					380				
Gly	Val	Val	Leu	Met	His	Asp	Ile	His	Gln	Thr	Thr	Ile	Asn	Ala	Leu
385					390					395					400

Pro Thr Val Met Glu Tyr Leu Lys Ala Glu Gly Tyr Glu Cys Val Thr
405 410 415
Val Ser Glu Leu Tyr Ala His Gln
420

<210> SEQ ID NO 19
<211> LENGTH: 1251
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 19

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atgcttaaga gactctggtt aattctaggt cctcttctta ttgcctttgt tttagtagtg      60
attactattt ttagttttcc tacacaactt gatcattcca tagctcagga aaaagcaa      120
gccgttgcca tcacagatag ttctttttaa aatgggttga ttaaaagaca agctttatca      180
gatgagactt gtcgttttgt gccttttttt ggttctagcg aatggagtcg aatggatagt      240
atgcaccctt cgggtgcttg agagcgctac aagcggagct atagaccatt tttaattggt      300
aagagaggat cagcatcttt gtcgcattat tatggtatac aacaaattac caatgaaatg      360
caaaagaaaa aagccatctt tgtagtatct cctcaatggt ttactgctca agggattaat      420
cctagtgcgg ttcagatgta cttgtctaac actcaagtga ttgaattttt actaaaagct      480
agaactgata aagaatcaca gtttgcagca aagcgtttgc ttgagcttaa ccctgggtgtg      540
tctaaatcaa acttattgaa aaaagtaagt aagggttaagt ctcttagtcg gttagacaga      600
gctattttga aatgtcaaca tcaagtagca ttgagagaag agtccctttt tagtttttta      660
ggcaaactta ctaactatga aaaaagaatt ttgcctcgcg ttaagggatt acctaaagta      720
ttttcgtata aacaattgaa tgcattagca actaagagag gccaattagc aacaaccaac      780
aaccgttttg ggattaaaaa tacattttat cgtaaacgaa tagcacctaa atacaatctt      840
tataagaatt tccaagttaa ttatagttac ctggcgtcac cagaatacaa tgattttcag      900
cttttattat cagaatttgc taaacgaaaa acagatgtac tctttgttat aactcctggt      960
aataaagctt gggcggatta taccggctta aatcaagata agtatcaagc ggcagttcgt     1020
aaaataaaat tccagttaaa gtcacaagga ttcatcgca ttgctgactt ctcaaaagat     1080
gggtggtgagt cctactttat gcaagatacc atccatctcg gttggaatgg ctggttagct     1140
tttgataaga aagtgcaacc atttctagaa acgaagcagc cagtgcccaa ctataaaatg     1200
aacccttatt tttatagtaa aatttgggca aataggaaag acttgcaata g               1251

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<210> SEQ ID NO 20
<211> LENGTH: 416
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 20

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Met Leu Lys Arg Leu Trp Leu Ile Leu Gly Pro Leu Leu Ile Ala Phe
1           5           10           15
Val Leu Val Val Ile Thr Ile Phe Ser Phe Pro Thr Gln Leu Asp His
20           25           30
Ser Ile Ala Gln Glu Lys Ala Asn Ala Val Ala Ile Thr Asp Ser Ser
35           40           45
Phe Lys Asn Gly Leu Ile Lys Arg Gln Ala Leu Ser Asp Glu Thr Cys
50           55           60
Arg Phe Val Pro Phe Phe Gly Ser Ser Glu Trp Ser Arg Met Asp Ser
65           70           75           80
Met His Pro Ser Val Leu Ala Glu Arg Tyr Lys Arg Ser Tyr Arg Pro
85           90           95
Phe Leu Ile Gly Lys Arg Gly Ser Ala Ser Leu Ser His Tyr Tyr Gly
100          105          110
Ile Gln Gln Ile Thr Asn Glu Met Gln Lys Lys Lys Ala Ile Phe Val
115          120          125
Val Ser Pro Gln Trp Phe Thr Ala Gln Gly Ile Asn Pro Ser Ala Val
130          135          140
Gln Met Tyr Leu Ser Asn Thr Gln Val Ile Glu Phe Leu Leu Lys Ala
145          150          155          160

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agaggtgtgc	ctaataattta	ttatggtaca	gagcagtatg	caacaggtga	taaagatcct	1200
aataatcgtg	gtgatatgcc	aagttttaat	aaagagtcac	aagcctataa	agtgattagt	1260
aagctagctc	ctttaagaaa	acaaaatcaa	gcttttagctt	atggaacaac	tgaacaacgt	1320
tggattagt	atcatgtttt	ggtatttgag	cgtaaatttg	gtaatcatgt	cgactagt	1380
gctattaata	gagatcaaac	gaatggttat	acaattacta	atgctaaaac	agccttgccc	1440
caaaatagct	acaaggacaa	attagaaggt	cttcttggcg	gtcaagaatt	aatagttgga	1500
gcagatggca	ctattagtag	ctttgaactt	ggagcggggc	aagtcgctgt	atggacttat	1560
gaaggagagg	acaagacacc	acaacttgga	gatgtcgatg	cttcagtggg	tattgctgga	1620
aataagatta	ctatttcagg	tcaaggtttt	ggtaattcta	aaggtcaagt	gacttttgga	1680
gaaatctctg	ctgagatcct	ttcttgggtca	gataccctta	tcaccttaaa	agtaccgacg	1740
gttccagcaa	attattataa	catttcagt	acaactgccg	ataagcaaac	cagcaatagt	1800
taccaagcct	ttgaagtatt	gactgataaa	caaattcctg	ttcgtttact	catcaatgat	1860
tttaagacag	taccagggga	acaactatat	ctcatgggtg	atgtttttga	gatgggggca	1920
aatgacgcta	agaatgctgt	tggtcctcta	tttaataaca	ctcagaccat	tgccaagtac	1980
ccaaactggg	tctttgatac	tcatctacca	atcaataaag	aaatagcagt	caaacttggt	2040
aaaaaagata	gtattgggaa	tgttttatgg	acaagtcctg	agacttatag	tataaagaca	2100
ggatcatgaag	cacaaacat	tactataaaa	aaataa			2136

<210> SEQ ID NO 22

<211> LENGTH: 711

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 22

Met	Arg	Glu	Leu	His	Ile	Lys	Thr	Tyr	Lys	Leu	Leu	Thr	Lys	Ser	Ala
1				5					10					15	
Val	Leu	Leu	Gly	Leu	Ile	Ser	Phe	Pro	Leu	Thr	Val	Ser	Ala	Ala	Asp
			20					25					30		
Asn	Ala	Ser	Val	Thr	Asn	Lys	Ala	Asp	Phe	Ser	Thr	Asp	Thr	Ile	Tyr
		35				40					45				
Gln	Ile	Val	Thr	Asp	Arg	Phe	Asn	Asp	Gly	Asn	Thr	Ser	Asn	Asn	Gly
	50					55				60					
Lys	Thr	Asp	Val	Phe	Asp	Lys	Asn	Asp	Leu	Lys	Lys	Tyr	His	Gly	Gly
65				70					75					80	
Asp	Trp	Gln	Gly	Ile	Ile	Ala	Lys	Ile	Lys	Asp	Gly	Tyr	Leu	Thr	Asp
			85					90					95		
Met	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Ser	Ser	Pro	Val	Glu	Asn	Ile	Asp
			100					105					110		
Ser	Ile	Asp	Pro	Ser	Asn	Gly	Ser	Ala	Ala	Tyr	His	Gly	Tyr	Trp	Ala
		115				120						125			
Lys	Asp	Phe	Phe	Lys	Thr	Asn	Gln	His	Phe	Gly	Thr	Glu	Ala	Asp	Phe
	130					135					140				
Gln	Gln	Leu	Val	Lys	Val	Ala	His	Gln	His	His	Ile	Lys	Val	Val	Ile
145					150					155				160	
Asp	Phe	Ala	Pro	Asn	His	Thr	Ser	Thr	Ala	Glu	Lys	Glu	Gly	Thr	Thr
			165					170						175	
Phe	Lys	Glu	Asp	Gly	Ala	Leu	Tyr	Lys	Asn	Gly	Lys	Leu	Val	Gly	Lys
		180						185					190		
Phe	Ser	Asp	Asp	Lys	Asp	Lys	Ile	Phe	Asn	His	Glu	Ser	Trp	Thr	Asp
	195					200						205			
Phe	Ser	Thr	Tyr	Glu	Asn	Ser	Ile	Tyr	His	Ser	Met	Tyr	Gly	Leu	Ala
	210					215					220				
Asp	Leu	Asn	Asn	Ile	Asn	Pro	Lys	Val	Asp	Gln	Tyr	Met	Lys	Glu	Ala
225					230					235				240	
Ile	Asp	Lys	Trp	Leu	Asp	Leu	Gly	Val	Asp	Gly	Ile	Arg	Val	Asp	Ala
			245					250						255	
Val	Lys	His	Met	Ser	Gln	Gly	Trp	Gln	Lys	Asn	Trp	Leu	Ser	His	Ile
			260					265					270		

Tyr	Glu	Lys	His	Asn	Val	Phe	Val	Phe	Gly	Glu	Trp	Phe	Ser	Gly	His
		275					280					285			
Thr	Asp	Asp	Asp	Tyr	Asp	Met	Thr	Thr	Phe	Ala	Asn	Asn	Ser	Gly	Met
	290					295					300				
Gly	Leu	Leu	Asp	Phe	Arg	Phe	Ala	Asn	Ala	Ile	Arg	Gln	Leu	Tyr	Thr
305					310					315					320
Gly	Phe	Ser	Thr	Phe	Thr	Met	Arg	Asp	Phe	Tyr	Lys	Val	Leu	Glu	Asn
				325					330					335	
Arg	Asp	Gln	Val	Thr	Asn	Glu	Val	Thr	Asp	Gln	Val	Thr	Phe	Ile	Asp
			340					345					350		
Asn	His	Asp	Met	Glu	Arg	Phe	Ala	Thr	Lys	Val	Ala	Asn	Asn	Gln	Thr
		355					360					365			
Ala	Val	Asn	Gln	Ala	Tyr	Ala	Leu	Leu	Leu	Thr	Ser	Arg	Gly	Val	Pro
	370					375					380				
Asn	Ile	Tyr	Tyr	Gly	Thr	Glu	Gln	Tyr	Ala	Thr	Gly	Asp	Lys	Asp	Pro
385					390					395					400
Asn	Asn	Arg	Gly	Asp	Met	Pro	Ser	Phe	Asn	Lys	Glu	Ser	Gln	Ala	Tyr
				405					410					415	
Lys	Val	Ile	Ser	Lys	Leu	Ala	Pro	Leu	Arg	Lys	Gln	Asn	Gln	Ala	Leu
			420					425					430		
Ala	Tyr	Gly	Thr	Thr	Glu	Gln	Arg	Trp	Ile	Ser	Asp	His	Val	Leu	Val
		435					440					445			
Phe	Glu	Arg	Lys	Phe	Gly	Asn	His	Val	Ala	Leu	Val	Ala	Ile	Asn	Arg
	450					455					460				
Asp	Gln	Thr	Asn	Gly	Tyr	Thr	Ile	Thr	Asn	Ala	Lys	Thr	Ala	Leu	Pro
465					470					475					480
Gln	Asn	Ser	Tyr	Lys	Asp	Lys	Leu	Glu	Gly	Leu	Leu	Gly	Gly	Gln	Glu
				485					490					495	
Leu	Ile	Val	Gly	Ala	Asp	Gly	Thr	Ile	Ser	Ser	Phe	Glu	Leu	Gly	Ala
			500					505					510		
Gly	Gln	Val	Ala	Val	Trp	Thr	Tyr	Glu	Gly	Glu	Asp	Lys	Thr	Pro	Gln
		515					520					525			
Leu	Gly	Asp	Val	Asp	Ala	Ser	Val	Gly	Ile	Ala	Gly	Asn	Lys	Ile	Thr
	530					535					540				
Ile	Ser	Gly	Gln	Gly	Phe	Gly	Asn	Ser	Lys	Gly	Gln	Val	Thr	Phe	Gly
545					550					555					560
Glu	Ile	Ser	Ala	Glu	Ile	Leu	Ser	Trp	Ser	Asp	Thr	Leu	Ile	Thr	Leu
				565					570					575	
Lys	Val	Pro	Thr	Val	Pro	Ala	Asn	Tyr	Tyr	Asn	Ile	Ser	Val	Thr	Thr
			580					585					590		
Ala	Asp	Lys	Gln	Thr	Ser	Asn	Ser	Tyr	Gln	Ala	Phe	Glu	Val	Leu	Thr
		595					600					605			
Asp	Lys	Gln	Ile	Pro	Val	Arg	Leu	Leu	Ile	Asn	Asp	Phe	Lys	Thr	Val
	610					615					620				
Pro	Gly														


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<210> SEQ ID NO 23
<211> LENGTH: 1248
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 23
atgaaatcat ggcaaaaagt tatcgtcggc ggagcaagtt tgacacttgc aagtaccttg      60
ttagtgggat gtggatcagg ttcaaaagat aaaaaggaag ctggcgctga ctcaaagact    120
attaaacttt ggggtaccgac tggctctaaa aaatcatatg cagataccat tgcaaaattt    180
gaaaaagatt ctggttacac cggttaaagtg gttgaatcag aagatccaaa agcacaagaa    240
aaaatcaaaa aagatgcctc aactgctgcc gatgtctttt cacttcctca tgatcaactt    300
ggtcaacttg tagaatctgg tactattcaa gaagttccag aaaagtacaa taaagaaatt    360
gctgctactt ctactgatca ggcgctcgtc ggtgcacagt acaaagggaa aacatatgct    420
ttcccatttg gtattgaatc acaagttctt ttctacaata aatcaaaatt agctgctgaa    480
gacgttactt catatgatac aattactaca aaagcaactt ttggtggtac ctttaaacia    540
gctaacactt acgctactgg tccattattc atgtcagttg gtaacacttt atttggggaa    600
aacgggtgaag atgtaaaagg tactaaactgg ggcaatgaaa aaggcgctgc tgttcttaaa    660
tggatcgtag accaagcttc aaataaaggt tttgttagct tagatgctaa caacgttatg    720
tctaaatttg gtgacggttc agtagcttcc tttgaatcag gaccgtggga ctatgaagct    780
gctcaaaaag ctatcggtaa agaaaacctt ggtgttgcta tttatccaaa agtaactatt    840
ggaggcgaaa cggttcaaca aaaagcattc ttgggtgtaa aactttacgc agtcaaccaa    900
gcaccagcta aaggtgatac aaaacgtatc gcagctagct acaaattggc atcctacttg    960
actaatgctg aaagccaaga aaaccaattc aaaactcgta acattgtccc agccaacaaa   1020
gaagttcaat cttcagaagc tgttcaatca aacgaacttg ctaaaaccgt tatcactatg   1080
ggttcttctt cagactacac tgtcgtaatg ccaaaactta gccaaatggg cacattctgg   1140
actgaaagtg ctgctattct tagtgatgcc ttcaacggta aaatcaaaga aaacgactac   1200
cttactaagt tgcaacaatt cgacaaagat atcgctgcaa caaaataa                   1248

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<210> SEQ ID NO 24
<211> LENGTH: 415
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 24
Met Lys Ser Trp Gln Lys Val Ile Val Gly Gly Ala Ser Leu Thr Leu
1      5      10      15
Ala Ser Thr Leu Leu Val Gly Cys Gly Ser Gly Ser Lys Asp Lys Lys
20     25     30
Glu Ala Gly Ala Asp Ser Lys Thr Ile Lys Leu Trp Val Pro Thr Gly
35     40     45
Ser Lys Lys Ser Tyr Ala Asp Thr Ile Ala Lys Phe Glu Lys Asp Ser
50     55     60
Gly Tyr Thr Val Lys Val Val Glu Ser Glu Asp Pro Lys Ala Gln Glu
65     70     75     80
Lys Ile Lys Lys Asp Ala Ser Thr Ala Ala Asp Val Phe Ser Leu Pro
85     90     95
His Asp Gln Leu Gly Gln Leu Val Glu Ser Gly Thr Ile Gln Glu Val
100    105    110
Pro Glu Lys Tyr Asn Lys Glu Ile Ala Ala Thr Ser Thr Asp Gln Ala
115    120    125
Leu Val Gly Ala Gln Tyr Lys Gly Lys Thr Tyr Ala Phe Pro Phe Gly
130    135    140
Ile Glu Ser Gln Val Leu Phe Tyr Asn Lys Ser Lys Leu Ala Ala Glu
145    150    155    160
Asp Val Thr Ser Tyr Asp Thr Ile Thr Thr Lys Ala Thr Phe Gly Gly
165    170    175
Thr Phe Lys Gln Ala Asn Thr Tyr Ala Thr Gly Pro Leu Phe Met Ser
180    185    190
Val Gly Asn Thr Leu Phe Gly Glu Asn Gly Glu Asp Val Lys Gly Thr

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	195		200		205										
Asn	Trp	Gly	Asn	Glu	Lys	Gly	Ala	Ala	Val	Leu	Lys	Trp	Ile	Ala	Asp
210						215					220				
Gln	Ala	Ser	Asn	Lys	Gly	Phe	Val	Ser	Leu	Asp	Ala	Asn	Asn	Val	Met
225					230					235					240
Ser	Lys	Phe	Gly	Asp	Gly	Ser	Val	Ala	Ser	Phe	Glu	Ser	Gly	Pro	Trp
			245			250								255	
Asp	Tyr	Glu	Ala	Ala	Gln	Lys	Ala	Ile	Gly	Lys	Glu	Asn	Leu	Gly	Val
		260				265							270		
Ala	Ile	Tyr	Pro	Lys	Val	Thr	Ile	Gly	Gly	Glu	Thr	Val	Gln	Gln	Lys
	275					280						285			
Ala	Phe	Leu	Gly	Val	Lys	Leu	Tyr	Ala	Val	Asn	Gln	Ala	Pro	Ala	Lys
290					295						300				
Gly	Asp	Thr	Lys	Arg	Ile	Ala	Ala	Ser	Tyr	Lys	Leu	Ala	Ser	Tyr	Leu
305				310						315					320
Thr	Asn	Ala	Glu	Ser	Gln	Glu	Asn	Gln	Phe	Lys	Thr	Arg	Asn	Ile	Val
			325					330					335		
Pro	Ala	Asn	Lys	Glu	Val	Gln	Ser	Ser	Glu	Ala	Val	Gln	Ser	Asn	Glu
		340					345					350			
Leu	Ala	Lys	Thr	Val	Ile	Thr	Met	Gly	Ser	Ser	Ser	Asp	Tyr	Thr	Val
	355					360						365			
Val	Met	Pro	Lys	Leu	Ser	Gln	Met	Gly	Thr	Phe	Trp	Thr	Glu	Ser	Ala
370					375						380				
Ala	Ile	Leu	Ser	Asp	Ala	Phe	Asn	Gly	Lys	Ile	Lys	Glu	Asn	Asp	Tyr
385				390					395						400
Leu	Thr	Lys	Leu	Gln	Gln	Phe	Asp	Lys	Asp	Ile	Ala	Ala	Thr	Lys	
			405					410						415	

<210> SEQ ID NO 25

<211> LENGTH: 837

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 25

atgattataa	aaaaaagaac	cgtagcaatt	ttagccatag	ctagtagctt	tttcttggtta	60
gcttggtcaag	ctactaaaag	tcttaaatca	ggagatgctt	ggggagttaa	ccaaaagcaa	120
aaaagtatta	cagttgggtt	tgacaatacg	tttggttccta	tgggctataa	ggatgaaagc	180
ggcagatgca	aagggttttga	tattgatttg	gctaaagaag	tttttcacca	atatggactc	240
aagggttaact	ttcaagctat	taattgggac	atgaaagaag	cagaactaaa	caatggtaaa	300
attgatgtaa	tctggaatgg	ttattcaata	actaaggagc	gtcaggataa	ggttgccttt	360
actgattcct	acatgagaaa	tgaacaaatt	attgttggtca	aaaaaagatc	tgatattaaa	420
acaatatcag	atatgaaaca	taaagtgtta	ggagcacaat	cagcttcac	aggttatgac	480
tccttggttaa	gaactcctaa	actgctgaaa	gattttatta	aaaataaaga	cgctaataca	540
tatgaaacct	ttacacaagc	ttttattgat	ttaaaatcag	atcgtatcga	tggaatattg	600
attgacaaag	tatatgccaa	ttactattta	gcaaaagaag	ggcaattaga	gaattatcgg	660
atgatcccaa	cgacctttga	aaatgaagca	ttttcggttg	gacttagaaa	agaagacaaa	720
acgttgcaag	caaaaattaa	tcgtgctttc	agggtgcttt	atcaaaatgg	caaatttcaa	780
gctattttctg	agaaatgggtt	tgagatgat	gttgccactg	ccaatattaa	atcttaa	837

<210> SEQ ID NO 26

<211> LENGTH: 278

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 26

Met	Ile	Ile	Lys	Lys	Arg	Thr	Val	Ala	Ile	Leu	Ala	Ile	Ala	Ser	Ser
1			5					10					15		
Phe	Phe	Leu	Val	Ala	Cys	Gln	Ala	Thr	Lys	Ser	Leu	Lys	Ser	Gly	Asp
			20				25						30		

Ile	His	Lys	Asn	Lys	Ala	Ser	Arg	Asp	Lys	Ala	Arg	Leu	Ala	Ala	Lys
65					70					75					80
Leu	Gly														

<210> SEQ ID NO 29

<211> LENGTH: 351

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 29

atgaaaagat	atgaagtgac	tgtcaatgga	caggtttatg	aagtgaagttt	acgtgaacta	60
gttgatggag	aaactgttga	agttagccag	ccagcagcac	ccgctactga	gaaagaaatg	120
aatgccaacg	ctgctggcgg	tggcattcag	gtaaaaggctc	caatgtcttg	aacagtcttg	180
tctatctttg	ctacagaagg	aaaagctgtt	aaaaaaggag	aagctgttct	ggctcttagag	240
gccatgaaaa	tggagaatga	aattctagca	cctgcagatg	gtctggtttc	aaaaattcat	300
gttgtggcta	accaaacggt	cgagtctgaa	caagttttga	tttcattcta	g	351

<210> SEQ ID NO 30

<211> LENGTH: 116

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 30

Met	Lys	Arg	Tyr	Glu	Val	Thr	Val	Asn	Gly	Gln	Val	Tyr	Glu	Val	Ser
1				5				10					15		
Leu	Arg	Glu	Leu	Val	Asp	Gly	Glu	Thr	Val	Glu	Val	Ser	Gln	Pro	Ala
			20					25					30		
Ala	Pro	Ala	Thr	Glu	Lys	Glu	Met	Asn	Ala	Asn	Ala	Ala	Gly	Gly	Gly
			35					40					45		
Ile	Gln	Val	Lys	Ala	Pro	Met	Ser	Gly	Thr	Val	Leu	Ser	Ile	Phe	Ala
	50					55					60				
Thr	Glu	Gly	Lys	Ala	Val	Lys	Lys	Gly	Glu	Ala	Val	Leu	Val	Leu	Glu
65					70					75					80
Ala	Met	Lys	Met	Glu	Asn	Glu	Ile	Leu	Ala	Pro	Ala	Asp	Gly	Leu	Val
				85					90					95	
Ser	Lys	Ile	His	Val	Val	Ala	Asn	Gln	Thr	Val	Glu	Ser	Glu	Gln	Val
			100					105					110		
Leu	Ile	Ser	Phe												
			115												

<210> SEQ ID NO 31

<211> LENGTH: 750

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 31

atggtaaaaa	aacaaaagcg	tcgaaaaata	aaatccatgt	cttgggcaag	aaaactacta	60
atagctgtac	ttttaattct	aggtttagca	ttgcttttta	acaaacctat	ccgaaataca	120
ttaattgctc	gaaactctaa	taaatatcaa	gtaacgaaag	tttcgaaaaa	acaaatcaaa	180
aagaataaag	aggctaagtc	aacatttgat	ttccaagccg	tagagccagt	tagtacagag	240
agtgtcttgc	aagcacaaat	ggcggctcag	caacttcctg	ttataggggg	cattgccata	300
ccagagcttg	gcattaatth	accaattttt	aaaggtttag	gaaataactga	gcttattttat	360
ggcgcaggaa	cgatgaaaaga	agaacaagtt	atgggaggag	aaaataatta	ttctcttgcc	420
agtcatacata	tttttggaat	tacaggttca	tctcaaagtc	tcttttcgcc	gcttgaaaga	480
gcacaaaatg	ggatgtccat	ctatttaaca	gataaagaaa	aaatttacga	atacatcata	540
aaagatgttt	tcacggtagc	tcctgaacgc	gttgatgtta	tcgatgatac	agctggctctc	600
aaagaagtga	ctttagtgac	ttgtacagat	atcgaagcaa	cagaacgtat	tattgtcaaa	660
ggagaactaa	aaacagaata	cgattttgat	aaagcgcccg	ccgatgtatt	gaaagctttt	720
aatcattctt	ataaccaagt	atctacctag				750

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<210> SEQ ID NO 32
<211> LENGTH: 249
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 32
Met Val Lys Lys Gln Lys Arg Arg Lys Ile Lys Ser Met Ser Trp Ala
1          5          10          15
Arg Lys Leu Leu Ile Ala Val Leu Leu Ile Leu Gly Leu Ala Leu Leu
20          25          30
Phe Asn Lys Pro Ile Arg Asn Thr Leu Ile Ala Arg Asn Ser Asn Lys
35          40          45
Tyr Gln Val Thr Lys Val Ser Lys Lys Gln Ile Lys Lys Asn Lys Glu
50          55          60
Ala Lys Ser Thr Phe Asp Phe Gln Ala Val Glu Pro Val Ser Thr Glu
65          70          75          80
Ser Val Leu Gln Ala Gln Met Ala Ala Gln Gln Leu Pro Val Ile Gly
85          90          95
Gly Ile Ala Ile Pro Glu Leu Gly Ile Asn Leu Pro Ile Phe Lys Gly
100         105         110
Leu Gly Asn Thr Glu Leu Ile Tyr Gly Ala Gly Thr Met Lys Glu Glu
115         120         125
Gln Val Met Gly Gly Glu Asn Asn Tyr Ser Leu Ala Ser His His Ile
130         135         140
Phe Gly Ile Thr Gly Ser Ser Gln Met Leu Phe Ser Pro Leu Glu Arg
145         150         155         160
Ala Gln Asn Gly Met Ser Ile Tyr Leu Thr Asp Lys Glu Lys Ile Tyr
165         170         175
Glu Tyr Ile Ile Lys Asp Val Phe Thr Val Ala Pro Glu Arg Val Asp
180         185         190
Val Ile Asp Asp Thr Ala Gly Leu Lys Glu Val Thr Leu Val Thr Cys
195         200         205
Thr Asp Ile Glu Ala Thr Glu Arg Ile Ile Val Lys Gly Glu Leu Lys
210         215         220
Thr Glu Tyr Asp Phe Asp Lys Ala Pro Ala Asp Val Leu Lys Ala Phe
225         230         235         240
Asn His Ser Tyr Asn Gln Val Ser Thr
245

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<210> SEQ ID NO 33
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 33
ttggaggaaa tcacaatggc attgaacatt gaaaacatta ttgctgaaat taaagaagct      60
tcaatccttg agcttaacga tcttgtaaaa gctatcgaag aagaatttgg tgtaactgca      120
gctgctcctg tagctgctgc agctgctggg ggtgctgaag aagctgctaa agattcattc      180
gacgttgaat tgacatctgc tggcgacaaa aaagttggcg ttatcaaagc tgttcgtgaa      240
atcacagggtc ttggtcttaa agaagctaaa ggtccttggt atggagcacc tgctaacgtt      300
aaagaaggcg ttgctgctgc agaagctgaa gaaatcaaag ctaaacttga agaagctgga      360
gcaacaatca ctcttaaata a                                     381

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<210> SEQ ID NO 34
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 34
Met Glu Glu Ile Thr Met Ala Leu Asn Ile Glu Asn Ile Ile Ala Glu

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1				5					10					15			
Ile	Lys	Glu	Ala	Ser	Ile	Leu	Glu	Leu	Asn	Asp	Leu	Val	Lys	Ala	Ile		
			20					25					30				
Glu	Glu	Glu	Phe	Gly	Val	Thr	Ala	Ala	Ala	Pro	Val	Ala	Ala	Ala	Ala		
		35					40					45					
Ala	Gly	Gly	Ala	Glu	Glu	Ala	Ala	Lys	Asp	Ser	Phe	Asp	Val	Glu	Leu		
	50					55					60						
Thr	Ser	Ala	Gly	Asp	Lys	Lys	Val	Gly	Val	Ile	Lys	Ala	Val	Arg	Glu		
65					70					75				80			
Ile	Thr	Gly	Leu	Gly	Leu	Lys	Glu	Ala	Lys	Gly	Leu	Val	Asp	Gly	Ala		
			85					90					95				
Pro	Ala	Asn	Val	Lys	Glu	Gly	Val	Ala	Ala	Ala	Glu	Ala	Glu	Glu	Ile		
		100						105					110				
Lys	Ala	Lys	Leu	Glu	Glu	Ala	Gly	Ala	Thr	Ile	Thr	Leu	Lys				
		115					120						125				

<210> SEQ ID NO 35

<211> LENGTH: 1764

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 35

atggctgttg	aaattattat	gccaaaactc	ggtgttgaca	tgcaagaagg	tgaatcatc	60
gagtggaaaa	aacaagaagg	tgatactgtc	aatgaaggcg	atattcttct	tgaatcatg	120
tcagataaaa	ccaatatgga	acttgaggca	gaagactcag	gtgttcttct	taaaattaca	180
cgtcaagcag	gtgaaacagt	acctgtaaca	gaagttatcg	gatataatcg	tgctgaaggt	240
gaatctgttg	aggtttctag	cccagctgct	tcagatgtga	atgttgctcg	tacaacagaa	300
gatttagaag	ctgctggact	tgaagtgcc	aaagcaccag	ctcaagctgc	ttcagctgca	360
ccaaaagctg	cacttgctga	tgatgagtat	gacatcatcg	ttgttggtgg	tggccctgca	420
ggttattatg	cagctattcg	tggtgctcaa	cttggtggta	aaattgccat	cgttgagaaa	480
tctgaatttg	gtggaacttg	cttgaacgta	gggtgatcc	caaccaaacc	ttaccttaaa	540
aatgctgaaa	tccttgatgg	tattaagatt	gcagcaggac	gtgggattaa	ccttgccctca	600
actaactata	ctattgacat	ggacaaaaca	gttgacttta	aaaacaccgt	tgtaaaaacc	660
ttaacaggcg	gcgttcaagg	tcttctaaaa	gctaataaag	tcactatctt	taatgggctt	720
ggtcaagtc	accctgacaa	gactgtaacc	attgggtcac	aaaccattaa	gggtcgcaac	780
gttatccttg	ctacagggtc	taaagtatca	cgtatcaata	tcccagggtat	tgactctaaa	840
cttgtcttaa	cgtcagatga	tatccttgac	ctccgtgaaa	tgccaaaatc	actagcagtt	900
atgggcgggtg	gtgttggttg	tatcgagctt	ggacttgttt	gggcatctta	cgggtgtggat	960
gttaccgtta	ttgaaatggc	tgaccgtatt	atcccagcta	tggataaaga	agtctctctt	1020
gaacttcaaa	aaatcctttc	taagaaaggc	atgaagatca	aaacatctgt	tgggtgtctct	1080
gaaattgttg	aagcaaataa	ccaattgact	ttgaaactta	acaatgggtga	agaagttggt	1140
gctgaaaaag	ctcttctttc	tatcggacgt	gtatcacaaa	tgaacgggtct	ggaaaatctt	1200
aaccttgaaa	tggatcgtaa	ccgtatcaaa	gttaatgact	accaagagac	atcaattcca	1260
ggtatctatg	cgccagggtga	cgttaacgga	acgaaaatgc	ttgctcacgc	tgcttaccgt	1320
atgggtgaag	tggctgcaga	aaatgcgatg	catggcaaca	caactcgtaa	agctaacctt	1380
aaatacactc	cagcagctgt	ttacacacac	cctgaagtgg	caatgggttg	tttaactgaa	1440
gaacaagcgc	gtgaacaata	tggatgatgt	cttattggta	aaaacagctt	tactggtaat	1500
ggacgcgcga	ttgcttcaaa	tgaagcacat	ggttttggtta	aagttattgc	tgatgccaaa	1560
taccacgaaa	tcttaggtgt	tcatattatt	ggtccagctg	cagctgagat	gattaacgaa	1620
gcagctacta	ttatggaatc	tgaattaacc	ggtgatgaat	tggtattatc	aattcatgga	1680
cacccaacct	tctctgaagt	gatgtacgaa	gcctttgcag	atgtgcttgg	cgaagctatc	1740
cataacccac	caaaacgtaa	gtaa				1764

<210> SEQ ID NO 36

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 36

Met	Ala	Val	Glu	Ile	Ile	Met	Pro	Lys	Leu	Gly	Val	Asp	Met	Gln	Glu	1	5	10	15
Gly	Glu	Ile	Ile	Glu	Trp	Lys	Lys	Gln	Glu	Gly	Asp	Thr	Val	Asn	Glu	20	25	30	
Gly	Asp	Ile	Leu	Leu	Glu	Ile	Met	Ser	Asp	Lys	Thr	Asn	Met	Glu	Leu	35	40	45	
Glu	Ala	Glu	Asp	Ser	Gly	Val	Leu	Leu	Lys	Ile	Thr	Arg	Gln	Ala	Gly	50	55	60	
Glu	Thr	Val	Pro	Val	Thr	Glu	Val	Ile	Gly	Tyr	Ile	Gly	Ala	Glu	Gly	65	70	75	80
Glu	Ser	Val	Glu	Val	Ser	Ser	Pro	Ala	Ala	Ser	Asp	Val	Asn	Val	Ala	85	90	95	
Arg	Thr	Thr	Glu	Asp	Leu	Glu	Ala	Ala	Gly	Leu	Glu	Val	Pro	Lys	Ala	100	105	110	
Pro	Ala	Gln	Ala	Ala	Ser	Ala	Ala	Pro	Lys	Ala	Ala	Leu	Ala	Asp	Asp	115	120	125	
Glu	Tyr	Asp	Ile	Ile	Val	Val	Gly	Gly	Gly	Pro	Ala	Gly	Tyr	Tyr	Ala	130	135	140	
Ala	Ile	Arg	Gly	Ala	Gln	Leu	Gly	Gly	Lys	Ile	Ala	Ile	Val	Glu	Lys	145	150	155	160
Ser	Glu	Phe	Gly	Gly	Thr	Cys	Leu	Asn	Val	Gly	Cys	Ile	Pro	Thr	Lys	165	170	175	
Thr	Tyr	Leu	Lys	Asn	Ala	Glu	Ile	Leu	Asp	Gly	Ile	Lys	Ile	Ala	Ala	180	185	190	
Gly	Arg	Gly	Ile	Asn	Leu	Ala	Ser	Thr	Asn	Tyr	Thr	Ile	Asp	Met	Asp	195	200	205	
Lys	Thr	Val	Asp	Phe	Lys	Asn	Thr	Val	Val	Lys	Thr	Leu	Thr	Gly	Gly	210	215	220	
Val	Gln	Gly	Leu	Leu	Lys	Ala	Asn	Lys	Val	Thr	Ile	Phe	Asn	Gly	Leu	225	230	235	240
Gly	Gln	Val	Asn	Pro	Asp	Lys	Thr	Val	Thr	Ile	Gly	Ser	Gln	Thr	Ile	245	250	255	
Lys	Gly	Arg	Asn	Val	Ile	Leu	Ala	Thr	Gly	Ser	Lys	Val	Ser	Arg	Ile	260	265	270	
Asn	Ile	Pro	Gly	Ile	Asp	Ser	Lys	Leu	Val	Leu	Thr	Ser	Asp	Asp	Ile	275	280	285	
Leu	Asp	Leu	Arg	Glu	Met	Pro	Lys	Ser	Leu	Ala	Val	Met	Gly	Gly	Gly	290	295	300	
Val	Val	Gly	Ile	Glu	Leu	Gly	Leu	Val	Trp	Ala	Ser	Tyr	Gly	Val	Asp	305	310	315	320
Val	Thr	Val	Ile	Glu	Met	Ala	Asp	Arg	Ile	Ile	Pro	Ala	Met	Asp	Lys	325	330	335	
Glu	Val	Ser	Leu	Glu	Leu	Gln	Lys	Ile	Leu	Ser	Lys	Lys	Gly	Met	Lys	340	345	350	
Ile	Lys	Thr	Ser	Val	Gly	Val	Ser	Glu	Ile	Val	Glu	Ala	Asn	Asn	Gln	355	360	365	
Leu	Thr	Leu	Lys	Leu	Asn	Asn	Gly	Glu	Glu	Val	Val	Ala	Glu	Lys	Ala	370	375	380	
Leu	Leu	Ser	Ile	Gly	Arg	Val	Ser	Gln	Met	Asn	Gly	Leu	Glu	Asn	Leu	385	390	395	400
Asn	Leu	Glu	Met	Asp	Arg	Asn	Arg	Ile	Lys	Val	Asn	Asp	Tyr	Gln	Glu	405	410	415	
Thr	Ser	Ile	Pro	Gly	Ile	Tyr	Ala	Pro	Gly	Asp	Val	Asn	Gly	Thr	Lys	420	425	430	
Met	Leu	Ala	His	Ala	Ala	Tyr	Arg	Met	Gly	Glu	Val	Ala	Ala	Glu	Asn	435	440	445	
Ala	Met	His	Gly	Asn	Thr	Thr	Arg	Lys	Ala	Asn	Leu	Lys	Tyr	Thr	Pro				

450	Ala Ala Val Tyr Thr His	455	Pro Glu Val Ala Met	460	Val Gly Leu Thr Glu
465	Glu Gln Ala Arg Glu Gln Tyr Gly Asp	470	Val Leu Ile Gly Lys Asn Ser	475	480
	485	490	495		
Phe Thr Gly Asn Gly Arg Ala Ile Ala Ser Asn Glu Ala His Gly Phe					
500	505	510			
Val Lys Val Ile Ala Asp Ala Lys Tyr His Glu Ile Leu Gly Val His					
515	520	525			
Ile Ile Gly Pro Ala Ala Ala Glu Met Ile Asn Glu Ala Ala Thr Ile					
530	535	540			
Met Glu Ser Glu Leu Thr Val Asp Glu Leu Leu Leu Ser Ile His Gly					
545	550	555			560
His Pro Thr Phe Ser Glu Val Met Tyr Glu Ala Phe Ala Asp Val Leu					
565	570	575			
Gly Glu Ala Ile His Asn Pro Pro Lys Arg Lys					
580	585				

<210> SEQ ID NO 37

<211> LENGTH: 3636

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 37

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acattacaat	cggcaatccg	ttcaatcgat	ggcttggaac	agcgttcaac	cggtttttca	120
tcgggtgtct	aaaaagctag	ttccatgttt	aaatccatgt	taggagcgaa	tttagccgga	180
caagctatct	cagcaatgac	aaggacagtg	tcatacaggc	ttggctctat	gcttggcgag	240
atgaatagtt	cagcgaaaagc	gtggaaaact	tttgacgcc	atttagcgga	cattgggttt	300
ggaaaaaac	aaattttggc	agctaaaacg	gcgatgcaag	actatgcaac	taaaacaatc	360
tactcggcat	cagatatggc	tagcacgtat	gcacagttag	cggcagttgg	tgtgaaagat	420
accggaaaagc	tcgtaaaaagc	ttttggcggg	ttagctgcat	ctgctgaaaa	cccgaagcag	480
gccatgaagt	ctatcagtca	acaaatgacg	caagcagtag	gaagaccaac	agttgcatgg	540
caagacttta	ggataatgct	ggaacaggcg	cctgcaggga	tggctaaagt	cgctaaatct	600
atgggtaaaa	atcttgatga	actcgtcgcc	gatatacagg	cgggtagggt	taaaaccagc	660
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caaccagcgt	ttgaaaaagt	gaaccaattt	ggaattagag	cgatcgaagc	aatcggtaaa	840
caactcgata	aagttgattt	ttctaagttt	gctagtaatc	ttgggaaatt	ccttgaagga	900
attaatatcg	ataaaaattgt	atctaataat	tcatacggcga	tttcatctgt	cacttcaaag	960
gttaaagaat	tttggggcgg	tttcaaacia	actggagcaa	ttagtgtctt	ttcaggagct	1020
ttaaaaagtg	tttgggggagc	gttaaaaaat	gtagctagcg	ctatgagtgg	aggcagttgg	1080
aaaaactttg	gctctattgt	aggcggaatt	gtaaagcatg	tgtctaattt	tgcaaaaagct	1140
attgctgatg	ttgtcggtaa	aatggaacct	ggcagattgc	aaagctggat	agccactttt	1200
gcagcagtcg	ggggaggggt	aaagttattt	gaaaagctaa	caggacaaaag	cgttgttggc	1260
tcttttttag	ataaaaatcag	tacaaaattt	ggattatttg	gcaaaaaagc	taaagaagga	1320
accgatcaag	cagcgaatgg	ctctcgtaaa	agtgggtgaa	tcatacagcca	aatctttaat	1380
ggcttgggta	atatcggtta	gtctgctggg	acagccatat	caacagctgc	aaaagggtatc	1440
ggtacagggg	ttaaaaaccgc	cttgtctggg	gcacctccta	tcattagttc	tctaggaacc	1500
gcaatatcaa	cagttgcgca	aggtataggc	actgggctag	caatcgcttt	tagaggttta	1560
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atggtaggag	cggctttttgc	cttagcagga	actcaggctg	atggcattag	tcaaattttta	1680
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ttactaacta	ttatcgcaaa	cgctattggc	tctatgttgc	caattgtagc	tggagctatc	1800
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aactccatta	gcgctgttat	ccaatcgcta	actgggtgtga	ttaccgcagt	attcaatggc	1980
atagctactg	ttatttcata	tgctcggttcg	actatcaaag	atgtattgac	gggtctagga	2040

accgcttttg	aaggatttgg	gaatggtgta	aaatcagctc	tagaaggtgt	tggggcagta	2100
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tctatgggga	ctgcggcact	taatgcaggc	cgtggcgta	aagagatggc	taaaggtatt	2220
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ggattggctg	caattaatgc	tccaatcact	atgtttaaag	ctcaactaat	gacaataaca	2580
ccagctctag	cacaagctgg	cgctggcctt	gccgcgtttg	ttgctcaatc	atcaacattt	2640
agtacaggtt	tagcatctgc	cggtcctaca	atagcagcat	tcaatgctaa	tttgatgagc	2700
ttatctgcaa	caacaggagt	gctagttgca	tcaatagctg	gtttatcagc	tgtgctttct	2760
gttgtagcag	ctggcttttag	ccaaataggg	gcttctgcga	cagcaactgt	tggtcaaata	2820
caagcttttg	cttctagtac	aacagttggt	tcgtcagcat	ttgctagcat	gcaatctatg	2880
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tctcaaatgc	aatcaatctt	atctcgaatg	ctatctcagg	ccaggacatt	tggtgtctcaa	3000
ctagagcaac	aaatgagaca	atcgggacag	cgttcaggac	aaaatcttgc	tcgggggcta	3060
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agagccaacg	cgggagctgg	tcctatgctg	caagctggag	cgtacatcgg	acaagggctt	3180
gcgcaaggaa	tgtattcagc	gctaggagct	gtaacagctg	cagcaaacgc	ccttgtagca	3240
caagccgaga	gagcagcaag	agccaaggcg	atgattcatt	cgccgtcaag	gttggttgca	3300
aaacgagttg	gtcaatatat	cccgaaggcg	gtagctatgg	gtatcgacaa	aaacgctgat	3360
gtcgttgacg	actctgttgg	cggtgtattt	gatagcatca	atagctttga	ttttaatatc	3420
gcagatagac	tgactagcat	tggagctaaa	ttccaagggtg	ttgtcaaata	agagagttcg	3480
caatcggttat	cgcagcaaca	agagtttgta	catacagctc	aaccagcgta	tataaacttt	3540
agtttaggcg	gaaacgaata	cgaagcattt	gtaagtgcata	tcactaatca	acaagcaaaa	3600
attgaaaaaa	tcagactaaa	gagaagcagc	tggttag			3636

<210> SEQ ID NO 38

<211> LENGTH: 1211

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 38

Met	Gly	Glu	Ser	Tyr	Ser	Val	Glu	Ala	Val	Leu	Thr	Ala	Val	Asp	Lys
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Thr	Phe	Gly	Lys	Thr	Leu	Gln	Ser	Ala	Ile	Arg	Ser	Ile	Asp	Gly	Leu
			20					25					30		
Glu	Lys	Arg	Ser	Thr	Gly	Phe	Ser	Ser	Val	Ser	Gln	Lys	Ala	Ser	Ser
		35					40					45			
Met	Phe	Lys	Ser	Met	Leu	Gly	Ala	Asn	Leu	Ala	Gly	Gln	Ala	Ile	Ser
	50					55				60					
Ala	Met	Thr	Arg	Thr	Val	Ser	Ser	Gly	Leu	Gly	Ser	Met	Leu	Gly	Glu
65					70				75					80	
Met	Asn	Ser	Ser	Ala	Lys	Ala	Trp	Lys	Thr	Phe	Asp	Ala	Asn	Leu	Ala
			85					90					95		
Asp	Ile	Gly	Phe	Gly	Lys	Lys	Gln	Ile	Leu	Ala	Ala	Lys	Thr	Ala	Met
		100					105						110		
Gln	Asp	Tyr	Ala	Thr	Lys	Thr	Ile	Tyr	Ser	Ala	Ser	Asp	Met	Ala	Ser
	115					120					125				
Thr	Tyr	Ala	Gln	Leu	Ala	Ala	Val	Gly	Val	Lys	Asp	Thr	Gly	Lys	Leu
	130				135						140				
Val	Lys	Ala	Phe	Gly	Gly	Leu	Ala	Ala	Ser	Ala	Glu	Asn	Pro	Lys	Gln
145				150					155					160	
Ala	Met	Lys	Ser	Ile	Ser	Gln	Gln	Met	Thr	Gln	Ala	Val	Gly	Arg	Pro
			165					170					175		
Thr	Val	Ala	Trp	Gln	Asp	Phe	Arg	Ile	Met	Leu	Glu	Gln	Ala	Pro	Ala
			180					185					190		

Gly	Met	Ala	Lys	Val	Ala	Lys	Ser	Met	Gly	Lys	Asn	Leu	Asp	Glu	Leu		
		195					200					205					
Val	Ala	Asp	Ile	Gln	Ala	Gly	Arg	Val	Lys	Thr	Ser	Asp	Phe	Leu	Glu		
		210					215					220					
Ala	Val	Lys	Lys	Ala	Gly	Asn	Asp	Lys	Ser	Phe	Gln	Lys	Met	Ala	Thr		
225						230					235				240		
Glu	Phe	Lys	Thr	Val	Asp	Gln	Ala	Ile	Asp	Gly	Met	Arg	Glu	Gly	Leu		
				245					250						255		
Ser	Asn	Lys	Leu	Gln	Pro	Ala	Phe	Glu	Lys	Val	Asn	Gln	Phe	Gly	Ile		
			260					265					270				
Arg	Ala	Ile	Glu	Ala	Ile	Gly	Lys	Gln	Leu	Asp	Lys	Val	Asp	Phe	Ser		
		275					280					285					
Lys	Phe	Ala	Ser	Asn	Leu	Gly	Lys	Phe	Leu	Glu	Gly	Ile	Asn	Ile	Asp		
		290				295					300						
Lys	Ile	Val	Ser	Asn	Ile	Ser	Ser	Ala	Ile	Ser	Ser	Val	Thr	Ser	Lys		
305					310					315					320		
Val	Lys	Glu	Phe	Trp	Gly	Gly	Phe	Lys	Gln	Thr	Gly	Ala	Ile	Ser	Ala		
				325						330					335		
Phe	Ser	Gly	Ala	Leu	Lys	Ser	Val	Trp	Gly	Ala	Leu	Lys	Asn	Val	Ala		
			340					345					350				
Ser	Ala	Met	Ser	Gly	Gly	Ser	Trp	Lys	Asn	Phe	Gly	Ser	Ile	Val	Gly		
		355					360				365						
Gly	Ile	Val	Lys	His	Val	Ser	Asn	Phe	Ala	Lys	Ala	Ile	Ala	Asp	Val		
		370				375					380						
Val	Gly	Lys	Met	Glu	Pro	Gly	Arg	Leu	Gln	Ser	Trp	Ile	Ala	Thr	Phe		
385					390					395					400		
Ala	Ala	Val	Gly	Gly	Gly	Leu	Lys	Leu	Phe	Glu	Lys	Leu	Thr	Gly	Gln		
				405					410						415		
Ser	Val	Val	Gly	Ser	Phe	Leu	Asp	Lys	Ile	Ser	Thr	Lys	Phe	Gly	Leu		
			420					425					430				
Phe	Gly	Lys	Lys	Ala	Lys	Glu	Gly	Thr	Asp	Gln	Ala	Ala	Asn	Gly	Ser		
		435					440					445					
Arg	Lys	Ser	Gly	Gly	Ile	Ile	Ser	Gln	Ile	Phe	Asn	Gly	Leu	Gly	Asn		
		450				455					460						
Ile	Val	Lys	Ser	Ala	Gly	Thr	Ala	Ile	Ser	Thr	Ala	Ala	Lys	Gly	Ile		
465					470					475					480		
Gly	Thr	Gly	Ile	Lys	Thr	Ala	Leu	Ser	Gly	Ala	Pro	Pro	Ile	Ile	Ser		
				485					490						495		
Ser	Leu	Gly	Thr	Ala	Ile	Ser	Thr	Val	Ala	Gln	Gly	Ile	Gly	Thr	Gly		
			500					505					510				
Leu	Ala	Ile	Ala	Phe	Arg	Gly	Leu	Gly	Ala	Ala	Ile	Ala	Met	Val	Pro		
		515					520					525					
Pro	Thr	Thr	Trp	Leu	Ala	Leu	Gly	Thr	Ala	Ile	Leu	Met	Val	Gly	Ala		
		530				535					540						
Ala	Phe	Ala	Leu	Ala	Gly	Thr	Gln	Ala	Asp	Gly	Ile	Ser	Gln	Ile	Leu		
545					550					555					560		
Arg	Thr	Ile	Gly	Asp	Val	Val	Val	Gln	Val	Leu	Gln	Gln	Val	Thr	Asp		
				565					570						575		
Ser	Leu	Ala	Thr	Leu	Leu	Thr	Ile	Ile	Ala	Asn	Ala	Ile	Gly	Ser	Met		
			580					585					590				
Leu	Pro	Ile	Val	Ala	Gly	Ala	Ile	Ser	Gln	Ile	Val	Gly	Ala	Val	Ala		
		595					600					605					
Gly	Gly	Leu	Ser	Gln	Leu	Ile	Ile	Ala	Val	Ser	Thr	Gly	Val	Ser	Leu		
		610				615					620						
Val	Ile	Gly	Ala	Phe	Thr	Gly	Leu	Leu	Gly	Gly	Ile	Ser	Gly	Val	Ile		
625					630					635					640		
Asn	Ser	Ile	Ser	Ala	Val	Ile	Gln	Ser	Leu	Thr	Gly	Val	Ile	Thr	Ala		

				645					650				655				
Val	Phe	Asn	Gly	Ile	Ala	Thr	Val	Ile	Ser	Ser	Val	Gly	Ser	Thr	Ile		
			660					665					670				
Lys	Asp	Val	Leu	Thr	Gly	Leu	Gly	Thr	Ala	Phe	Glu	Gly	Phe	Gly	Asn		
		675					680					685					
Gly	Val	Lys	Ser	Ala	Leu	Glu	Gly	Val	Gly	Ala	Val	Ile	Glu	Ser	Phe		
	690					695					700						
Gly	Ser	Ala	Val	Arg	Asn	Val	Leu	Asp	Gly	Val	Ala	Asn	Ile	Leu	Asp		
705				710					715						720		
Ser	Met	Gly	Thr	Ala	Ala	Leu	Asn	Ala	Gly	Arg	Gly	Val	Lys	Glu	Met		
			725					730						735			
Ala	Lys	Gly	Ile	Lys	Met	Leu	Val	Asp	Leu	Ser	Leu	Gly	Asp	Leu	Val		
		740					745						750				
Ala	Thr	Leu	Ala	Ala	Val	Ala	Ser	Gly	Leu	Gly	Lys	Met	Ala	Ser	Ser		
	755					760						765					
Ala	Gly	Glu	Met	Thr	Thr	Leu	Gly	Ser	Ala	Met	Ser	Lys	Val	Ala	Asn		
	770					775					780						
Gly	Met	Thr	Arg	Leu	Ala	Thr	Ser	Ala	Thr	Ile	Ala	Ile	Thr	Gly	Leu		
785				790						795					800		
Thr	Val	Phe	Ala	Thr	Thr	Met	Ala	Thr	Ile	Lys	Thr	Ala	Val	Ala	Thr		
			805					810						815			
Leu	Pro	Pro	Val	Leu	Thr	Met	Ala	Ala	Ser	Gly	Phe	Thr	Thr	Phe	Thr		
		820					825						830				
Thr	Gln	Ala	Val	Ala	Ala	Val	Thr	Gly	Leu	Ala	Ala	Ile	Asn	Ala	Pro		
	835					840						845					
Ile	Thr	Met	Phe	Lys	Ala	Gln	Leu	Met	Thr	Ile	Thr	Pro	Ala	Leu	Ala		
	850					855					860						
Gln	Ala	Gly	Ala	Gly	Phe	Ala	Ala	Phe	Val	Ala	Gln	Ser	Ser	Thr	Phe		
865				870					875						880		
Ser	Thr	Gly	Leu	Ala	Ser	Ala	Gly	Pro	Thr	Ile	Ala	Ala	Phe	Asn	Ala		
			885					890						895			
Asn	Leu	Met	Ser	Leu	Ser	Ala	Thr	Thr	Gly	Val	Leu	Val	Ala	Ser	Ile		
		900						905					910				
Ala	Gly	Leu	Ser	Ala	Val	Leu	Ser	Val	Val	Ser	Ala	Gly	Phe	Ser	Gln		
	915					920						925					
Ile	Gly	Ala	Ser	Ala	Thr	Ala	Thr	Val	Gly	Gln	Ile	Gln	Ala	Phe	Ala		
	930					935					940						
Ser	Ser	Thr	Thr	Val	Val	Ser	Ser	Ala	Phe	Ala	Ser	Met	Gln	Ser	Met		
945				950						955					960		
Ile	Gln	Ser	Ala	Met	Ala	Ala	Ile	Val	Ser	Ser	Ile	Ile	Thr	Ser	Phe		
			965					970						975			
Asn	Gln	Ala	Ala	Ser	Gln	Met	Gln	Ser	Ile	Leu	Ser	Arg	Met	Leu	Ser		
		980					985						990				
Gln	Ala	Arg	Thr	Phe	Gly	Ser	Gln	Leu	Glu	Gln	Gln	Met	Arg	Gln	Ser		
	995						1000					1005					
Gly	Gln	Arg	Ser	Gly	Gln	Asn	Leu	Ala	Arg	Gly	Leu	Ser	Ser	Gln			
	1010					1015					1020						
Gln	Gly	Ala	Val	Ile	Asn	Ala	Ile	Ser	Ser	Met	Val	Asn	Ala	Ala			
	1025					1030					1035						
Val	Ser	Arg	Ala	Asn	Ala	Gly	Ala	Gly	Pro	Met	Arg	Gln	Ala	Gly			
	1040					1045					1050						
Ala	Tyr	Ile	Gly	Gln	Gly	Leu	Ala	Gln	Gly	Met	Tyr	Ser	Ala	Leu			
	1055					1060					1065						
Gly	Ala	Val	Thr	Ala	Ala	Ala	Asn	Ala	Leu	Val	Ala	Gln	Ala	Glu			
	1070					1075					1080						
Arg	Ala	Ala	Arg	Ala	Lys	Ala	Met	Ile	His	Ser	Pro	Ser	Arg	Leu			
	1085					1090					1095						

Phe	Ala	Lys	Arg	Val	Gly	Gln	Tyr	Ile	Pro	Gln	Gly	Val	Ala	Met
1100						1105					1110			
Gly	Ile	Asp	Lys	Asn	Ala	Asp	Val	Val	Asp	Asp	Ser	Val	Gly	Gly
1115						1120					1125			
Leu	Phe	Asp	Ser	Ile	Asn	Ser	Phe	Asp	Phe	Asn	Ile	Ala	Asp	Arg
1130						1135					1140			
Leu	Thr	Ser	Ile	Gly	Ala	Lys	Phe	Gln	Gly	Val	Val	Lys	Ser	Glu
1145						1150					1155			
Ser	Ser	Gln	Ser	Leu	Ser	Gln	Gln	Gln	Glu	Phe	Val	His	Thr	Ala
1160						1165					1170			
Gln	Pro	Ala	Tyr	Ile	Asn	Phe	Ser	Leu	Gly	Gly	Asn	Glu	Tyr	Glu
1175						1180					1185			
Ala	Phe	Val	Ser	Asp	Ile	Thr	Asn	Gln	Gln	Ala	Lys	Ile	Glu	Lys
1190						1195					1200			
Ile	Arg	Leu	Lys	Arg	Ser	Trp								
1205						1210								

<210> SEQ ID NO 39

<211> LENGTH: 1206

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 39

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ggtgaagggtg	tcttgacact	tcgtgaattg	actaacgacc	gcgatgctga	tattaacgac	180
tttgttaaaag	ctggcgacac	agttgaagta	cttgttcttc	gtcaagtagt	aggtaaagat	240
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aaacttgttg	gtcgtgaagg	cgaagttggt	actgttaaag	gtaccctgtc	tgtaaagggt	360
ggcctttcag	ttgaatttga	aggacttcgt	ggatttatcc	ctgcttcaat	gattgacact	420
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ggtgatgcag	cagaaaaccg	tttcatccta	tcacgtcgtg	aagttatcga	agaggccgct	540
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gtagcgcgtt	taacaagttt	tggtgctttc	attgaccttg	gtggtgttga	cggacttggt	660
cacgtgactg	aattgtctca	cgaacgtaac	gtgtcaccta	aatcagttgt	ttcagttggt	720
gaagaagttg	aagttaaaagt	tctttcaatt	gacgaagaag	ctggtcgtgt	gtcactttca	780
cttaaagcaa	caacacctgg	accatgggac	ggcgttgaac	aaaaacttgc	tcaaggtgat	840
gttgttgaag	gtaaagtaaa	acgcttgact	gacttcggtg	cttttgttga	agtattacca	900
ggtattgatg	gacttggtca	tatttcacaa	atttcacaca	aacgtggtga	aaatccaaaa	960
gatgtacttt	ctgtaggaca	agaagtaaca	gttaaagtcc	ttgaagtga	tgcagctgat	1020
gagcgcgtat	cattatcaat	caaagctctt	gaagaacgcc	cagcgcaagc	tgaaggagac	1080
aacaaagaag	aaaaacgtca	atcacgccc	cgctcgccaa	aacgtgaatc	aagacgtgac	1140
tacgaactcc	cagaaacaca	aactggattc	tcaatggctg	atcttttcgg	tgatattgaa	1200
ttgtaa						1206

<210> SEQ ID NO 40

<211> LENGTH: 401

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 40

Met	Asn	Glu	Phe	Glu	Asp	Leu	Leu	Asn	Ser	Val	Ser	Glu	Val	Asn	Pro
1				5					10					15	
Gly	Asp	Val	Val	Thr	Ala	Glu	Val	Leu	Thr	Val	Asp	Asn	Gly	Gln	Ala
			20					25					30		
Asn	Val	Val	Ile	Glu	Gly	Thr	Gly	Val	Glu	Gly	Val	Leu	Thr	Leu	Arg
		35				40					45				
Glu	Leu	Thr	Asn	Asp	Arg	Asp	Ala	Asp	Ile	Asn	Asp	Phe	Val	Lys	Ala
	50					55					60				

Gly	Asp	Thr	Val	Glu	Val	Leu	Val	Leu	Arg	Gln	Val	Val	Gly	Lys	Asp	65	70	75	80
Thr	Asp	Thr	Val	Thr	Phe	Leu	Val	Ser	Lys	Lys	Arg	Leu	Glu	Ala	Arg	85	90	95	
Lys	Ala	Trp	Asp	Lys	Leu	Val	Gly	Arg	Glu	Gly	Glu	Val	Val	Thr	Val	100	105	110	
Lys	Gly	Thr	Arg	Ala	Val	Lys	Gly	Gly	Leu	Ser	Val	Glu	Phe	Glu	Gly	115	120	125	
Leu	Arg	Gly	Phe	Ile	Pro	Ala	Ser	Met	Ile	Asp	Thr	Arg	Phe	Val	Arg	130	135	140	
Asn	Thr	Glu	Lys	Phe	Val	Gly	Gln	Glu	Phe	Asp	Ala	Lys	Ile	Lys	Glu	145	150	155	160
Val	Asp	Ala	Ala	Glu	Asn	Arg	Phe	Ile	Leu	Ser	Arg	Arg	Glu	Val	Ile	165	170	175	
Glu	Glu	Ala	Ala	Lys	Glu	Ala	Arg	Ala	Glu	Val	Phe	Ser	Lys	Ile	Ser	180	185	190	
Glu	Gly	Ala	Val	Val	Thr	Gly	Thr	Val	Ala	Arg	Leu	Thr	Ser	Phe	Gly	195	200	205	
Ala	Phe	Ile	Asp	Leu	Gly	Gly	Val	Asp	Gly	Leu	Val	His	Val	Thr	Glu	210	215	220	
Leu	Ser	His	Glu	Arg	Asn	Val	Ser	Pro	Lys	Ser	Val	Val	Ser	Val	Gly	225	230	235	240
Glu	Glu	Val	Glu	Val	Lys	Val	Leu	Ser	Ile	Asp	Glu	Glu	Ala	Gly	Arg	245	250	255	
Val	Ser	Leu	Ser	Leu	Lys	Ala	Thr	Thr	Pro	Gly	Pro	Trp	Asp	Gly	Val	260	265	270	
Glu	Gln	Lys	Leu	Ala	Gln	Gly	Asp	Val	Val	Glu	Gly	Lys	Val	Lys	Arg	275	280	285	
Leu	Thr	Asp	Phe	Gly	Ala	Phe	Val	Glu	Val	Leu	Pro	Gly	Ile	Asp	Gly	290	295	300	
Leu	Val	His	Ile	Ser	Gln	Ile	Ser	His	Lys	Arg	Val	Glu	Asn	Pro	Lys	305	310	315	320
Asp	Val	Leu	Ser	Val	Gly	Gln	Glu	Val	Thr	Val	Lys	Val	Leu	Glu	Val	325	330	335	
Asn	Ala	Ala	Asp	Glu	Arg	Val	Ser	Leu	Ser	Ile	Lys	Ala	Leu	Glu	Glu	340	345	350	
Arg	Pro	Ala	Gln	Ala	Glu	Gly	Asp	Asn	Lys	Glu	Glu	Lys	Arg	Gln	Ser	355	360	365	
Arg	Pro	Arg	Arg	Pro	Lys	Arg	Glu	Ser	Arg	Arg	Asp	Tyr	Glu	Leu	Pro	370	375	380	
Glu	Thr	Gln	Thr	Gly	Phe	Ser	Met	Ala	Asp	Leu	Phe	Gly	Asp	Ile	Glu	385	390	395	400
Leu																			

<210> SEQ ID NO 41

<211> LENGTH: 900

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 41

atgttatact	attcttatct	taataaagga	gttactatga	agaaatcagt	tacattactg	60
tctatcggac	ttgccagcct	tttattggca	gcatgtgcgc	cacatcaatc	tcaaaaatca	120
agttgggaca	ctatcaaaga	aaaaggggtg	ttaaaagtag	ctaccccagg	aacctatcag	180
ccaacttctt	tttacaacga	taataatgag	ttagtaggtt	acgaagtaga	tatggtcaaa	240
gaaatcggta	aacgacttaa	cattaaagtc	aagtttggtg	aaacaggatt	tgaccaagcc	300
tttacctcag	ttgatagtgg	tcgagtggat	atttctttga	acaactttga	cattacccca	360
aaacgtcaga	aaaaatacaa	tatctctacg	ccttataaat	acggggtagg	aggcatgatt	420
gtccgtgctg	atggcagctc	aaacatagct	aaaaaagatc	ttagcgactg	gaaaggaaaa	480

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aaagcagccg gcgcttctgg aacagaatac atgaaagtag cgcaaaaaca gggagctgaa 540
ctgggtgacct acgataatgt tacaggagat gtttatctaa acgatgtggc taacgggtcga 600
acagattttca tcccaaatga ttaccagct caaaaattat ttgtggatta catgttatct 660
caaaatccaa atctaaatgt caaaatgagc gatgttcagt acaacccaac cgaacaagga 720
attgttatga acaaaaaaga cgatagcctc aagaaaaaaa tagatgctgt tattaaagac 780
atgataaaaag atggtagctt gaagaaaatc tctgaaacct actatgctgg tcaagatctg 840
acaaaacctt ttggcaaaga caaaaaaatt cccgtcattg atacgaaaga cgtaaactaa 900

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<210> SEQ ID NO 42

<211> LENGTH: 299

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 42

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Met Leu Tyr Tyr Ser Tyr Leu Asn Lys Gly Val Thr Met Lys Lys Ser
1      5      10      15
Val Thr Leu Leu Ser Ile Gly Leu Ala Ser Leu Leu Leu Ala Ala Cys
20     25     30
Ala Pro His Gln Ser Gln Lys Ser Ser Trp Asp Thr Ile Lys Glu Lys
35     40     45
Gly Val Leu Lys Val Ala Thr Pro Gly Thr Tyr Gln Pro Thr Ser Phe
50     55     60
Tyr Asn Asp Asn Asn Glu Leu Val Gly Tyr Glu Val Asp Met Val Lys
65     70     75     80
Glu Ile Gly Lys Arg Leu Asn Ile Lys Val Lys Phe Val Glu Thr Gly
85     90     95
Phe Asp Gln Ala Phe Thr Ser Val Asp Ser Gly Arg Val Asp Ile Ser
100    105    110
Leu Asn Asn Phe Asp Ile Thr Pro Lys Arg Gln Lys Lys Tyr Asn Ile
115    120    125
Ser Thr Pro Tyr Lys Tyr Gly Val Gly Gly Met Ile Val Arg Ala Asp
130    135    140
Gly Ser Ser Asn Ile Ala Lys Lys Asp Leu Ser Asp Trp Lys Gly Lys
145    150    155    160
Lys Ala Ala Gly Ala Ser Gly Thr Glu Tyr Met Lys Val Ala Gln Lys
165    170    175
Gln Gly Ala Glu Leu Val Thr Tyr Asp Asn Val Thr Gly Asp Val Tyr
180    185    190
Leu Asn Asp Val Ala Asn Gly Arg Thr Asp Phe Ile Pro Asn Asp Tyr
195    200    205
Pro Ala Gln Lys Leu Phe Val Asp Tyr Met Leu Ser Gln Asn Pro Asn
210    215    220
Leu Asn Val Lys Met Ser Asp Val Gln Tyr Asn Pro Thr Glu Gln Gly
225    230    235    240
Ile Val Met Asn Lys Lys Asp Asp Ser Leu Lys Lys Lys Ile Asp Ala
245    250    255
Val Ile Lys Asp Met Ile Lys Asp Gly Ser Leu Lys Lys Ile Ser Glu
260    265    270
Thr Tyr Tyr Ala Gly Gln Asp Leu Thr Lys Pro Phe Gly Lys Asp Lys
275    280    285
Lys Ile Pro Val Ile Asp Thr Lys Asp Val Asn
290    295

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<210> SEQ ID NO 43

<211> LENGTH: 2052

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 43

Lys	Met	Lys	Phe	Glu	Tyr	Gly	Thr	Leu	Gly	Asn	His	Glu	Phe	Asp	Glu	130	135	140
Gly	Leu	Asp	Glu	Phe	Asn	Arg	Ile	Met	Thr	Gly	Gln	Ala	Pro	Asp	Pro	145	150	155
Glu	Ser	Thr	Ile	Asn	Asp	Ile	Thr	Lys	Gln	Tyr	Glu	His	Glu	Ala	Ser	165	170	175
His	Gln	Thr	Ile	Val	Ile	Ala	Asn	Val	Ile	Asp	Lys	Lys	Thr	Lys	Asp	180	185	190
Ile	Pro	Tyr	Gly	Trp	Lys	Pro	Tyr	Ala	Ile	Lys	Asp	Ile	Ala	Ile	Asn	195	200	205
Asp	Lys	Ile	Val	Lys	Ile	Gly	Phe	Ile	Gly	Val	Val	Thr	Thr	Glu	Ile	210	215	220
Pro	Asn	Leu	Val	Leu	Lys	Gln	Asn	Tyr	Glu	His	Tyr	Gln	Phe	Leu	Asp	225	230	235
Val	Ala	Glu	Thr	Ile	Ala	Lys	Tyr	Ala	Lys	Glu	Leu	Gln	Glu	Gln	His	245	250	255
Val	His	Ala	Ile	Val	Val	Leu	Ala	His	Val	Pro	Ala	Thr	Ser	Lys	Asp	260	265	270
Gly	Val	Val	Asp	His	Glu	Met	Ala	Thr	Val	Met	Glu	Lys	Val	Asn	Gln	275	280	285
Ile	Tyr	Pro	Glu	His	Ser	Ile	Asp	Ile	Ile	Phe	Ala	Gly	His	Asn	His	290	295	300
Gln	Tyr	Thr	Asn	Gly	Thr	Ile	Gly	Lys	Thr	Arg	Ile	Val	Gln	Ala	Leu	305	310	315
Ser	Gln	Gly	Lys	Ala	Tyr	Ala	Asp	Val	Arg	Gly	Thr	Leu	Asp	Thr	Asp	325	330	335
Thr	Asn	Asp	Phe	Ile	Lys	Thr	Pro	Ser	Ala	Asn	Val	Val	Ala	Val	Ala	340	345	350
Pro	Gly	Ile	Lys	Thr	Glu	Asn	Ser	Asp	Ile	Lys	Ala	Ile	Ile	Asn	His	355	360	365
Ala	Asn	Asp	Ile	Val	Lys	Thr	Val	Thr	Glu	Arg	Lys	Ile	Gly	Thr	Ala	370	375	380
Thr	Asn	Ser	Ser	Thr	Ile	Ser	Lys	Thr	Glu	Asn	Ile	Asp	Lys	Glu	Ser	385	390	395
Pro	Val	Gly	Asn	Leu	Ala	Thr	Thr	Ala	Gln	Leu	Thr	Ile	Ala	Lys	Lys	405	410	415
Thr	Phe	Pro	Thr	Val	Asp	Phe	Ala	Met	Thr	Asn	Asn	Gly	Gly	Ile	Arg	420	425	430
Ser	Asp	Leu	Val	Val	Lys	Asn	Asp	Arg	Thr	Ile	Thr	Trp	Gly	Ala	Ala	435	440	445
Gln	Ala	Val	Gln	Pro	Phe	Gly	Asn	Ile	Leu	Gln	Val	Ile	Gln	Met	Thr	450	455	460
Gly	Gln	His	Ile	Tyr	Asp	Val	Leu	Asn	Gln	Gln	Tyr	Asp	Glu	Asn	Gln	465	470	475
Thr	Tyr	Phe	Leu	Gln	Met	Ser	Gly	Leu	Thr	Tyr	Thr	Tyr	Thr	Asp	Asn	485	490	495
Asp	Pro	Lys	Asn	Ser	Asp	Thr	Pro	Phe	Lys	Ile	Val	Lys	Val	Tyr	Lys	500	505	510
Asp	Asn	Gly	Glu	Glu	Ile	Asn	Leu	Thr	Thr	Thr	Tyr	Thr	Val	Val	Val	515	520	525
Asn	Asp	Phe	Leu	Tyr	Gly	Gly	Gly	Asp	Gly	Phe	Ser	Ala	Phe	Lys	Lys	530	535	540
Ala	Lys	Leu	Ile	Gly	Ala	Ile	Asn	Thr	Asp	Thr	Glu	Ala	Phe	Ile	Thr	545	550	555
Tyr	Ile	Thr	Asn	Leu	Glu	Ala	Ser	Gly	Lys	Thr	Val	Asn	Ala	Thr	Ile	565	570	575
Lys	Gly	Val	Lys	Asn	Tyr	Val	Thr	Ser	Asn	Leu	Glu	Ser	Ser	Thr	Lys			

			580					585				590					
Val	Asn	Ser	Ala	Gly	Lys	His	Ser	Ile	Ile	Ser	Lys	Val	Phe	Arg	Asn		
	595						600					605					
Arg	Asp	Gly	Asn	Thr	Val	Ser	Ser	Glu	Val	Ile	Ser	Asp	Leu	Leu	Thr		
	610					615					620						
Ser	Thr	Glu	Asn	Thr	Asn	Asn	Ser	Leu	Gly	Lys	Lys	Glu	Thr	Thr	Thr		
625					630					635					640		
Asn	Lys	Asn	Thr	Ile	Ser	Ser	Ser	Thr	Leu	Pro	Ile	Thr	Gly	Asp	Asn		
			645					650					655				
Tyr	Lys	Met	Ser	Pro	Ile	Met	Thr	Ile	Leu	Ala	Leu	Ile	Ser	Leu	Gly		
	660							665					670				
Gly	Leu	Asn	Ala	Phe	Ile	Lys	Lys	Arg	Lys	Ser							
	675						680										

<210> SEQ ID NO 45

<211> LENGTH: 3027

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 45

atgaagaaac	atcttaaaac	agttgccttg	accctcacta	cagtatcggt	agtcacccac	60
aatcaggaag	tttttagttt	agtcaaagag	ccaattctta	aacaaactca	agcttcttca	120
tcgatttctg	gcgctgacta	cgcagaaagt	agcggtaaaa	gcaagttaaa	gattaatgaa	180
acttctggcc	ctgttgatga	tacagtcact	gacttatttt	cggataaacg	tactactcct	240
gaaaaataa	aagataatct	tgctaaaggt	ccgagagaac	aagagttaaa	ggcagtaaca	300
gagaatacag	aatcagaaaa	gcagatcact	tctggatctc	aactagaaca	atcaaaagag	360
tctctttctt	taaataaaaac	agtgccatca	acgtctaatt	gggagatttg	tgattttatt	420
actaagggga	atacccttgt	tggtccttca	aaatcagggt	ttgaaaagtt	atctcaaact	480
gatcatctcg	tattgcctag	tcaagcagca	gatggaactc	aattgataca	agtagctagt	540
tttgctttta	ctccagataa	aaagacggca	attgcagaat	ataccagtag	ggctggagaa	600
aatggggaaa	taagccaact	agatgtggat	ggaaaagaaa	ttattaacga	aggtgagggt	660
tttaattctt	atctactaaa	gaaggtaaca	atcccaactg	gttataaaca	tattggtcaa	720
gatgcttttg	tggacaataa	gaatattgct	gaggttaatc	ttcctgaaag	cctcgagact	780
atttctgact	atgcttttgc	tcacctagct	ttgaaacaga	tcgatttgcc	agataattta	840
aaagcgattg	gagaattagc	tttttttgat	aatcaaatta	caggtaaact	ttctttgcc	900
cgtcagttaa	tgcgattagc	agaacgtgct	ttaaatcaa	accatatcaa	aacaattgag	960
tttagaggaa	atagtctaaa	agtgataggg	gaagctagtt	ttcaagataa	tgactctgag	1020
caactaatgc	tacctgacgg	tcttgaaaaa	atagaatcag	aagcttttac	aggaaatcca	1080
ggagatgata	actacaataa	ccgtgttggt	ttgtggacaa	aatctggaaa	aaatccttct	1140
ggtcttgcta	ctgaaaatac	ctatgttaat	cctgataagt	cactatggca	ggaaagtcct	1200
gagattgatt	atactaaatg	gttagaggaa	gattttacct	atcaaaaaaa	tagtggtaca	1260
ggtttttcaa	ataaaggcct	acaaaaagta	aaacgtaata	aaaacttaga	aattccaaaa	1320
cagcacaatg	gtgttactat	tactgaaatt	ggtgataatg	cttttcgcaa	tgttgatttt	1380
caaaataaaa	ctttacgtaa	atatgatttg	gaagaagtaa	agcttccttc	aactattcgg	1440
aaaatagggt	cttttgcttt	tcaatcta	aacttgaaat	cttttgaa	aagtgcgat	1500
ttagaagaga	ttaaagagg	agcctttatg	aataatcgta	ttgaaacctt	ggaattaaaa	1560
gataaattag	ttactattgg	tgatgcggct	ttccatatta	atcatattta	tgccattggt	1620
cttccagaat	ctgtacaaga	aatagggcgt	tcagcatttc	ggcaaaatgg	tgcaataaat	1680
cttattttta	tgggaagtaa	ggttaagacc	ttaggtgaga	tggcattttt	atcaaataga	1740
cttgaacatc	tggatctttc	tgagcaaaaa	cagtttacag	agattcctgt	tcaagccttt	1800
tcagacaatg	ccttgaaaaga	agtattatta	ccagcatcac	tgaaaacgat	tcgagaagaa	1860
gccttcaaaa	agaatcattt	aaaacaactg	gaagtggcat	ctgccttgct	ccatattgct	1920
tttaatgctt	tagatgataa	tgatggtgat	gaacaatttg	ataataaagt	ggttggttaa	1980
acgcataata	attcctacgc	actagcagat	ggtgagcatt	ttatcgttga	tccagataag	2040
ttatcttcta	caatagtaga	ccttgaaaag	attttaaaaa	taatcgaagg	tttagattat	2100
tctacattac	gtcagactac	tcaaaactcag	tttagagaca	tgactactgc	aggtaaagcg	2160
ttgttggtcaa	aatctaacct	ccgacaagga	gaaaaacaaa	aattccttca	agaagcacia	2220
tttttccttg	gccgcgttga	tttggataaa	gccatagcta	aagctgagaa	ggcttttagtg	2280

accaagaagg	caacaaagaa	tggtcagttg	cttgaaagaa	gtattaacaa	agcgggtatta	2340
gcttataata	atagcgctat	taaaaaagct	aatgttaagc	gcttggaata	agagtttagac	2400
ttgctaacag	gattagttga	gggaaaagga	ccattagcgc	aagctacaat	ggtacaagga	2460
gtttatttat	taaagacgcc	tttgccattg	ccagaatatt	atatcggatt	gaacgtttat	2520
tttgacaagt	ctggaaaatt	gatttatgca	cttgatatga	gtgatactat	tggtcgaggga	2580
caaaaagacg	cttatggtaa	tcctatatta	aatgttgacg	aggataatga	aggttatcat	2640
gccttggcag	ttgccacttt	agctgattat	gaggggctcg	acatcaaac	aattttaaat	2700
agtaagctta	gtcaattaac	atctattcgt	caggtaccga	ctgcagccta	tcatagagcc	2760
ggtattttcc	aagctatcca	aaatgcagcg	gcagaagcag	agcagttatt	gcctaaacca	2820
ggtacgcact	ctgagaagtc	aagctcaagt	gaatctgcta	actctaaaga	tagaggattg	2880
caatcaaacc	caaaaacgaa	tagaggacga	cactctgcaa	tattgcctag	gacagggtca	2940
aaaggcagct	ttgtctatgg	aatcttaggt	tacactagcg	ttgctttact	gtcactaata	3000
actgctataa	aaaagaaaaa	atattaa				3027

<210> SEQ ID NO 46

<211> LENGTH: 1008

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 46

Met	Lys	Lys	His	Leu	Lys	Thr	Val	Ala	Leu	Thr	Leu	Thr	Thr	Val	Ser
1				5					10					15	
Val	Val	Thr	His	Asn	Gln	Glu	Val	Phe	Ser	Leu	Val	Lys	Glu	Pro	Ile
			20					25					30		
Leu	Lys	Gln	Thr	Gln	Ala	Ser	Ser	Ser	Ile	Ser	Gly	Ala	Asp	Tyr	Ala
		35					40					45			
Glu	Ser	Ser	Gly	Lys	Ser	Lys	Leu	Lys	Ile	Asn	Glu	Thr	Ser	Gly	Pro
	50					55					60				
Val	Asp	Asp	Thr	Val	Thr	Asp	Leu	Phe	Ser	Asp	Lys	Arg	Thr	Thr	Pro
65					70					75					80
Glu	Lys	Ile	Lys	Asp	Asn	Leu	Ala	Lys	Gly	Pro	Arg	Glu	Gln	Glu	Leu
				85					90					95	
Lys	Ala	Val	Thr	Glu	Asn	Thr	Glu	Ser	Glu	Lys	Gln	Ile	Thr	Ser	Gly
			100					105					110		
Ser	Gln	Leu	Glu	Gln	Ser	Lys	Glu	Ser	Leu	Ser	Leu	Asn	Lys	Thr	Val
		115					120					125			
Pro	Ser	Thr	Ser	Asn	Trp	Glu	Ile	Cys	Asp	Phe	Ile	Thr	Lys	Gly	Asn
	130					135					140				
Thr	Leu	Val	Gly	Leu	Ser	Lys	Ser	Gly	Val	Glu	Lys	Leu	Ser	Gln	Thr
145					150					155					160
Asp	His	Leu	Val	Leu	Pro	Ser	Gln	Ala	Ala	Asp	Gly	Thr	Gln	Leu	Ile
				165					170					175	
Gln	Val	Ala	Ser	Phe	Ala	Phe	Thr	Pro	Asp	Lys	Lys	Thr	Ala	Ile	Ala
		180						185					190		
Glu	Tyr	Thr	Ser	Arg	Ala	Gly	Glu	Asn	Gly	Glu	Ile	Ser	Gln	Leu	Asp
	195						200					205			
Val	Asp	Gly	Lys	Glu	Ile	Ile	Asn	Glu	Gly	Glu	Val	Phe	Asn	Ser	Tyr
	210					215					220				
Leu	Leu	Lys	Lys	Val	Thr	Ile	Pro	Thr	Gly	Tyr	Lys	His	Ile	Gly	Gln
225					230					235					240
Asp	Ala	Phe	Val	Asp	Asn	Lys	Asn	Ile	Ala	Glu	Val	Asn	Leu	Pro	Glu
			245						250					255	
Ser	Leu	Glu	Thr	Ile	Ser	Asp	Tyr	Ala	Phe	Ala	His	Leu	Ala	Leu	Lys
		260						265					270		
Gln	Ile	Asp	Leu	Pro	Asp	Asn	Leu	Lys	Ala	Ile	Gly	Glu	Leu	Ala	Phe
	275						280					285			
Phe	Asp	Asn	Gln	Ile	Thr	Gly	Lys	Leu	Ser	Leu	Pro	Arg	Gln	Leu	Met
	290						295					300			

Arg	Leu	Ala	Glu	Arg	Ala	Phe	Lys	Ser	Asn	His	Ile	Lys	Thr	Ile	Glu	305	310	315	320
Phe	Arg	Gly	Asn	Ser	Leu	Lys	Val	Ile	Gly	Glu	Ala	Ser	Phe	Gln	Asp	325	330	335	
Asn	Asp	Leu	Ser	Gln	Leu	Met	Leu	Pro	Asp	Gly	Leu	Glu	Lys	Ile	Glu	340	345	350	
Ser	Glu	Ala	Phe	Thr	Gly	Asn	Pro	Gly	Asp	Asp	His	Tyr	Asn	Asn	Arg	355	360	365	
Val	Val	Leu	Trp	Thr	Lys	Ser	Gly	Lys	Asn	Pro	Ser	Gly	Leu	Ala	Thr	370	375	380	
Glu	Asn	Thr	Tyr	Val	Asn	Pro	Asp	Lys	Ser	Leu	Trp	Gln	Glu	Ser	Pro	385	390	395	400
Glu	Ile	Asp	Tyr	Thr	Lys	Trp	Leu	Glu	Glu	Asp	Phe	Thr	Tyr	Gln	Lys	405	410	415	
Asn	Ser	Val	Thr	Gly	Phe	Ser	Asn	Lys	Gly	Leu	Gln	Lys	Val	Lys	Arg	420	425	430	
Asn	Lys	Asn	Leu	Glu	Ile	Pro	Lys	Gln	His	Asn	Gly	Val	Thr	Ile	Thr	435	440	445	
Glu	Ile	Gly	Asp	Asn	Ala	Phe	Arg	Asn	Val	Asp	Phe	Gln	Asn	Lys	Thr	450	455	460	
Leu	Arg	Lys	Tyr	Asp	Leu	Glu	Glu	Val	Lys	Leu	Pro	Ser	Thr	Ile	Arg	465	470	475	480
Lys	Ile	Gly	Ala	Phe	Ala	Phe	Gln	Ser	Asn	Asn	Leu	Lys	Ser	Phe	Glu	485	490	495	
Ala	Ser	Asp	Asp	Leu	Glu	Glu	Ile	Lys	Glu	Gly	Ala	Phe	Met	Asn	Asn	500	505	510	
Arg	Ile	Glu	Thr	Leu	Glu	Leu	Lys	Asp	Lys	Leu	Val	Thr	Ile	Gly	Asp	515	520	525	
Ala	Ala	Phe	His	Ile	Asn	His	Ile	Tyr	Ala	Ile	Val	Leu	Pro	Glu	Ser	530	535	540	
Val	Gln	Glu	Ile	Gly	Arg	Ser	Ala	Phe	Arg	Gln	Asn	Gly	Ala	Asn	Asn	545	550	555	560
Leu	Ile	Phe	Met	Gly	Ser	Lys	Val	Lys	Thr	Leu	Gly	Glu	Met	Ala	Phe	565	570	575	
Leu	Ser	Asn	Arg	Leu	Glu	His	Leu	Asp	Leu	Ser	Glu	Gln	Lys	Gln	Phe	580	585	590	
Thr	Glu	Ile	Pro	Val	Gln	Ala	Phe	Ser	Asp	Asn	Ala	Leu	Lys	Glu	Val	595	600	605	
Leu	Leu	Pro	Ala	Ser	Leu	Lys	Thr	Ile	Arg	Glu	Glu	Ala	Phe	Lys	Lys	610	615	620	
Asn	His	Leu	Lys	Gln	Leu	Glu	Val	Ala	Ser	Ala	Leu	Ser	His	Ile	Ala	625	630	635	640
Phe	Asn	Ala	Leu	Asp	Asp	Asn	Asp	Gly	Asp	Glu	Gln	Phe	Asp	Asn	Lys	645	650	655	
Val	Val	Val	Lys	Thr	His	His	Asn	Ser	Tyr	Ala	Leu	Ala	Asp	Gly	Glu	660	665	670	
His	Phe	Ile	Val	Asp	Pro	Asp	Lys	Leu	Ser	Ser	Thr	Ile	Val	Asp	Leu	675	680	685	
Glu	Lys	Ile	Leu	Lys	Leu	Ile	Glu	Gly	Leu	Asp	Tyr	Ser	Thr	Leu	Arg	690	695	700	
Gln	Thr	Thr	Gln	Thr	Gln	Phe	Arg	Asp	Met	Thr	Thr	Ala	Gly	Lys	Ala	705	710	715	720
Leu	Leu	Ser	Lys	Ser	Asn	Leu	Arg	Gln	Gly	Glu	Lys	Gln	Lys	Phe	Leu	725	730	735	
Gln	Glu	Ala	Gln	Phe	Phe	Leu	Gly	Arg	Val	Asp	Leu	Asp	Lys	Ala	Ile	740	745	750	
Ala	Lys	Ala	Glu	Lys	Ala	Leu	Val	Thr	Lys	Lys	Ala	Thr	Lys	Asn	Gly				

tcaataggtta ccaacacaaaa accggaaaaa gatttctcaat caaagaataa aaaatcaggg 1260
gtggataaat ag 1272

<210> SEQ ID NO 48

<211> LENGTH: 423

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 48

Met	Ser	Lys	Arg	Gly	Lys	Ile	Lys	Ile	Thr	Thr	Lys	Thr	Lys	Leu	Ile
1				5					10					15	
Thr	Ala	Ser	Val	Ile	Thr	Leu	Val	Leu	Ile	Ile	Thr	Gly	Ile	Val	Leu
			20					25					30		
Trp	Lys	Gln	Arg	Asn	Thr	Leu	Thr	Ala	Asp	Ile	Ala	Lys	Glu	Pro	
		35				40					45				
Tyr	Ser	Thr	Val	Ser	Val	Thr	Glu	Gly	Ser	Ile	Ala	Ser	Ser	Thr	Leu
	50					55					60				
Leu	Ser	Gly	Thr	Val	Lys	Ala	Leu	Ser	Glu	Glu	Tyr	Ile	Tyr	Phe	Asp
65					70					75					80
Ala	Asn	Lys	Gly	Asn	Asp	Ala	Thr	Val	Thr	Val	Lys	Val	Gly	Asp	Gln
				85					90					95	
Val	Thr	Gln	Gly	Gln	Gln	Leu	Val	Gln	Tyr	Asn	Thr	Thr	Thr	Ala	Gln
			100					105					110		
Ser	Ala	Tyr	Asp	Thr	Ala	Val	Arg	Ser	Leu	Asn	Lys	Ile	Gly	Arg	Gln
		115				120						125			
Ile	Asn	His	Leu	Lys	Thr	Tyr	Gly	Val	Pro	Ala	Val	Ser	Thr	Glu	Thr
	130					135						140			
Asn	Arg	Asp	Glu	Ala	Thr	Gly	Glu	Glu	Thr	Thr	Thr	Thr	Val	Gln	Pro
145					150					155					160
Ser	Ala	Gln	Gln	Asn	Ala	Asn	Tyr	Lys	Gln	Gln	Leu	Gln	Asp	Leu	Asn
				165					170					175	
Asp	Ala	Tyr	Ala	Asp	Ala	Gln	Ala	Glu	Val	Asn	Lys	Ala	Gln	Ile	Ala
			180						185					190	
Leu	Asn	Asp	Thr	Val	Val	Ile	Ser	Ser	Val	Ser	Gly	Thr	Val	Val	Glu
		195					200					205			
Val	Asn	Asn	Asp	Ile	Asp	Pro	Ser	Ser	Lys	Asn	Ser	Gln	Thr	Leu	Val
	210					215					220				
His	Val	Ala	Thr	Glu	Gly	Gln	Leu	Gln	Val	Lys	Gly	Thr	Leu	Thr	Glu
225					230						235				240
Tyr	Asp	Leu	Ala	Asn	Val	Lys	Val	Gly	Gln	Ser	Val	Lys	Ile	Lys	Ser
				245					250					255	
Lys	Val	Tyr	Ser	Asn	Gln	Glu	Trp	Thr	Gly	Lys	Ile	Ser	Tyr	Val	Ser
			260					265					270		
Asn	Tyr	Pro	Thr	Glu	Ser	Asn	Ala	Gly	Ser	Thr	Thr	Pro	Ala	Gly	Ser
		275					280						285		
Thr	Gly	Ala	Gly	Ser	Ser	Thr	Gly	Ala	Thr	Tyr	Asp	Tyr	Lys	Ile	Asp
	290					295					300				
Ile	Ile	Ser	Pro	Leu	Asn	Gln	Leu	Lys	Gln	Gly	Phe	Thr	Val	Ser	Val
305					310					315					320
Glu	Val	Val	Asn	Glu	Ala	Lys	Gln	Ala	Leu	Val	Pro	Leu	Thr	Ala	Val
				325					330					335	
Ile	Lys	Lys	Asp	Lys	Lys	His	Tyr	Val	Trp	Thr	Tyr	Asp	Asp	Ala	Thr
			340					345					350		
Gly	Lys	Ala	Lys	Lys	Val	Glu	Val	Thr	Leu	Gly	Asn	Ala	Asp	Ala	Gln
		355					360					365			
Gln	Gln	Glu	Ile	His	Lys	Gly	Val	Ala	Val	Gly	Asp	Ile	Val	Ile	Ala
	370					375					380				
Asn	Pro	Asp	Lys	Asn	Ile	Lys	Pro	Asp	Lys	Lys	Leu	Glu	Gly	Val	Ile

Ala Glu Val Thr Phe Asn Glu Val Val Leu Val Gly Gly Asp Lys Thr
35 40 45
Val Val Gly Thr Pro Val Val Glu Gly Ala Thr Val Val Gly Thr Val
50 55 60
Glu Lys Gln Gly Lys Gln Lys Lys Val Val Thr Phe Lys Tyr Lys Pro
65 70 75 80
Lys Lys Gly Ser His Arg Lys Gln Gly His Arg Gln Pro Tyr Thr Lys
85 90 95
Val Val Ile Asn Ala Ile Asn Ala
100

<210> SEQ ID NO 53
<211> LENGTH: 1293
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 53

atgatactat tgaaaagcct ctataagggc ttttttgctg caatgaagga ggaaaathtt 60
gaggcaagat gttataatag agaaaaagga ggggtgtgtct tgattaaaac tatgcaatac 120
aaaaaaacga tggcaacagt tgttgctctt atcgtcgcac ttttgctatt tggcttgatt 180
tatgatattac ttgggggttca aaaaaatgag cttagcagctc aaaaatctgc tcagccaaag 240
gtcaaaacag cgcgtgttgt agctaattggc gacattttta ttcattgatat tctctacatg 300
agtgctagaa aagctgacga tacctatgat ttcactcctt attttgaata tgtaaggac 360
tggattagcg gtgctgactt agctattgga gattatgaag ggaccattag cccagattat 420
cccttagcag gctatccctt attcaatgct ccagaagaga ttgcaggtgc tctgaaaaat 480
actggctatg atgtagtcga ttttagcccat aatcatatct tagattccca attagacggt 540
gcccttaaca ctaaaaaggt ttttcatcaa ttaggtatag acagtattgg catctatgac 600
aaggatcggt caaaaagaatc cttcttaatt aaaaatgtca atggtatcaa aattgcaatt 660
ttaggttatt cttatgggtta taacggcatg gaggccacac ttagccaaga agactatgag 720
aaacacatgt ctgatattaga tgaagctaag ataaaaaaag aacttcagct agctgaaaaa 780
aaggctgacg tgaccattgt tatgccacaa atgggaacag aatatgcctt agaaccgaca 840
gcagaacaaa aagaacttta ccacaaaatg attgattggg gagctgacgt cgtcctagga 900
ggccatccgc atgttattga accttcagag acagttataa aaggtaggca aaagaaattc 960
attatttact ctatgggaaa ttttatttca aatcagcggc ttgaaaccgt agatgatatc 1020
tggactgagc gtggcctatt gatggacctt acttttgaga aaaaagataa caaaacaaaa 1080
attaaaaacag ttgaggccca tccaaccatg gttttagcca aaggtaaagg cattgtgggt 1140
aaagaagggt ttgaaactata caattatcga acaatgggtt tagaagattt tatcaaagg 1200
ggaaaatacc acgacaagat tgatgaggaa accaaagcaa aagtagcact tgcctatcag 1260
gaaattaatg atttagttaa cctgaaatgg taa 1293

<210> SEQ ID NO 54
<211> LENGTH: 430
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 54

Met Ile Leu Leu Lys Ser Leu Tyr Lys Gly Phe Phe Ala Ala Met Lys
1 5 10 15
Glu Glu Asn Phe Glu Ala Arg Cys Tyr Asn Arg Glu Lys Gly Gly Cys
20 25 30
Val Leu Ile Lys Thr Met Gln Tyr Lys Lys Thr Met Ala Thr Val Val
35 40 45
Ala Leu Ile Val Ala Leu Leu Phe Gly Leu Ile Tyr Asp Leu Leu
50 55 60
Gly Val Gln Lys Asn Glu Leu Ala Ala Gln Lys Ser Ala Gln Pro Lys
65 70 75 80
Val Lys Thr Ala Arg Val Val Ala Asn Gly Asp Ile Leu Ile His Asp
85 90 95
Ile Leu Tyr Met Ser Ala Arg Lys Ala Asp Asp Thr Tyr Asp Phe Thr

			100					105				110					
Pro	Tyr	Phe	Glu	Tyr	Val	Lys	Asp	Trp	Ile	Ser	Gly	Ala	Asp	Leu	Ala		
		115					120					125					
Ile	Gly	Asp	Tyr	Glu	Gly	Thr	Ile	Ser	Pro	Asp	Tyr	Pro	Leu	Ala	Gly		
	130					135					140						
Tyr	Pro	Leu	Phe	Asn	Ala	Pro	Glu	Glu	Ile	Ala	Gly	Ala	Leu	Lys	Asn		
145				150						155					160		
Thr	Gly	Tyr	Asp	Val	Val	Asp	Leu	Ala	His	Asn	His	Ile	Leu	Asp	Ser		
			165						170					175			
Gln	Leu	Asp	Gly	Ala	Leu	Asn	Thr	Lys	Lys	Val	Phe	His	Gln	Leu	Gly		
		180						185					190				
Ile	Asp	Ser	Ile	Gly	Ile	Tyr	Asp	Lys	Asp	Arg	Ser	Lys	Glu	Ser	Phe		
	195						200					205					
Leu	Ile	Lys	Asn	Val	Asn	Gly	Ile	Lys	Ile	Ala	Ile	Leu	Gly	Tyr	Ser		
	210					215					220						
Tyr	Gly	Tyr	Asn	Gly	Met	Glu	Ala	Thr	Leu	Ser	Gln	Glu	Asp	Tyr	Glu		
225				230						235					240		
Lys	His	Met	Ser	Asp	Leu	Asp	Glu	Ala	Lys	Ile	Lys	Lys	Glu	Leu	Gln		
			245						250					255			
Leu	Ala	Glu	Lys	Lys	Ala	Asp	Val	Thr	Ile	Val	Met	Pro	Gln	Met	Gly		
		260						265					270				
Thr	Glu	Tyr	Ala	Leu	Glu	Pro	Thr	Ala	Glu	Gln	Lys	Glu	Leu	Tyr	His		
	275						280					285					
Lys	Met	Ile	Asp	Trp	Gly	Ala	Asp	Val	Val	Leu	Gly	Gly	His	Pro	His		
	290					295					300						
Val	Ile	Glu	Pro	Ser	Glu	Thr	Val	Ile	Lys	Gly	Arg	Gln	Lys	Lys	Phe		
305				310						315					320		
Ile	Ile	Tyr	Ser	Met	Gly	Asn	Phe	Ile	Ser	Asn	Gln	Arg	Leu	Glu	Thr		
			325					330					335				
Val	Asp	Asp	Ile	Trp	Thr	Glu	Arg	Gly	Leu	Leu	Met	Asp	Leu	Thr	Phe		
		340						345				350					
Glu	Lys	Lys	Asp	Asn	Lys	Thr	Lys	Ile	Lys	Thr	Val	Glu	Ala	His	Pro		
	355						360					365					
Thr	Met	Val	Leu	Ala	Lys	Gly	Lys	Gly	Ile	Val	Gly	Lys	Glu	Gly	Phe		
	370					375					380						
Glu	Leu	Tyr	Asn	Tyr	Arg	Thr	Met	Val	Leu	Glu	Asp	Phe	Ile	Lys	Gly		
385				390						395					400		
Gly	Lys	Tyr	His	Asp	Lys	Ile	Asp	Glu	Glu	Thr	Lys	Ala	Lys	Val	Ala		
			405					410					415				
Leu	Ala	Tyr	Gln	Glu	Ile	Asn	Asp	Leu	Val	Asn	Leu	Lys	Trp				
		420						425				430					

<210> SEQ ID NO 55

<211> LENGTH: 2217

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 55

ttggagatga	catctttagg	aaaaaacgat	aaggaagttg	ctactgtgaa	gaaatttaaa	60
acacttatca	caggttttat	caacacaaga	ttgggtttta	taattactct	actcttttgt	120
tactggataa	agaccctgtg	ggcatatcat	acagactttt	cactagattt	gggaaatata	180
taccaagtct	ttctaactat	tatcaatcca	atcccactag	cttttttact	tttggggggt	240
gctcttttacg	ttaagaatac	ccgagccttt	tatatctgtt	cttgggtggt	ttatattaca	300
cttaacattc	tcttgatatc	aaattctata	tattaccgag	aattttcaga	ctttattaca	360
gtgagtgccca	tgctagctag	tagtaaagtc	tccgctggat	taggggactc	tgctttaaac	420
cttttacgca	tctgggatat	tatctatatt	cttgatttta	ttattcta	tagtttatct	480
atcgctaaaa	aaatcaaaaa	tgatcaacgt	ccttttaaca	agcgcgcagc	atttgccatc	540
accgctttat	ctagtctatt	gctttctatt	aatctttttt	tagcagaaat	tgatcgctcg	600


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gaactattaa cacgtggcctt ttcaaatact tatattgtga gagctttagg actaccagcg      660
tttaccctct atagcggcaa tcaaacctat caagctcaaa aagaacgaaa tggagctact      720
gcagaagaat taattgatgt taaaacttat gtcaaaggac attatgcagc acctgatcct      780
cagtattttg gaattggaaa aggcaaaaat attattgttc ttcatttaga aagctttcaa      840
caattcttaa tagattataa actaaaagaa ggagataaag aatatgaggt aacgcctttt      900
atcaactcac tttatcactc aaatgctacc ttagcattcc ctaacttttt tcatcagggt      960
aaagcaggta aaacttctga tgctgaaacc atgatggaga attccttatt tggtttaaat     1020
agtgggttctt ttatggtgaa ctacggtggt gaaaatacac aatttgctac tccaagtatt     1080
ttagcccaaa aagggtggcta taccagcgct gtctttcatg gtaacgttg gtaacgttg     1140
aatcgcaata atgcttataa acaatggggc tataattatt tttttgattc tagctacttc     1200
tctaaacaaa atagtaagaa ctcttttcaa tatgggttaa atgataagta catgtttaag     1260
gattccataa aatatcttga acagatgcaa caaccttttt ataccaagtt tatcactgtg     1320
agtaatcact atccttatac tagtctaaaa ggcgaaagta gtgaagaagg ttttccttta     1380
gccaaaacag acgatgaaac gatcaatggt tactttgcta ctgccaatta tttagacgct     1440
gcccttaaat ctttttttga ttacttgaaa gccactgggt tgtacgacaa ttctattttt     1500
gttttatatg gtgatcatta tggatattca aattctcgta attctagtct tgctccactt     1560
cttggtaaa gattctgaaac ttggtctgaa tatgataatg ctatgctaca acgagtcccc     1620
tatatgatcc atattccagg ttatacgaat ggtagtatca aagaaacctt tggcggtgaa     1680
atcgatgctc ttcctacttt actccacata cttgggtattg acactagtca gtttgttcaa     1740
ttaggacaag atttattatc acctcaaaat agccagattg tggcacaacg aacatctggg     1800
acttatatga ctctgaata cactaactat agtggacgtc tgtacaacac gcaaacaggt     1860
ttagaaatca ctaatcccga tgaaatgact atagccaaaa ctaaggaaat tcgctctgct     1920
gttgctcaac aactagcagc tagcgacgct attcaaacgg gtgatctcct gcgctttgat     1980
actcaaaatg gtctaaaagc tattgatcct aaccagttta tctacactaa gcagttaaaa     2040
caactgaaa g atatttcagc aaaactcgga tcagagtcaa caagtttata cagtaaaaaa     2100
ggtcataaat caactcagaa acttttttaa gcaccatctt acttagaact aaatcccgta     2160
gaagctgacg cggcaacttc tgaactaaaa gaggataacc ccaaaaataa agaataa      2217

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<210> SEQ ID NO 56

<211> LENGTH: 738

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 56

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Met Glu Met Thr Ser Leu Gly Lys Asn Asp Lys Glu Val Ala Thr Val
1          5          10          15
Lys Lys Phe Lys Thr Leu Ile Thr Gly Phe Ile Asn Thr Arg Leu Gly
20        25        30
Phe Ile Ile Thr Leu Leu Phe Cys Tyr Trp Ile Lys Thr Leu Trp Ala
35        40        45
Tyr His Thr Asp Phe Ser Leu Asp Leu Gly Asn Ile Tyr Gln Val Phe
50        55        60
Leu Thr Ile Ile Asn Pro Ile Pro Leu Ala Phe Leu Leu Leu Gly Val
65        70        75        80
Ala Leu Tyr Val Lys Asn Thr Arg Ala Phe Tyr Ile Cys Ser Trp Val
85        90        95
Val Tyr Ile Ile Leu Asn Ile Leu Leu Ile Ser Asn Ser Ile Tyr Tyr
100       105       110
Arg Glu Phe Ser Asp Phe Ile Thr Val Ser Ala Met Leu Ala Ser Ser
115       120       125
Lys Val Ser Ala Gly Leu Gly Asp Ser Ala Leu Asn Leu Leu Arg Ile
130       135       140
Trp Asp Ile Ile Tyr Ile Leu Asp Phe Ile Ile Leu Ile Ser Leu Ser
145       150       155       160
Ile Ala Lys Lys Ile Lys Asn Asp Gln Arg Pro Phe Asn Lys Arg Ala
165       170       175
Ala Phe Ala Ile Thr Ala Leu Ser Ser Leu Leu Leu Ser Ile Asn Leu
180       185       190

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Phe	Leu	Ala	Glu	Ile	Asp	Arg	Pro	Glu	Leu	Leu	Thr	Arg	Gly	Phe	Ser	195	200	205
Asn	Thr	Tyr	Ile	Val	Arg	Ala	Leu	Gly	Leu	Pro	Ala	Phe	Thr	Leu	Tyr	210	215	220
Ser	Gly	Asn	Gln	Thr	Tyr	Gln	Ala	Gln	Lys	Glu	Arg	Asn	Gly	Ala	Thr	225	230	235
Ala	Glu	Glu	Leu	Ile	Asp	Val	Lys	Thr	Tyr	Val	Lys	Gly	His	Tyr	Ala	245	250	255
Ala	Pro	Asp	Pro	Gln	Tyr	Phe	Gly	Ile	Gly	Lys	Gly	Lys	Asn	Ile	Ile	260	265	270
Val	Leu	His	Leu	Glu	Ser	Phe	Gln	Gln	Phe	Leu	Ile	Asp	Tyr	Lys	Leu	275	280	285
Lys	Glu	Gly	Asp	Lys	Glu	Tyr	Glu	Val	Thr	Pro	Phe	Ile	Asn	Ser	Leu	290	295	300
Tyr	His	Ser	Asn	Ala	Thr	Leu	Ala	Phe	Pro	Asn	Phe	Phe	His	Gln	Val	305	310	315
Lys	Ala	Gly	Lys	Thr	Ser	Asp	Ala	Glu	Thr	Met	Met	Glu	Asn	Ser	Leu	325	330	335
Phe	Gly	Leu	Asn	Ser	Gly	Ser	Phe	Met	Val	Asn	Tyr	Gly	Gly	Glu	Asn	340	345	350
Thr	Gln	Phe	Ala	Thr	Pro	Ser	Ile	Leu	Ala	Gln	Lys	Gly	Gly	Tyr	Thr	355	360	365
Ser	Ala	Val	Phe	His	Gly	Asn	Val	Gly	Thr	Phe	Trp	Asn	Arg	Asn	Asn	370	375	380
Ala	Tyr	Lys	Gln	Trp	Gly	Tyr	Asn	Tyr	Phe	Phe	Asp	Ser	Ser	Tyr	Phe	385	390	395
Ser	Lys	Gln	Asn	Ser	Lys	Asn	Ser	Phe	Gln	Tyr	Gly	Leu	Asn	Asp	Lys	405	410	415
Tyr	Met	Phe	Lys	Asp	Ser	Ile	Lys	Tyr	Leu	Glu	Gln	Met	Gln	Gln	Pro	420	425	430
Phe	Tyr	Thr	Lys	Phe	Ile	Thr	Val	Ser	Asn	His	Tyr	Pro	Tyr	Thr	Ser	435	440	445
Leu	Lys	Gly	Glu	Ser	Ser	Glu	Glu	Gly	Phe	Pro	Leu	Ala	Lys	Thr	Asp	450	455	460
Asp	Glu	Thr	Ile	Asn	Gly	Tyr	Phe	Ala	Thr	Ala	Asn	Tyr	Leu	Asp	Ala	465	470	475
Ala	Leu	Lys	Ser	Phe	Phe	Asp	Tyr	Leu	Lys	Ala	Thr	Gly	Leu	Tyr	Asp	485	490	495
Asn	Ser	Ile	Phe	Val	Leu	Tyr	Gly	Asp	His	Tyr	Gly	Ile	Ser	Asn	Ser	500	505	510
Arg	Asn	Ser	Ser	Leu	Ala	Pro	Leu	Leu	Gly	Lys	Asp	Ser	Glu	Thr	Trp	515	520	525
Ser	Glu	Tyr	Asp	Asn	Ala	Met	Leu	Gln	Arg	Val	Pro	Tyr	Met	Ile	His	530	535	540
Ile	Pro	Gly	Tyr	Thr	Asn	Gly	Ser	Ile	Lys	Glu	Thr	Phe	Gly	Gly	Glu	545	550	555
Ile	Asp	Ala	Leu	Pro	Thr	Leu	Leu	His	Ile	Leu	Gly	Ile	Asp	Thr	Ser	565	570	575
Gln	Phe	Val	Gln	Leu	Gly	Gln	Asp	Leu	Leu	Ser	Pro	Gln	Asn	Ser	Gln	580	585	590
Ile	Val	Ala	Gln	Arg	Thr	Ser	Gly	Thr	Tyr	Met	Thr	Pro	Glu	Tyr	Thr	595	600	605
Asn	Tyr	Ser	Gly	Arg	Leu	Tyr	Asn	Thr	Gln	Thr	Gly	Leu	Glu	Ile	Thr	610	615	620
Asn	Pro	Asp	Glu	Met	Thr	Ile	Ala	Lys	Thr	Lys	Glu	Ile	Arg	Ser	Ala	625	630	635
Val	Ala	Gln	Gln	Leu	Ala	Ala	Ser	Asp	Ala	Ile	Gln	Thr	Gly	Asp	Leu			

				645					650					655			
Leu	Arg	Phe	Asp	Thr	Gln	Asn	Gly	Leu	Lys	Ala	Ile	Asp	Pro	Asn	Gln		
			660					665					670				
Phe	Ile	Tyr	Thr	Lys	Gln	Leu	Lys	Gln	Leu	Lys	Asp	Ile	Ser	Ala	Lys		
		675					680					685					
Leu	Gly	Ser	Glu	Ser	Thr	Ser	Leu	Tyr	Ser	Lys	Asn	Gly	His	Lys	Ser		
	690					695					700						
Thr	Gln	Lys	Leu	Phe	Lys	Ala	Pro	Ser	Tyr	Leu	Glu	Leu	Asn	Pro	Val		
705					710				715						720		
Glu	Ala	Asp	Ala	Ala	Thr	Ser	Glu	Leu	Lys	Glu	Asp	Asn	Pro	Lys	Asn		
				725				730						735			
Lys	Glu																

<210> SEQ ID NO 57

<211> LENGTH: 813

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 57

atgaatttta	aaaaaataag	atttggtttt	ttgctttgcc	tcctacttta	tccttttagca	60
gcttgtaaca	agtctgaaca	acttaatcac	tacgaaagaa	ttaaaaaac	aagaaaatta	120
gtcgttgctg	taagccctga	ttatgctcct	tttgaattta	aagctttagt	taatggaaaa	180
gatactattg	ttggagcaga	tgttcaatta	gctcaggcta	ttgctgatga	attagacgtt	240
gatcttgagc	tttcaccaat	gagttttgat	aatgttttgt	ctagttttaca	gactggtaaa	300
gctgatcttg	ctatttcagg	aatctcacat	actaaagaaa	gagctaaagt	atatgatttt	360
tcaattcctt	actatcaggc	agaaaacgct	atagtgatga	gagcatctga	tgctaaagtg	420
acaaaaaata	ttagtgacct	aaacggtaag	aaagtagccg	ctcaaaaagg	tagtatcgag	480
gaagggtttag	ttaaaataca	attaccaaag	gccaatctga	tttctttgac	tgctatggga	540
gaagccatta	atgaactaaa	agcaggacaa	gtctatgcag	ttaccttaga	agcacctgta	600
gctgctgggt	ttttagccca	acataaggat	ctggcttttag	cacccttttag	cttaaaaacc	660
agtgatggag	atgccaaagc	agtggccctt	cctaaaaata	gtggagactt	aaccaaagcc	720
gttaataagg	ttattgctaa	gtagatgag	caagaacggt	acaagtcatt	tattgcagag	780
acaatagcac	taacgaaaaa	tactatgaag	taa			813

<210> SEQ ID NO 58

<211> LENGTH: 270

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 58

Met	Asn	Phe	Lys	Lys	Ile	Arg	Phe	Gly	Phe	Leu	Leu	Cys	Leu	Leu	Leu
1			5					10					15		
Tyr	Pro	Leu	Ala	Ala	Cys	Asn	Lys	Ser	Glu	Gln	Leu	Asn	His	Tyr	Glu
		20					25					30			
Arg	Ile	Lys	Lys	Thr	Arg	Lys	Leu	Val	Val	Ala	Val	Ser	Pro	Asp	Tyr
		35				40					45				
Ala	Pro	Phe	Glu	Phe	Lys	Ala	Leu	Val	Asn	Gly	Lys	Asp	Thr	Ile	Val
	50				55				60						
Gly	Ala	Asp	Val	Gln	Leu	Ala	Gln	Ala	Ile	Ala	Asp	Glu	Leu	Asp	Val
65			70					75					80		
Asp	Leu	Glu	Leu	Ser	Pro	Met	Ser	Phe	Asp	Asn	Val	Leu	Ser	Ser	Leu
		85					90					95			
Gln	Thr	Gly	Lys	Ala	Asp	Leu	Ala	Ile	Ser	Gly	Ile	Ser	His	Thr	Lys
		100					105					110			
Glu	Arg	Ala	Lys	Val	Tyr	Asp	Phe	Ser	Ile	Pro	Tyr	Tyr	Gln	Ala	Glu
	115					120					125				
Asn	Ala	Ile	Val	Met	Arg	Ala	Ser	Asp	Ala	Lys	Val	Thr	Lys	Asn	Ile
	130				135					140					
Ser	Asp	Leu	Asn	Gly	Lys	Lys	Val	Ala	Ala	Gln	Lys	Gly	Ser	Ile	Glu

145		150		155		160
Glu Gly Leu Val	Lys Ile Gln Leu Pro	Lys Ala Asn Leu Ile	Ser Leu			
	165	170	175			
Thr Ala Met Gly	Glu Ala Ile Asn Glu Leu Lys	Ala Gly Gln Val Tyr				
	180	185	190			
Ala Val Thr Leu	Glu Ala Pro Val Ala Ala Gly	Phe Leu Ala Gln His				
	195	200	205			
Lys Asp Leu Ala	Leu Ala Pro Phe Ser Leu Lys	Thr Ser Asp Gly Asp				
	210	215	220			
Ala Lys Ala Val	Ala Leu Pro Lys Asn Ser Gly	Asp Leu Thr Lys Ala				
	225	230	235			240
Val Asn Lys Val	Ile Ala Lys Leu Asp Glu Gln	Glu Arg Tyr Lys Ser				
	245	250	255			
Phe Ile Ala Glu	Thr Ile Ala Leu Thr Lys Asn	Thr Met Lys				
	260	265	270			

<210> SEQ ID NO 59

<211> LENGTH: 2733

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 59

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agtgttgaag	aagttacttc	acgccaaaat	ttgacttatg	ccaatgaaat	cgtaacacaa	120
aggccaaaga	gagaatctgt	tattagtgat	aaatcgaatt	ttcccgtcat	atcaccttac	180
ctagcaagtg	tggatttttg	tgagagaaaa	acacctttgc	caacacctga	taaaggagta	240
aaagtaacta	ctgaacagtc	tattgctcaa	gtaagaaaagg	ggcctgaaga	aagaccctat	300
actgttactg	gcaagattac	gagtgtgatc	aatggctggg	gaggctatgg	cttttatatt	360
caagatagtg	aaggatttgg	actttatggt	tatcctcaaa	aagatttagg	atacagtaag	420
ggagatattg	ttcaattaac	aggtacactt	actcgcttta	aagggtgattt	acaactccaa	480
cagggtgactg	cacacaaaaa	gttagagtta	tcttttccga	cttctgttaa	agaagcagta	540
atatcagaat	tagaaacaac	aacaccctca	acattagtta	agttatctca	cgtgacagtt	600
ggagaattat	caactgatca	atataacaac	acatctttcc	ttgtaaggga	tgatagtggg	660
aaaagtatag	ttgttcatat	agatcatcgt	acaggggtta	aaggggctga	tgttggtact	720
aaaataagtc	aggggtgattt	gattaacctc	acagccatat	tgtctattgt	tgatgggtcaa	780
ttacaattaa	gaccgttttc	tcttgaacaa	ttggaagtgg	ttaaaaagg	cacaagctca	840
aatagtgatg	cttcatctcg	taatattgtg	aaaataggcg	agattcaagg	agctagtcac	900
acgtcgccac	ttctcaaaaa	agcggtcacc	gtagaacagg	ttgttgtcac	ttatttagac	960
gattccactc	atttttatgt	tcaagatctt	aatgggtgatg	gtgatttagc	gacttcagat	1020
ggatttcgtg	tttttgctaa	aaacgctaag	gttcaagtcg	gcatgtttt	gaccatttca	1080
gggtgaagtgg	aagaattctt	tggtcgtggg	tatgaggaac	gtaagcagac	tgaccttacc	1140
atcacccaaa	ttgtggctaa	agcagtgacc	aaaacagggg	cagctcaagt	tccatcacccg	1200
cttgtttttag	ggaaagatcg	tatcgcgcca	gccaatatta	ttgataatga	tggcttgctg	1260
gtgtttgatc	cagaagaaga	cgctattgat	tattgggaat	caatggaagg	catgttagtg	1320
gcggttgatg	atgctaaaat	ccttgggtcca	atgaaaaata	aagaaattta	tgtcttacct	1380
ggctctagta	caagaccggt	aaataattca	gggtggagtat	tacttccagc	taattcttat	1440
aacacagatg	tgattcctgt	tcttttcaaa	aaaggcaaac	aaattattaa	agcaggagac	1500
tcttacaaaag	gaagatttagc	tgggccagta	tcttatagct	atggtaatta	caaggctctt	1560
gttgatgaca	gcaaaaaacat	gccaaagtta	atggatgggtc	atctaaaacc	tgaaaaaaca	1620
aacttgcaaa	aagaccttag	caagttaagc	attgcttctt	acaatattga	aaacttctca	1680
gccaatcctt	cttcaactaa	agatgagaag	gtcaaacgga	ttgccgaatc	ctttattcat	1740
gatctgaatg	ctccagacat	tattggatta	attgaagtcc	aagataataa	tgggccgact	1800
gatgatggga	caacggatgc	gacacaaagc	gcgcaacgcc	tcattgatgc	tattaaaaaa	1860
ctaggtggcc	caacttatcg	ttatgttgat	attgctccag	aaaataatgt	tgacggaggt	1920
caaccaggtg	gtaatatctg	aacaggattc	ctttatcaac	cagagcgcgt	cagcctttct	1980
gataagccaa	aaggcggtgc	tcgtgatgct	ctaacttggg	ttaatggaga	attaaacctt	2040
agtgttggtc	gaattgatcc	aactaacgcc	gcttggaagg	atgttcgtaa	atcactagca	2100
gcagaattta	tcttccaagg	tcgtaaaagtc	gttggtgttg	caaatcattt	gaactctaag	2160

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cgtgggggata atgctcttta tggttgtgtg caaccagtca cttttaaatc tgagcaaaga 2220
cgtcacgtct tggctaatat gctagcaciaa tttgcgaaag aaggggcaaa acaccaagct 2280
aatattgtga tgctaggtga ctttaaatgat tttgaattca caaagacgat tcaattaatc 2340
gaagaagggtg acatgggttaa cttgggtgagc cgacatgata tttcagatcg gtattcttat 2400
tttcaccaag gcaataatca gacccttgat aatatattag tttcacgcca tttacttgat 2460
cactacgaat ttgacatggt tcatgtgaat tccccattta tggaagctca cggacgcgca 2520
tcagatcatg atccattggt acttcaatta tcatttttcca aagaaaatga taaggcagag 2580
tcttctaaac aaagtgtaaa agctaaaaaaa acttcaaaaag gaaaactggt gccaaaaaca 2640
ggagatagtc ttgtttatgt gataacgcta ctaggaacgg ctagttttatt agtgcctatt 2700
ttattattga ctaaaggcaa aaaggaatca tag 2733

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<210> SEQ ID NO 60

<211> LENGTH: 910

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 60

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Met Ile Asn Lys Lys Cys Ile Ile Pro Val Ser Leu Leu Thr Leu Ala
1           5           10           15
Ile Thr Leu Thr Ser Val Glu Glu Val Thr Ser Arg Gln Asn Leu Thr
20           25           30
Tyr Ala Asn Glu Ile Val Thr Gln Arg Pro Lys Arg Glu Ser Val Ile
35           40           45
Ser Asp Lys Ser Asn Phe Pro Val Ile Ser Pro Tyr Leu Ala Ser Val
50           55           60
Asp Phe Gly Glu Arg Lys Thr Pro Leu Pro Thr Pro Asp Lys Gly Val
65           70           75           80
Lys Val Thr Thr Glu Gln Ser Ile Ala Gln Val Arg Lys Gly Pro Glu
85           90           95
Glu Arg Pro Tyr Thr Val Thr Gly Lys Ile Thr Ser Val Ile Asn Gly
100          105          110
Trp Gly Gly Tyr Gly Phe Tyr Ile Gln Asp Ser Glu Gly Ile Gly Leu
115          120          125
Tyr Val Tyr Pro Gln Lys Asp Leu Gly Tyr Ser Lys Gly Asp Ile Val
130          135          140
Gln Leu Thr Gly Thr Leu Thr Arg Phe Lys Gly Asp Leu Gln Leu Gln
145          150          155          160
Gln Val Thr Ala His Lys Lys Leu Glu Leu Ser Phe Pro Thr Ser Val
165          170          175
Lys Glu Ala Val Ile Ser Glu Leu Glu Thr Thr Thr Pro Ser Thr Leu
180          185          190
Val Lys Leu Ser His Val Thr Val Gly Glu Leu Ser Thr Asp Gln Tyr
195          200          205
Asn Asn Thr Ser Phe Leu Val Arg Asp Asp Ser Gly Lys Ser Ile Val
210          215          220
Val His Ile Asp His Arg Thr Gly Val Lys Gly Ala Asp Val Val Thr
225          230          235          240
Lys Ile Ser Gln Gly Asp Leu Ile Asn Leu Thr Ala Ile Leu Ser Ile
245          250          255
Val Asp Gly Gln Leu Gln Leu Arg Pro Phe Ser Leu Glu Gln Leu Glu
260          265          270
Val Val Lys Lys Val Thr Ser Ser Asn Ser Asp Ala Ser Ser Arg Asn
275          280          285
Ile Val Lys Ile Gly Glu Ile Gln Gly Ala Ser His Thr Ser Pro Leu
290          295          300
Leu Lys Lys Ala Val Thr Val Glu Gln Val Val Val Thr Tyr Leu Asp
305          310          315          320
Asp Ser Thr His Phe Tyr Val Gln Asp Leu Asn Gly Asp Gly Asp Leu

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Ala	Thr	Ser	Asp	Gly	Ile	Arg	Val	Phe	Ala	Lys	Asn	Ala	Lys	Val	Gln	325	330	335
																340	345	350
Val	Gly	Asp	Val	Leu	Thr	Ile	Ser	Gly	Glu	Val	Glu	Glu	Phe	Phe	Gly			
																355	360	365
Arg	Gly	Tyr	Glu	Glu	Arg	Lys	Gln	Thr	Asp	Leu	Thr	Ile	Thr	Gln	Ile			
																370	375	380
Val	Ala	Lys	Ala	Val	Thr	Lys	Thr	Gly	Thr	Ala	Gln	Val	Pro	Ser	Pro			
																385	390	400
Leu	Val	Leu	Gly	Lys	Asp	Arg	Ile	Ala	Pro	Ala	Asn	Ile	Ile	Asp	Asn			
																405	410	415
Asp	Gly	Leu	Arg	Val	Phe	Asp	Pro	Glu	Glu	Asp	Ala	Ile	Asp	Tyr	Trp			
																420	425	430
Glu	Ser	Met	Glu	Gly	Met	Leu	Val	Ala	Val	Asp	Asp	Ala	Lys	Ile	Leu			
																435	440	445
Gly	Pro	Met	Lys	Asn	Lys	Glu	Ile	Tyr	Val	Leu	Pro	Gly	Ser	Ser	Thr			
																450	455	460
Arg	Pro	Leu	Asn	Asn	Ser	Gly	Gly	Val	Leu	Leu	Pro	Ala	Asn	Ser	Tyr			
																465	470	475
Asn	Thr	Asp	Val	Ile	Pro	Val	Leu	Phe	Lys	Lys	Gly	Lys	Gln	Ile	Ile			
																485	490	495
Lys	Ala	Gly	Asp	Ser	Tyr	Lys	Gly	Arg	Leu	Ala	Gly	Pro	Val	Ser	Tyr			
																500	505	510
Ser	Tyr	Gly	Asn	Tyr	Lys	Val	Phe	Val	Asp	Asp	Ser	Lys	Asn	Met	Pro			
																515	520	525
Ser	Leu	Met	Asp	Gly	His	Leu	Lys	Pro	Glu	Lys	Thr	Asn	Leu	Gln	Lys			
																530	535	540
Asp	Leu	Ser	Lys	Leu	Ser	Ile	Ala	Ser	Tyr	Asn	Ile	Glu	Asn	Phe	Ser			
																545	550	555
Ala	Asn	Pro	Ser	Ser	Thr	Lys	Asp	Glu	Lys	Val	Lys	Arg	Ile	Ala	Glu			
																565	570	575
Ser	Phe	Ile	His	Asp	Leu	Asn	Ala	Pro	Asp	Ile	Ile	Gly	Leu	Ile	Glu			
																580	585	590
Val	Gln	Asp	Asn	Asn	Gly	Pro	Thr	Asp	Asp	Gly	Thr	Thr	Asp	Ala	Thr			
																595	600	605
Gln	Ser	Ala	Gln	Arg	Leu	Ile	Asp	Ala	Ile	Lys	Lys	Leu	Gly	Gly	Pro			
																610	615	620
Thr	Tyr	Arg	Tyr	Val	Asp	Ile	Ala	Pro	Glu	Asn	Asn	Val	Asp	Gly	Gly			
																625	630	635
Gln	Pro	Gly	Gly	Asn	Ile	Arg	Thr	Gly	Phe	Leu	Tyr	Gln	Pro	Glu	Arg			
																645	650	655
Val	Ser	Leu	Ser	Asp	Lys	Pro	Lys	Gly	Gly	Ala	Arg	Asp	Ala	Leu	Thr			
																660	665	670
Trp	Val	Asn	Gly	Glu	Leu	Asn	Leu	Ser	Val	Gly	Arg	Ile	Asp	Pro	Thr			
																675	680	685
Asn	Ala	Ala	Trp	Lys	Asp	Val	Arg	Lys	Ser	Leu	Ala	Ala	Glu	Phe	Ile			
																690	695	700
Phe	Gln	Gly	Arg	Lys	Val	Val	Val	Val	Ala	Asn	His	Leu	Asn	Ser	Lys			
																705	710	715
Arg	Gly	Asp	Asn	Ala	Leu	Tyr	Gly	Cys	Val	Gln	Pro	Val	Thr	Phe	Lys			
																725	730	735
Ser	Glu	Gln	Arg	His	Val	Leu	Ala	Asn	Met	Leu	Ala	Gln	Phe	Ala				
																740	745	750
Lys	Glu	Gly	Ala	Lys	His	Gln	Ala	Asn	Ile	Val	Met	Leu	Gly	Asp	Phe			
																755	760	765
Asn	Asp	Phe	Glu	Phe	Thr	Lys	Thr	Ile	Gln	Leu	Ile	Glu	Glu	Gly	Asp			
																770	775	780

Met	Val	Asn	Leu	Val	Ser	Arg	His	Asp	Ile	Ser	Asp	Arg	Tyr	Ser	Tyr
785					790					795					800
Phe	His	Gln	Gly	Asn	Asn	Gln	Thr	Leu	Asp	Asn	Ile	Leu	Val	Ser	Arg
			805						810					815	
His	Leu	Leu	Asp	His	Tyr	Glu	Phe	Asp	Met	Val	His	Val	Asn	Ser	Pro
			820					825					830		
Phe	Met	Glu	Ala	His	Gly	Arg	Ala	Ser	Asp	His	Asp	Pro	Leu	Leu	Leu
		835					840					845			
Gln	Leu	Ser	Phe	Ser	Lys	Glu	Asn	Asp	Lys	Ala	Glu	Ser	Ser	Lys	Gln
	850					855					860				
Ser	Val	Lys	Ala	Lys	Lys	Thr	Ser	Lys	Gly	Lys	Leu	Leu	Pro	Lys	Thr
865					870					875					880
Gly	Asp	Ser	Leu	Val	Tyr	Val	Ile	Thr	Leu	Leu	Gly	Thr	Ala	Ser	Leu
			885						890					895	
Leu	Val	Pro	Ile	Leu	Leu	Leu	Thr	Lys	Gly	Lys	Lys	Glu	Ser		
			900					905					910		

<210> SEQ ID NO 61

<211> LENGTH: 6180

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 61

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ttcagccaat	ctaattggcgt	gatggttgta	aaggctgcgg	aagtgccggc	gacagattta	180
tcacgtcagg	cgtctgattc	ggagagggtg	gatgaatcgt	ctttattgca	gaaagaaaac	240
ttatcagtag	attcatttaa	attagaaaat	ttaaattggat	gggaagctga	aaatgatata	300
gcaggtaatt	tggggaaaatt	taaagatcca	gatagtccgg	gctatcaaaa	tattttgaca	360
tcatctggaa	agaatatcag	tgtagctgtt	gctcccaaag	gttcaggtaa	aatgaacatt	420
aaagtaacta	aaagatcaaa	ttttcagggt	ggatattatg	taggtggtct	tagaactcaa	480
actccggtat	tgaagttaaa	tgatgtttat	cgatattcct	ttacaactaa	aaaattatca	540
ggaaattcct	cagagttcaa	aacgagagtt	aagcccgttg	aatctaataa	taaactaggg	600
aaagagcttg	ttattagggt	ggataataaa	aatgtatcta	ctaagcatga	ttggcttcca	660
gacatctctg	atggaaactca	tactgtggac	ttcactggtc	ttgataaaaa	attatctgtt	720
gcttttcagat	tttctccaag	acaaacttcg	aatgttgttt	acgaattttc	taacataaat	780
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agcgtcttgt	cgggtactgc	aatatcttct	ggagatacat	tagaaaaaag	aaaatcgfff	900
gatggcgata	tcctaagagt	ttataaagat	agcaaaatca	ttgctagaac	agtaataaaa	960
ggcaataagt	gggatgttaa	actttcaaag	cctcttattg	caggtgaaaa	attagatttt	1020
gagattttgc	atccgagatc	tcaaaacggt	agtaaaaaaa	tttcaaaaca	agtcgaagct	1080
aaaccatttg	atccagcttc	ctataaagaa	aaagttatag	ccaaattaaa	gccggtttat	1140
gaagctacta	gtgaaaaaat	cacaaatgat	gcttggttgg	atgaaaatgc	gaaggatttg	1200
caaaaaacaaa	aattagaaga	acaatatatt	tctggaaaag	tagcgatatc	agaggctgga	1260
actaaacaag	aagctataga	tgcagcatat	aataaatatt	caagtcaaac	agatccagac	1320
tctcttccta	gtcagtataa	acaaggtaat	aaagaaaatg	aacaagaaaa	agggcgtaaa	1380
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agtgttaatc	aaacagtatc	attagaacag	ttgaagcaac	ggttaatagt	gtataaagct	1560
tctgaaaaag	attcagagaa	aaaagaatat	cctgagtcaa	ttcctaatac	gcatattcca	1620
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actcttgaaa	aaatcaatca	agataaatgg	ttgacgccag	accaacaagc	tgaacagtta	1740
aaacaagcgg	aagttacttt	taaaaaaggc	caagaagcaa	ttaaaagtgc	tcagacttta	1800
actcagcttg	agacagactt	agctgattat	gtttctgaga	atgaaggtaa	gggaaattct	1860
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cttaaggaag	ctcacgaagc	tactaaacaa	gcaatttgaa	aagatccatg	gttgagtccg	1980
gaacagaaaa	aagctcaaaa	agaaaaagcc	aaagcaagac	tagatgaggg	cttgaaagct	2040
cttaaagctg	cagatagttt	agagatttct	aaagtgcag	aagaagcttt	cgttgataaa	2100

gaaaaaaatc	cagattcaat	tccaaatcaa	cataaagctg	gaactgctga	tcaagctaga	2160
aaacaagctt	tagatagttt	agataaggag	gttcaaaaag	agttagagtc	aattgataac	2220
gataatactc	taacaactga	tgagaaaagca	gctgctaaga	aaaaagtcaa	tgacgcttat	2280
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gatgagtctt	tatctaattt	acctcataaa	caaggaacgc	cgcttaaaga	tcaacaatct	2400
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aaaacattac	caagagacga	aaaagagaaa	caaattgctg	actctaagga	acgcttaaaa	2520
tctgacacgc	aaaaagttaa	agatgctaaa	aatgctgatg	ctattaaaaa	agcatttgaa	2580
gaagggaaaag	tgaatattcc	tcaagcacat	atcccagggtg	atttgaacaa	ggataaagaa	2640
aaacttcttg	cagaattgaa	gcaaaaagca	gatgatactg	aaaaagctat	tgatgttgat	2700
aaaactctga	cagaagatga	gaaaaaagag	caaaaagtca	aaacaaaagc	tgaacttgaa	2760
aaagctaaaa	ctgatgttaa	aaatactcag	acacgtgaag	aactagataa	aaaagttcca	2820
gaacttaaga	aagctattga	agacactcac	gttaaaggta	atcttgaagg	tgtaagaat	2880
aaggctattg	aagatcttaa	aaaagctcat	actgaaacag	ttgctaaaaa	aaatgggtgat	2940
gatacccttg	acaaagctac	taaagaagct	caagtgaag	aagtgacaa	agctttggca	3000
gcaggtaaaag	atgcgatcac	taaagcagat	gatgctgata	aagtaagtac	agctgttaca	3060
gagcacacac	caaaaattaa	agcagcacat	aaaactgggtg	accttaaaaa	agctcaagta	3120
gatgctaaca	cagctcttga	caaagcagct	gaaaaagaac	gtggagaaat	caataaagat	3180
gctacactaa	cgacagaaga	taaagcaaaa	caactgaaag	aagttgagac	agctcttact	3240
aaagctaaag	ataacgtgaa	agctgctaag	acagcagacg	ctatcaatga	cgacagtgat	3300
aaaggcgtag	caacaattga	tgccgtccat	aaagcaggtc	aagacttagg	tgctcgtaag	3360
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<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 62

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Leu Gly Val Ala Val Pro Thr Gly Phe Ser Gln Ser Asn Gly Val Met
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Val Val Lys Ala Ala Glu Val Pro Ala Thr Asp Leu Ser Arg Gln Ala
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Ser Asp Ser Glu Arg Val Asp Glu Ser Ser Leu Leu Gln Lys Glu Asn
65           70           75           80
Leu Ser Val Asp Ser Phe Lys Leu Glu Asn Leu Asn Gly Trp Glu Ala
          85           90           95
Glu Asn Asp Thr Ala Gly Asn Leu Gly Lys Phe Lys Asp Pro Asp Ser
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Ser Gly Tyr Gln Asn Ile Leu Thr Ser Ser Gly Lys Asn Ile Ser Val
          115          120          125
Ala Val Ala Pro Lys Gly Ser Gly Lys Met Asn Ile Lys Val Thr Lys
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Arg Ser Asn Phe Gln Gly Gly Tyr Tyr Val Gly Gly Leu Arg Thr Gln
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Lys Lys Leu Ser Gly Asn Ser Ser Glu Phe Lys Thr Arg Val Lys Pro
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Val Glu Ser Asn Asn Lys Leu Gly Lys Glu Leu Val Ile Arg Val Asp
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Gly Thr His Thr Val Asp Phe Thr Gly Leu Asp Lys Lys Leu Ser Val
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Ser Asn Ile Asn Ile Lys Asn Ile Ser Pro Ala Ser Val Pro Ala Ile
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Pro Ser Lys Val Leu Glu Gly Thr Ser Val Leu Ser Gly Thr Ala Ile
          275          280          285
Ser Ser Gly Asp Thr Leu Glu Lys Arg Lys Ser Phe Asp Gly Asp Ile
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Leu Arg Val Tyr Lys Asp Ser Lys Ile Ile Ala Arg Thr Val Ile Lys
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Gln	Lys	Gln	Lys	Leu	Glu	Glu	Gln	Tyr	Ile	Ser	Gly	Lys	Val	Ala	Ile	
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Thr	Arg	Asp	Leu	Thr	Leu	Lys	Ala	Ile	Gln	Glu	Asp	Lys	Trp	Leu	Thr	
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Glu	Gln	Glu	Lys	Thr	Ile	Gln	Lys	Glu	Glu	Ala	Leu	Lys	Ala	Phe	Glu	
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Thr	Gly	Ile	Glu	Ser	Val	Asn	Gln	Thr	Val	Ser	Leu	Glu	Gln	Leu	Lys	
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Gln	Arg	Leu	Ile	Val	Tyr	Lys	Ala	Ser	Glu	Lys	Asp	Ser	Glu	Lys	Lys	
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Glu	Val	Lys	Ala	Ala	Lys	Gln	Glu	Glu	Leu	Lys	Lys	Leu	His	Asp	Thr	
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Thr	Leu	Glu	Lys	Ile	Asn	Gln	Asp	Lys	Trp	Leu	Thr	Pro	Asp	Gln	Gln	
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Leu	Lys	Glu	Ala	His	Glu	Ala	Thr	Lys	Gln	Ala	Ile	Glu	Lys	Asp	Pro	
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Asp	Ser	Ile	Pro	Asn	Gln	His	Lys	Ala	Gly	Thr	Ala	Asp	Gln	Ala	Arg	
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Ile Glu Gly Asp Lys Thr Leu Pro Arg Asp Glu Lys Glu Lys Gln Ile				
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Lys Leu Leu Ala Glu Leu Lys Gln Lys Ala Asp Asp Thr Glu Lys Ala				
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Ile Asp Val Asp Lys Thr Leu Thr Glu Asp Glu Lys Lys Glu Gln Lys				
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Val Lys Thr Lys Ala Glu Leu Glu Lys Ala Lys Thr Asp Val Lys Asn				
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Thr Gln Thr Arg Glu Glu Leu Asp Lys Lys Val Pro Glu Leu Lys Lys				
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Ala Ile Glu Asp Thr His Val Lys Gly Asn Leu Glu Gly Val Lys Asn				
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Lys Glu Ala Asp Lys Ala Leu Ala Ala Gly Lys Asp Ala Ile Thr Lys				
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Pro Lys Ile Lys Ala Ala His Lys Thr Gly Asp Leu Lys Lys Ala				
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Gln Asp Leu Gly Ala Arg Lys Ser Gly Gln Val Ala Lys Leu Glu				
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Glu Leu Lys Lys Ala Ile Glu Ala Val Asn Ala Ala Asp Thr Ala				
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1895	Glu Asn	Leu Gly Thr Val	1900	Ala Ile Arg Ser Ala	1905	Tyr Val Ala Gly
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tctaaaggta aaatgacagc agccgagtac aaagattact acactactgg ttataaaaact      1200
gacgtggaac aaatcaaaat caatggtaag aaaaagacca tgacctttgt tcgtaatggg      1260
gaaaagaaaa ccttcactta cacatacgcc ggcaaagaaa tcttgacctt tccaaaagga      1320
aatcgcgggg ttcgtttcat gtttgaagct aaagaagcag atgctggcga attcaaatac      1380
gttcaattca gtgaccatgc cattgctcct gaaaaagcaa agcatttcca cctgtactgg      1440
ggtggtgaca gccaagaaaa attacataaa gagttagaac attggccaac ttactacggt      1500
tcagacttat ctggtcgtga aatcgcccaa gaaatcaatg ctcattaa      1548

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<210> SEQ ID NO 64
<211> LENGTH: 515
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 64
Met Lys Lys Lys Ile Leu Leu Met Met Ser Leu Ile Ser Val Phe Phe
1          5          10          15
Ala Trp Gln Leu Thr Gln Ala Lys Gln Val Leu Ala Glu Gly Lys Val
20          25          30
Lys Val Val Thr Thr Phe Tyr Pro Val Tyr Glu Phe Thr Lys Gly Val
35          40          45
Ile Gly Asn Asp Gly Asp Val Phe Met Leu Met Lys Ala Gly Thr Asp
50          55          60
Pro His Asp Phe Glu Pro Ser Thr Lys Ala Ile Lys Lys Ile Gln Asp
65          70          75          80
Ala Asp Ala Phe Val Tyr Met Asp Asp Asn Met Glu Thr Trp Val Ser
85          90          95
Asp Val Lys Lys Ser Leu Thr Ser Lys Lys Val Thr Ile Val Lys Gly
100         105         110
Thr Gly Asn Met Leu Leu Val Ala Gly Ala Gly His Asp His Pro His
115         120         125
Glu Asp Ala Asp Lys Lys His Glu His Asn Lys His Ser Glu Glu Gly
130         135         140
His Asn His Ala Phe Asp Pro His Val Trp Leu Ser Pro Tyr Arg Ser
145         150         155         160

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Ile	Thr	Val	Val	Glu	Asn	Ile	Arg	Asp	Ser	Leu	Ser	Lys	Ala	Tyr	Pro		
				165					170					175			
Glu	Lys	Ala	Glu	Asn	Phe	Lys	Ala	Asn	Ala	Ala	Thr	Tyr	Ile	Glu	Lys		
			180					185					190				
Leu	Lys	Glu	Leu	Asp	Lys	Asp	Tyr	Thr	Ala	Ala	Leu	Ser	Asp	Ala	Lys		
		195				200						205					
Gln	Lys	Ser	Phe	Val	Thr	Gln	His	Ala	Ala	Phe	Gly	Tyr	Met	Ala	Leu		
	210				215						220						
Asp	Tyr	Gly	Leu	Asn	Gln	Ile	Ser	Ile	Asn	Gly	Val	Thr	Pro	Asp	Ala		
225				230					235					240			
Glu	Pro	Ser	Ala	Lys	Arg	Ile	Ala	Thr	Leu	Ser	Lys	Tyr	Val	Lys	Lys		
			245						250					255			
Tyr	Gly	Ile	Lys	Tyr	Ile	Tyr	Phe	Glu	Glu	Asn	Ala	Ser	Ser	Lys	Val		
	260						265						270				
Ala	Lys	Thr	Leu	Ala	Lys	Glu	Ala	Gly	Val	Lys	Ala	Ala	Val	Leu	Ser		
	275					280						285					
Pro	Leu	Glu	Gly	Leu	Thr	Glu	Lys	Glu	Met	Lys	Ala	Gly	Gln	Asp	Tyr		
	290				295					300							
Phe	Thr	Val	Met	Arg	Lys	Asn	Leu	Glu	Thr	Leu	Arg	Leu	Thr	Thr	Asp		
305				310					315					320			
Val	Ala	Gly	Lys	Glu	Ile	Leu	Pro	Glu	Lys	Asp	Thr	Thr	Lys	Thr	Val		
			325					330					335				
Tyr	Asn	Gly	Tyr	Phe	Lys	Asp	Lys	Glu	Val	Lys	Asp	Arg	Gln	Leu	Ser		
	340					345						350					
Asp	Trp	Ser	Gly	Ser	Trp	Gln	Ser	Val	Tyr	Pro	Tyr	Leu	Gln	Asp	Gly		
	355				360							365					
Thr	Leu	Asp	Gln	Val	Trp	Asp	Tyr	Lys	Ala	Lys	Lys	Ser	Lys	Gly	Lys		
	370				375						380						
Met	Thr	Ala	Ala	Glu	Tyr	Lys	Asp	Tyr	Tyr	Thr	Thr	Gly	Tyr	Lys	Thr		
385				390					395				400				
Asp	Val	Glu	Gln	Ile	Lys	Ile	Asn	Gly	Lys	Lys	Lys	Thr	Met	Thr	Phe		
			405					410					415				
Val	Arg	Asn	Gly	Glu	Lys	Lys	Thr	Phe	Thr	Tyr	Thr	Tyr	Ala	Gly	Lys		
		420					425						430				
Glu	Ile	Leu	Thr	Tyr	Pro	Lys	Gly	Asn	Arg	Gly	Val	Arg	Phe	Met	Phe		
	435					440						445					
Glu	Ala	Lys	Glu	Ala	Asp	Ala	Gly	Glu	Phe	Lys	Tyr	Val	Gln	Phe	Ser		
	450				455						460						
Asp	His	Ala	Ile	Ala	Pro	Glu	Lys	Ala	Lys	His	Phe	His	Leu	Tyr	Trp		
465				470					475				480				
Gly	Gly	Asp	Ser	Gln	Glu	Lys	Leu	His	Lys	Glu	Leu	Glu	His	Trp	Pro		
			485				490						495				
Thr	Tyr	Tyr	Gly	Ser	Asp	Leu	Ser	Gly	Arg	Glu	Ile	Ala	Gln	Glu	Ile		
			500				505						510				
Asn	Ala	His															
		515															

<210> SEQ ID NO 65

<211> LENGTH: 1248

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 65

atggcctacc	gtctatctat	aaaatatatt	ttattggagg	cttttcctaa	aatggcaaaa	60
gaaaaatacg	atcgtagtaa	acccacggtt	aacattggta	caatcggaca	cgttgaccat	120
ggtaaaacta	ctttaacagc	tgcaatcaca	actgtattgg	cacgtcgctt	gccttcacat	180
gttaaccaac	caaaaagatta	cgcttctatc	gatgctgctc	cagaagaacg	cgaacgcgga	240
atcactatca	acactgcaca	cgttgagtac	gaaactgcaa	ctcgtcacta	tgcgcacatc	300

gacgctccag	gacacgcgga	ctacgttaaa	aacatgatca	ctggtgccgc	tcaaattggac	360
ggagctatcc	ttgtagttgc	ttcaactgat	ggaccaatgc	cacaaactcg	tgagcacatc	420
cttctttcac	gtcaggttgg	tgtaaacac	cttatcgtgt	tcatgaacaa	agttgacctt	480
gttgatgacg	aagagttgct	tgaattagtt	gagatggaaa	ttcgtgacct	tctttcagaa	540
tacgatttcc	caggtgatga	ccttccagtt	atccaaggtt	cagctcttaa	agctcttgaa	600
ggcgacacta	aatttgaaga	catcatcatg	gaattgatgg	atactgttga	ttcatacatt	660
ccagaaccag	aacgcgacac	tgacaaacca	ttgcttcttc	cagtcgaaga	cgtattctca	720
attacaggtc	gtggtacagt	tgcttcagga	cgtatcgacc	gtggtactgt	tcgtgtcaac	780
gacgaaatcg	aaatcgttgg	tatcaaagaa	gaaactaaaa	aagctgttgt	tactggtgtt	840
gaaatgttcc	gtaaacaact	tgacgaaggt	cttgcaggag	acaacgtagg	tatccttctt	900
cgtggtgttc	aacgtgacga	aatcgaacgt	ggccaagtta	ttgctaaacc	aagttcaatc	960
aacccacaca	ctaaattcaa	aggtgaagta	tatatccttt	ctaaagacga	aggtggacgt	1020
cacactccat	tcttcaacaa	ctaccgtcca	caattctact	tccgtacaac	tgacgtaaca	1080
ggttcaatcg	aacttccagc	aggtacagaa	atgggttatgc	ctgggtgataa	cgtgacaatc	1140
aacggttgagt	tgatccaccc	aatcgccgta	gaacaaggta	ctactttctc	aatccgtgaa	1200
ggtggacgta	ctggttggttc	aggtatcgtt	tcagaaatcg	aagcttaa		1248

<210> SEQ ID NO 66

<211> LENGTH: 415

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 66

Met	Ala	Tyr	Arg	Leu	Ser	Ile	Lys	Tyr	Ile	Leu	Leu	Glu	Ala	Phe	Pro
1				5					10					15	
Lys	Met	Ala	Lys	Glu	Lys	Tyr	Asp	Arg	Ser	Lys	Pro	His	Val	Asn	Ile
			20					25					30		
Gly	Thr	Ile	Gly	His	Val	Asp	His	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Ala
		35					40					45			
Ile	Thr	Thr	Val	Leu	Ala	Arg	Arg	Leu	Pro	Ser	Ser	Val	Asn	Gln	Pro
	50					55					60				
Lys	Asp	Tyr	Ala	Ser	Ile	Asp	Ala	Ala	Pro	Glu	Glu	Arg	Glu	Arg	Gly
65				70						75				80	
Ile	Thr	Ile	Asn	Thr	Ala	His	Val	Glu	Tyr	Glu	Thr	Ala	Thr	Arg	His
			85					90					95		
Tyr	Ala	His	Ile	Asp	Ala	Pro	Gly	His	Ala	Asp	Tyr	Val	Lys	Asn	Met
			100					105					110		
Ile	Thr	Gly	Ala	Ala	Gln	Met	Asp	Gly	Ala	Ile	Leu	Val	Val	Ala	Ser
	115						120					125			
Thr	Asp	Gly	Pro	Met	Pro	Gln	Thr	Arg	Glu	His	Ile	Leu	Leu	Ser	Arg
	130					135					140				
Gln	Val	Gly	Val	Lys	His	Leu	Ile	Val	Phe	Met	Asn	Lys	Val	Asp	Leu
145				150					155					160	
Val	Asp	Asp	Glu	Glu	Leu	Leu	Glu	Leu	Val	Glu	Met	Glu	Ile	Arg	Asp
			165					170					175		
Leu	Leu	Ser	Glu	Tyr	Asp	Phe	Pro	Gly	Asp	Asp	Leu	Pro	Val	Ile	Gln
		180						185					190		
Gly	Ser	Ala	Leu	Lys	Ala	Leu	Glu	Gly	Asp	Thr	Lys	Phe	Glu	Asp	Ile
	195						200					205			
Ile	Met	Glu	Leu	Met	Asp	Thr	Val	Asp	Ser	Tyr	Ile	Pro	Glu	Pro	Glu
	210					215					220				
Arg	Asp	Thr	Asp	Lys	Pro	Leu	Leu	Leu	Pro	Val	Glu	Asp	Val	Phe	Ser
225				230						235				240	
Ile	Thr	Gly	Arg	Gly	Thr	Val	Ala	Ser	Gly	Arg	Ile	Asp	Arg	Gly	Thr
			245					250					255		
Val	Arg	Val	Asn	Asp	Glu	Ile	Glu	Ile	Val	Gly	Ile	Lys	Glu	Glu	Thr
		260					265					270			
Lys	Lys	Ala	Val	Val	Thr	Gly	Val	Glu	Met	Phe	Arg	Lys	Gln	Leu	Asp

<400> SEQUENCE: 69

```
atgaaaatta cagttgtagg cattggatac gttggattat cgatagggct cctacttgca      60
aaggaacacg acgtcacctt ttttgatatt gataataaaa aaattgattt aataaataaaa    120
aggcaatccc ctcttaaaga agcagctata aacaaacttt tatgtaaggc aaaaaatatt    180
aatgcaactt cttctgaaga attagcatat aaggatgcga ctttcataat cttgtctttg    240
ccaaccaacc taaaatttaa taagcttgat acttccatta tcgaaatttc tgtaagtaat    300
attttaaaga taaacaaaaa ggctacaatt gtaataaagt cgacagttcc aattggtttt    360
acagaatatt taaggaatcg atttcactac aacgatatca ttttttcacc tgagttcctt    420
agggaaggat caactattca tgatcaattg tatecttcga gaactatagt tggaaatgaa    480
tctagaaatt ctcaattatt cttagacata ctaacagata tatcggttga aaaagactcg    540
ccatctttat tagttggctc ttctgaagca gaagcgataa agttattttc gaatgcatac    600
ttggcacaaa aaattgcttt ttttaatgag ttggatacgt ttgctgaaat gcaaaatttg    660
gactcaaaaa aaattattga ggctatggga tatgaccaga gaataggaaa ttcgcacaat    720
aatccttctt tcggttttgg tgggtactgt cttcctaagg atattaagca attagagtat    780
catttttaaag aaattccagc accaattatt accagtataa gtgaatctaa tttattaaga    840
aaaattcata tagcaaaaaa gattttgaac agctcagcta aaacaatagg aatttataga    900
attaattcca aaaaagattc ggataattgt agggaatctt ctacaattga tgttgctaaa    960
cttctaaaaa gcagtggtaa ggatgtttatc atctttgagc ccttaattaa caaaaaaag   1020
tttttggggt gccctttaag taatgatttt aatgaattta ttaaattttc ggatattata   1080
gttgccaata gaatagatga tgctctgaga aaatgtaatt caaaagtttt tacacgtgat   1140
atttttcagt atgattaa                                     1158
```

<210> SEQ ID NO 70

<211> LENGTH: 385

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 70

```
Met Lys Ile Thr Val Val Gly Ile Gly Tyr Val Gly Leu Ser Ile Gly
1          5          10          15
Leu Leu Leu Ala Lys Glu His Asp Val Thr Phe Phe Asp Ile Asp Asn
20        25        30
Lys Lys Ile Asp Leu Ile Asn Lys Arg Gln Ser Pro Leu Lys Glu Ala
35        40        45
Ala Ile Asn Lys Leu Leu Cys Lys Ala Lys Asn Ile Asn Ala Thr Ser
50        55        60
Ser Glu Glu Leu Ala Tyr Lys Asp Ala Thr Phe Ile Ile Leu Ser Leu
65        70        75        80
Pro Thr Asn Leu Lys Phe Asn Lys Leu Asp Thr Ser Ile Ile Glu Ile
85        90        95
Ser Val Ser Asn Ile Leu Lys Ile Asn Lys Lys Ala Thr Ile Val Ile
100       105       110
Lys Ser Thr Val Pro Ile Gly Phe Thr Glu Tyr Leu Arg Asn Arg Phe
115       120       125
His Tyr Asn Asp Ile Ile Phe Ser Pro Glu Phe Leu Arg Glu Gly Ser
130       135       140
Thr Ile His Asp Gln Leu Tyr Pro Ser Arg Thr Ile Val Gly Asn Glu
145       150       155       160
Ser Arg Asn Ser Gln Leu Phe Leu Asp Ile Leu Thr Asp Ile Ser Val
165       170       175
Glu Lys Asp Ser Pro Ser Leu Leu Val Gly Ser Ser Glu Ala Glu Ala
180       185       190
Ile Lys Leu Phe Ser Asn Ala Tyr Leu Ala Gln Lys Ile Ala Phe Phe
195       200       205
Asn Glu Leu Asp Thr Phe Ala Glu Met Gln Asn Leu Asp Ser Lys Lys
210       215       220
Ile Ile Glu Ala Met Gly Tyr Asp Gln Arg Ile Gly Asn Ser His Asn
225       230       235       240
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Asn	Pro	Ser	Phe	Gly	Phe	Gly	Gly	Tyr	Cys	Leu	Pro	Lys	Asp	Ile	Lys
				245					250					255	
Gln	Leu	Glu	Tyr	His	Phe	Lys	Glu	Ile	Pro	Ala	Pro	Ile	Ile	Thr	Ser
			260					265					270		
Ile	Ser	Glu	Ser	Asn	Leu	Leu	Arg	Lys	Ile	His	Ile	Ala	Lys	Met	Ile
		275					280					285			
Leu	Asn	Ser	Ser	Ala	Lys	Thr	Ile	Gly	Ile	Tyr	Arg	Ile	Asn	Ser	Lys
	290					295					300				
Lys	Asp	Ser	Asp	Asn	Cys	Arg	Glu	Ser	Ser	Thr	Ile	Asp	Val	Ala	Lys
305					310					315				320	
Leu	Leu	Lys	Ser	Ser	Gly	Lys	Asp	Val	Ile	Ile	Phe	Glu	Pro	Leu	Ile
				325				330						335	
Asn	Gln	Lys	Lys	Phe	Leu	Gly	Cys	Pro	Leu	Ser	Asn	Asp	Phe	Asn	Glu
		340						345					350		
Phe	Ile	Lys	Tyr	Ser	Asp	Ile	Ile	Val	Ala	Asn	Arg	Ile	Asp	Asp	Ala
	355					360					365				
Leu	Arg	Lys	Cys	Asn	Ser	Lys	Val	Phe	Thr	Arg	Asp	Ile	Phe	Gln	Tyr
	370					375					380				
Asp															
385															

<210> SEQ ID NO 71

<211> LENGTH: 1170

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 71

atgattatta	ctaaaaagag	cttattttgtg	acaagtgtcg	ctttgtcggt	agtacctttg	60
gcgacagcgc	aggcacaaga	gtggacacca	cgatcgggta	cagaaatcaa	gtctgaactc	120
gtcctagttg	ataatgtttt	tacttatact	gtaaaatacg	gtgacacttt	aagcacaatt	180
gctgaagcaa	tggggattga	tgtgcatgtc	ttaggagata	ttaatcatat	tgctaattat	240
gacctaattt	ttccagacac	gatcctaaca	gcaaactaca	atcaacacgg	tcaggcaacg	300
aatttgacgg	ttcaagcacc	tgcttctagt	ccagctagcg	ttagtcatgt	acctagcagt	360
gagccattac	cccaagcatc	tgccacctct	caaccgactg	ttcctatggc	accacctgcg	420
acaccatctg	atgtcccaac	gacaccattc	gcctctgcaa	agccagatag	ttctgtgaca	480
gcgtcatctg	agctcacatc	gtcaacgaat	gatgtttcga	ctgagttgtc	tagcgaatca	540
caaaagcagc	cagaagtacc	acaagaagca	gttccaactc	ctaaagcagc	tgaaacgact	600
gaagtcgaac	ctaagacaga	catctcagaa	gccccaaactt	cagctaatag	gcctgtacct	660
aacgagagtg	cttcagaaga	agtttcttct	gcggccccag	cacaagcccc	agcagaaaaa	720
gaagaaacct	ctgcgccagc	agcacaaaaa	gctgtagctg	acaccacaag	tggtgcaacc	780
tcaaatggcc	tttcttacgc	tccaaaccat	gcctacaatc	caatgaatgc	agggcttcaa	840
ccacaaacag	cagccttcaa	agaagaagtg	gcttctgcct	ttgggtattac	gtcatttagt	900
ggttaccgtc	caggtgatcc	aggagatcat	ggtaaagggt	tggccattga	ttttatgggtg	960
cctgaaaatt	ctgctcttgg	tgatcaagtt	gctcaatatg	ccattgacca	tatggcagag	1020
cgtgggtatt	catacgttat	ttggaaacag	cgattctatg	cgccatttgc	aagtattttac	1080
ggaccagcct	acacatggaa	ccccatgcca	gatcgcggca	gtattacaga	aaaccattat	1140
gatcatgttc	atgtctcctt	taatgcttaa				1170

<210> SEQ ID NO 72

<211> LENGTH: 389

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 72

Met	Ile	Ile	Thr	Lys	Lys	Ser	Leu	Phe	Val	Thr	Ser	Val	Ala	Leu	Ser
1				5					10					15	
Leu	Val	Pro	Leu	Ala	Thr	Ala	Gln	Ala	Gln	Glu	Trp	Thr	Pro	Arg	Ser
			20				25					30			
Val	Thr	Glu	Ile	Lys	Ser	Glu	Leu	Val	Leu	Val	Asp	Asn	Val	Phe	Thr

atggctatcg	taggtcgtct	tggacgtgtc	cttggacctc	gtaacttgat	gccaaaccct	420
aaaactggta	cagtaacgat	ggatgttgct	aaagccgttg	aagagtctaa	aggtggtaaa	480
atcacttacc	gtgctgacaa	agcaggtaat	gttcaagctc	ttattggtaa	agtttcattt	540
gatgctgaca	aattggttga	aaacttcaaa	gccttccacg	atgtaatggc	taaagctaaa	600
cctgcaacag	ctaaaggaac	ttacatggca	aacgtctcaa	tcacatcaac	acaaggtgtt	660
ggatatcaagg	ttgatcctaa	ctcacttttaa				690

<210> SEQ ID NO 74

<211> LENGTH: 228

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 74

Met	Ala	Lys	Lys	Ser	Lys	Gln	Met	Arg	Ala	Ala	Leu	Glu	Lys	Val	Asp	
1				5					10					15		
Ser	Thr	Lys	Ala	Tyr	Ser	Val	Glu	Glu	Ala	Val	Ala	Leu	Val	Lys	Glu	
		20						25					30			
Thr	Asn	Phe	Ala	Lys	Phe	Asp	Ala	Ser	Val	Glu	Val	Ala	Tyr	Asn	Leu	
	35						40						45			
Asn	Ile	Asp	Val	Arg	Lys	Ala	Asp	Gln	Gln	Ile	Arg	Gly	Ala	Met	Val	
	50					55					60					
Leu	Pro	Asn	Gly	Thr	Gly	Lys	Thr	Gln	Arg	Val	Leu	Val	Phe	Ala	Arg	
65					70					75					80	
Gly	Ala	Lys	Ala	Glu	Glu	Ala	Lys	Ala	Ala	Gly	Ala	Asp	Phe	Val	Gly	
				85					90					95		
Glu	Asp	Asp	Leu	Val	Ala	Lys	Ile	Asn	Gly	Gly	Trp	Leu	Asp	Phe	Asp	
			100					105					110			
Val	Val	Ile	Ala	Thr	Pro	Asp	Met	Met	Ala	Ile	Val	Gly	Arg	Leu	Gly	
	115						120						125			
Arg	Val	Leu	Gly	Pro	Arg	Asn	Leu	Met	Pro	Asn	Pro	Lys	Thr	Gly	Thr	
	130					135						140				
Val	Thr	Met	Asp	Val	Ala	Lys	Ala	Val	Glu	Glu	Ser	Lys	Gly	Gly	Lys	
145					150					155					160	
Ile	Thr	Tyr	Arg	Ala	Asp	Lys	Ala	Gly	Asn	Val	Gln	Ala	Leu	Ile	Gly	
			165					170						175		
Lys	Val	Ser	Phe	Asp	Ala	Asp	Lys	Leu	Val	Glu	Asn	Phe	Lys	Ala	Phe	
			180					185					190			
His	Asp	Val	Met	Ala	Lys	Ala	Lys	Pro	Ala	Thr	Ala	Lys	Gly	Thr	Tyr	
	195						200						205			
Met	Ala	Asn	Val	Ser	Ile	Thr	Ser	Thr	Gln	Gly	Val	Gly	Ile	Lys	Val	
	210					215					220					
Asp	Pro	Asn	Ser													
225																

<210> SEQ ID NO 75

<211> LENGTH: 498

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 75

atgcaatatt	gcatatctgt	gggaggtaaa	aatctcaatt	accgccaaaa	ccacaacagg	60
aggattttta	aaatggctaa	aaaagtcgaa	aaacttgtaa	aacttcaa	ccctgctggt	120
aaagctacac	cagctccacc	agttggacca	gctcttggtc	aagcagggtat	caacatcatg	180
ggcttcacta	aagaatttaa	cgctcgtaca	gctgatcaag	ctggtatgat	catcccagtt	240
ggtatctcag	tttatgaaga	caaatcattt	gatttcatca	ctaaaacacc	accagctgct	300
gttcttttga	aaaaagctgc	aggtgttgaa	aaaggatcag	gtacacctaa	cactactaag	360
gttgcgacag	ttactcgtgc	acaagtacaa	gaaattgctg	aaactaagat	gccagatttg	420
aacgctgcaa	acattgaagc	tgcaatgcgt	atgatcgaag	gtactgctcg	ttctatggga	480
ttcactgtta	ctgactag					498

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<210> SEQ ID NO 76
<211> LENGTH: 165
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 76
Met Gln Tyr Cys Ile Ser Val Gly Gly Lys Asn Leu Asn Tyr Arg Gln
1          5          10          15
Asn His Asn Arg Arg Ile Phe Lys Met Ala Lys Lys Val Glu Lys Leu
20          25          30
Val Lys Leu Gln Ile Pro Ala Gly Lys Ala Thr Pro Ala Pro Pro Val
35          40          45
Gly Pro Ala Leu Gly Gln Ala Gly Ile Asn Ile Met Gly Phe Thr Lys
50          55          60
Glu Phe Asn Ala Arg Thr Ala Asp Gln Ala Gly Met Ile Ile Pro Val
65          70          75          80
Val Ile Ser Val Tyr Glu Asp Lys Ser Phe Asp Phe Ile Thr Lys Thr
85          90          95
Pro Pro Ala Ala Val Leu Leu Lys Lys Ala Ala Gly Val Glu Lys Gly
100         105         110
Ser Gly Thr Pro Asn Thr Thr Lys Val Ala Thr Val Thr Arg Ala Gln
115         120         125
Val Gln Glu Ile Ala Glu Thr Lys Met Pro Asp Leu Asn Ala Ala Asn
130         135         140
Ile Glu Ala Ala Met Arg Met Ile Glu Gly Thr Ala Arg Ser Met Gly
145         150         155         160
Phe Thr Val Thr Asp
165

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<210> SEQ ID NO 77
<211> LENGTH: 807
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 77
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gaatctgttg accgcgctat aaaaggcgat aaatacattg atgaaaaaac tgccaaagaa      120
gaaagcgaag cagcttctaa agcctatgaa gaaagcattc aaaaagctct caaagctgat      180
gctagccaat ttccacaact aaccaaagaa gtcggcaag aagaagctaa ggtagctaat      240
aggacaagtc aaggggacat tacccttaag ttattcccaa aatatgctcc ctagctgtt      300
gagaacttcc tcacccatgc taaaaaaggc tactatgata accttacctt ccacgtgtg      360
atcaacgact ttatgattca atcaggtgac ccaaaggag atggcacagg tggtagaatc      420
atttgaaaag gcaaggatcc taaaaaagat gctggcaatg gctttgtcaa cgaaatctct      480
ccatttttat atcatattcg cggtgctctt gccatggcaa atgctggtgc taatactaac      540
ggtagccaat tttatatcaa ccaaacaag aaaaatcaaa gcaagggtat atcaagtacc      600
aactacccaa aacctatcat ctctgcctat gagcatggcg gcaatccaag ctagatggc      660
ggttatactg tatttggtca agtcattgat ggtatggatg ttgtcgataa aattgccgct      720
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gtcaaaagatt atcgctttaa aaactaa
807

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<210> SEQ ID NO 78
<211> LENGTH: 268
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 78
Met Lys Lys Leu Leu Ser Leu Ser Leu Val Ala Ile Ser Leu Leu Asn
1          5          10          15
Leu Ser Ala Cys Glu Ser Val Asp Arg Ala Ile Lys Gly Asp Lys Tyr

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ggtaaagcca	tctattcaga	gtctgtcgac	tttaaagaca	taaaagatag	cctaggttat	1380
gataaatcgc	atcaatttgc	ttatgtcaaaa	gagtcaactg	atgcgggtta	taacgcacaa	1440
gacgttaaag	gtaaaattgc	tttaattgaa	cgtgatccca	ataaaaccta	tgacgaaatg	1500
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caatcaaaacc	gctcaatgcy	tctaaccagct	aatgggatgg	ggataccatc	tgctttcata	1620
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gtcccagcca	atggaaaaagt	gactgtaaag	gttaccatgg	atgtctcaca	gttcacaaaa	2340
gagctaacaa	aacagatgcc	aaatgggttac	tatctagaag	gttttgctcg	ctttagagat	2400
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aatagtgaca	ttagatttgc	aaaatcaacg	accctgttag	gcacagcatt	ttctggaaaa	2940
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tcaactgggtg atcataaggt tatgtcaaaa aataattcac aggctttgac agcctctgcc	4800
acaccaacca agtcaacgac ctcagcaaca gcaaaagccc taccatcaac gggtgaaaaa	4860
atgggtctca agttgcgcat agtaggtctt gtgttactcg gacttacttg cgtctttagc	4920
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<210> SEQ ID NO 80

<211> LENGTH: 1647

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 80

Met	Glu	Lys	Lys	Gln	Arg	Phe	Ser	Leu	Arg	Lys	Tyr	Lys	Ser	Gly	Thr
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Phe	Ser	Val	Leu	Ile	Gly	Ser	Val	Phe	Leu	Val	Met	Thr	Thr	Thr	Val
			20					25					30		
Ala	Ala	Asp	Glu	Leu	Ser	Thr	Met	Ser	Glu	Pro	Thr	Ile	Thr	Asn	His
		35					40					45			
Ala	Gln	Gln	Gln	Ala	Gln	His	Leu	Thr	Asn	Thr	Glu	Leu	Ser	Ser	Ala
	50					55					60				
Glu	Ser	Lys	Ser	Gln	Asp	Thr	Ser	Gln	Ile	Thr	Leu	Lys	Thr	Asn	Arg
65					70					75					80
Glu	Lys	Glu	Gln	Ser	Gln	Asp	Leu	Val	Ser	Glu	Pro	Thr	Thr	Thr	Glu
				85					90					95	
Leu	Ala	Asp	Thr	Asp	Ala	Ala	Ser	Met	Ala	Asn	Thr	Gly	Ser	Asp	Ala
			100					105					110		
Thr	Gln	Lys	Ser	Ala	Ser	Leu	Pro	Pro	Val	Asn	Thr	Asp	Val	His	Asp
		115					120					125			
Trp	Val	Lys	Thr	Lys	Gly	Ala	Trp	Asp	Lys	Gly	Tyr	Lys	Gly	Gln	Gly
	130					135					140				
Lys	Val	Val	Ala	Val	Ile	Asp	Thr	Gly	Ile	Asp	Pro	Ala	His	Gln	Ser
145					150					155					160
Met	Arg	Ile	Ser	Asp	Val	Ser	Thr	Ala	Lys	Val	Lys	Ser	Lys	Glu	Asp
				165					170					175	
Met	Leu	Ala	Arg	Gln	Lys	Ala	Ala	Gly	Ile	Asn	Tyr	Gly	Ser	Trp	Ile
			180					185					190		
Asn	Asp	Lys	Val	Val	Phe	Ala	His	Asn	Tyr	Val	Glu	Asn	Ser	Asp	Asn
		195					200					205			
Ile	Lys	Glu	Asn	Gln	Phe	Glu	Asp	Phe	Asp	Glu	Asp	Trp	Glu	Asn	Phe
	210					215					220				
Glu	Phe	Asp	Ala	Glu	Ala	Glu	Pro	Lys	Ala	Ile	Lys	Lys	His	Lys	Ile
225					230					235					240
Tyr	Arg	Pro	Gln	Ser	Thr	Gln	Ala	Pro	Lys	Glu	Thr	Val	Ile	Lys	Thr
				245					250					255	
Glu	Glu	Thr	Asp	Gly	Ser	His	Asp	Ile	Asp	Trp	Thr	Gln	Thr	Asp	Asp
			260					265					270		
Asp	Thr	Lys	Tyr	Glu	Ser	His	Gly	Met	His	Val	Thr	Gly	Ile	Val	Ala
		275					280					285			
Gly	Asn	Ser	Lys	Glu	Ala	Ala	Ala	Thr	Gly	Glu	Arg	Phe	Leu	Gly	Ile
	290					295					300				
Ala	Pro	Glu	Ala	Gln	Val	Met	Phe	Met	Arg	Val	Phe	Ala	Asn	Asp	Ile
305					310					315					320
Met	Gly	Ser	Ala	Glu	Ser	Leu	Phe	Ile	Lys	Ala	Ile	Glu	Asp	Ala	Val
				325					330					335	
Ala	Leu	Gly	Ala	Asp	Val	Ile	Asn	Leu	Ser	Leu	Gly	Thr	Ala	Asn	Gly
			340					345					350		
Ala	Gln	Leu	Ser	Gly	Ser	Lys	Pro	Leu	Met	Glu	Ala	Ile	Glu	Lys	Ala

		355					360				365					
Lys	Lys	Ala	Gly	Val	Ser	Val	Val	Val	Ala	Ala	Gly	Asn	Glu	Arg	Val	
	370					375					380					
Tyr	Gly	Ser	Asp	His	Asp	Asp	Pro	Leu	Ala	Thr	Asn	Pro	Asp	Tyr	Gly	
385					390						395				400	
Leu	Val	Gly	Ser	Pro	Ser	Thr	Gly	Arg	Thr	Pro	Thr	Ser	Val	Ala	Ala	
				405					410					415		
Ile	Asn	Ser	Lys	Trp	Val	Ile	Gln	Arg	Leu	Met	Thr	Val	Lys	Glu	Leu	
			420					425					430			
Glu	Asn	Arg	Ala	Asp	Leu	Asn	His	Gly	Lys	Ala	Ile	Tyr	Ser	Glu	Ser	
		435					440					445				
Val	Asp	Phe	Lys	Asp	Ile	Lys	Asp	Ser	Leu	Gly	Tyr	Asp	Lys	Ser	His	
	450					455					460					
Gln	Phe	Ala	Tyr	Val	Lys	Glu	Ser	Thr	Asp	Ala	Gly	Tyr	Asn	Ala	Gln	
465					470					475					480	
Asp	Val	Lys	Gly	Lys	Ile	Ala	Leu	Ile	Glu	Arg	Asp	Pro	Asn	Lys	Thr	
				485					490					495		
Tyr	Asp	Glu	Met	Ile	Ala	Leu	Ala	Lys	Lys	His	Gly	Ala	Leu	Gly	Val	
			500					505					510			
Leu	Ile	Phe	Asn	Asn	Lys	Pro	Gly	Gln	Ser	Asn	Arg	Ser	Met	Arg	Leu	
		515					520					525				
Thr	Ala	Asn	Gly	Met	Gly	Ile	Pro	Ser	Ala	Phe	Ile	Ser	His	Glu	Phe	
	530					535					540					
Gly	Lys	Ala	Met	Ser	Gln	Leu	Asn	Gly	Asn	Gly	Thr	Gly	Ser	Leu	Glu	
545					550					555					560	
Phe	Asp	Ser	Val	Val	Ser	Lys	Ala	Pro	Ser	Gln	Lys	Gly	Asn	Glu	Met	
				565					570					575		
Asn	His	Phe	Ser	Asn	Trp	Gly	Leu	Thr	Ser	Asp	Gly	Tyr	Leu	Lys	Pro	
			580					585					590			
Asp	Ile	Thr	Ala	Pro	Gly	Gly	Asp	Ile	Tyr	Ser	Thr	Tyr	Asn	Asp	Asn	
		595					600					605				
His	Tyr	Gly	Ser	Gln	Thr	Gly	Thr	Ser	Met	Ala	Ser	Pro	Gln	Ile	Ala	
	610					615					620					
Gly	Ala	Ser	Leu	Leu	Val	Lys	Gln	Tyr	Leu	Glu	Lys	Thr	Gln	Pro	Asn	
625					630					635					640	
Leu	Pro	Lys	Glu	Lys	Ile	Ala	Asp	Ile	Val	Lys	Asn	Leu	Leu	Met	Ser	
				645					650					655		
Asn	Ala	Gln	Ile	His	Val	Asn	Pro	Glu	Thr	Lys	Thr	Thr	Thr	Ser	Pro	
			660					665					670			
Arg	Gln	Gln	Gly	Ala	Gly	Leu	Leu	Asn	Ile	Asp	Gly	Ala	Val	Thr	Ser	
		675					680					685				
Gly	Leu	Tyr	Val	Thr	Gly	Lys	Asp	Asn	Tyr	Gly	Ser	Ile	Ser	Leu	Gly	
	690					695				700						
Asn	Ile	Thr	Asp	Thr	Met	Thr	Phe	Asp	Val	Thr	Val	His	Asn	Leu	Ser	
705					710					715					720	
Asn	Lys	Asp	Lys	Thr	Leu	Arg	Tyr	Asp	Thr	Glu	Leu	Leu	Thr	Asp	His	
				725					730					735		
Val	Asp	Pro	Gln	Lys	Gly	Arg	Phe	Thr	Leu	Thr	Ser	His	Ser	Leu	Lys	
		740						745					750			
Thr	Tyr	Gln	Gly	Gly	Glu	Val	Thr	Val	Pro	Ala	Asn	Gly	Lys	Val	Thr	
		755					760					765				
Val	Arg	Val	Thr	Met	Asp	Val	Ser	Gln	Phe	Thr	Lys	Glu	Leu	Thr	Lys	
	770					775					780					
Gln	Met	Pro	Asn	Gly	Tyr	Tyr	Leu	Glu	Gly	Phe	Val	Arg	Phe	Arg	Asp	
785					790					795					800	
Ser	Gln	Asp	Asp	Gln	Leu	Asn	Arg	Val	Asn	Ile	Pro	Phe	Val	Gly	Phe	
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Lys	Gly	Gln	Phe	Glu	Asn	Leu	Ala	Val	Ala	Glu	Glu	Ser	Ile	Tyr	Arg		
			820					825					830				
Leu	Lys	Ser	Gln	Gly	Lys	Thr	Gly	Phe	Tyr	Phe	Asp	Glu	Ser	Gly	Pro		
		835					840					845					
Lys	Asp	Asp	Ile	Tyr	Val	Gly	Lys	His	Phe	Thr	Gly	Leu	Val	Thr	Leu		
	850					855					860						
Gly	Ser	Glu	Thr	Asn	Val	Ser	Thr	Lys	Thr	Ile	Ser	Asp	Asn	Gly	Leu		
865				870						875					880		
His	Thr	Leu	Gly	Thr	Phe	Lys	Asn	Ala	Asp	Gly	Lys	Phe	Ile	Leu	Glu		
			885						890					895			
Lys	Asn	Ala	Gln	Gly	Asn	Pro	Val	Leu	Ala	Ile	Ser	Pro	Asn	Gly	Asp		
		900						905					910				
Asn	Asn	Gln	Asp	Phe	Ala	Ala	Phe	Lys	Gly	Val	Phe	Leu	Arg	Lys	Tyr		
	915						920					925					
Gln	Gly	Leu	Lys	Ala	Ser	Val	Tyr	His	Ala	Ser	Asp	Lys	Glu	His	Lys		
930						935					940						
Asn	Pro	Leu	Trp	Val	Ser	Pro	Glu	Ser	Phe	Lys	Gly	Asp	Lys	Asn	Phe		
945				950						955					960		
Asn	Ser	Asp	Ile	Arg	Phe	Ala	Lys	Ser	Thr	Thr	Leu	Leu	Gly	Thr	Ala		
		965							970					975			
Phe	Ser	Gly	Lys	Ser	Leu	Thr	Gly	Ala	Glu	Leu	Pro	Asp	Gly	His	Tyr		
	980						985					990					
His	Tyr	Val	Val	Ser	Tyr	Tyr	Pro	Asp	Val	Val	Gly	Ala	Lys	Arg	Gln		
	995						1000					1005					
Glu	Met	Thr	Phe	Asp	Met	Ile	Leu	Asp	Arg	Gln	Lys	Pro	Val	Leu			
1010						1015					1020						
Ser	Gln	Ala	Thr	Phe	Asp	Pro	Glu	Thr	Asn	Arg	Phe	Lys	Pro	Glu			
1025						1030					1035						
Pro	Leu	Lys	Asp	Arg	Gly	Leu	Ala	Gly	Val	Arg	Lys	Asp	Ser	Val			
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Phe	Tyr	Leu	Glu	Arg	Lys	Asp	Asn	Lys	Pro	Tyr	Thr	Val	Thr	Ile			
1055						1060					1065						
Asn	Asp	Ser	Tyr	Lys	Tyr	Val	Ser	Val	Glu	Asp	Asn	Lys	Thr	Phe			
1070						1075					1080						
Val	Glu	Arg	Gln	Ala	Asp	Gly	Ser	Phe	Ile	Leu	Pro	Leu	Asp	Lys			
1085						1090					1095						
Ala	Lys	Leu	Gly	Asp	Phe	Tyr	Tyr	Met	Val	Glu	Asp	Phe	Ala	Gly			
1100						1105					1110						
Asn	Val	Ala	Ile	Ala	Lys	Leu	Gly	Asp	His	Leu	Pro	Gln	Thr	Leu			
1115						1120					1125						
Gly	Lys	Thr	Pro	Ile	Lys	Leu	Lys	Leu	Thr	Asp	Gly	Asn	Tyr	Gln			
1130						1135					1140						
Thr	Lys	Glu	Thr	Leu	Lys	Asp	Asn	Leu	Glu	Met	Thr	Gln	Ser	Asp			
1145						1150					1155						
Thr	Gly	Leu	Val	Thr	Asn	Gln	Ala	Gln	Leu	Ala	Val	Val	His	Arg			
1160						1165					1170						
Asn	Gln	Pro	Gln	Ser	Gln	Leu	Thr	Lys	Met	Asn	Gln	Asp	Phe	Phe			
1175						1180					1185						
Ile	Ser	Pro	Asn	Glu	Asp	Gly	Asn	Lys	Asp	Phe	Val	Ala	Phe	Lys			
1190						1195					1200						
Gly	Leu	Lys	Asn	Asn	Val	Tyr	Asn	Asp	Leu	Thr	Val	Asn	Val	Tyr			
1205						1210					1215						
Ala	Lys	Asp	Asp	His	Gln	Lys	Gln	Thr	Pro	Ile	Trp	Ser	Ser	Gln			
1220						1225					1230						
Ala	Gly	Ala	Ser	Val	Ser	Ala	Ile	Glu	Ser	Thr	Ala	Trp	Tyr	Gly			
1235						1240					1245						
Ile	Thr	Ala	Arg	Gly	Ser	Lys	Val	Met	Pro	Gly	Asp	Tyr	Gln	Tyr			

1250	Val Val Thr Tyr Arg Asp	1255	Glu His Gly Lys Glu	1260	His Gln Lys Gln
1265	Tyr Thr Ile Ser Val Asn	1270	Asp Lys Lys Pro Met	1275	Ile Thr Gln Gly
1280	Arg Phe Asp Thr Ile Asn	1285	Gly Val Asp His Phe	1290	Thr Pro Asp Lys
1295	Thr Lys Ala Leu Asp Ser	1300	Ser Gly Ile Val Arg	1305	Glu Glu Val Phe
1310	Tyr Leu Ala Lys Lys Asn	1315	Gly Arg Lys Phe Asp	1320	Val Thr Glu Gly
1325	Lys Asp Gly Ile Thr Val	1330	Ser Asp Asn Lys Val	1335	Tyr Ile Pro Lys
1340	Asn Pro Asp Gly Ser Tyr	1345	Thr Ile Ser Lys Arg	1350	Asp Gly Val Thr
1355	Leu Ser Asp Tyr Tyr Tyr	1360	Leu Val Glu Asp Arg	1365	Ala Gly Asn Val
1370	Ser Phe Ala Thr Leu Arg	1375	Asp Leu Lys Ala Val	1380	Gly Lys Asp Lys
1385	Ala Val Val Asn Phe Gly	1390	Leu Asp Leu Pro Val	1395	Pro Glu Asp Lys
1400	Gln Ile Val Asn Phe Thr	1405	Tyr Leu Val Arg Asp	1410	Ala Asp Gly Lys
1415	Pro Ile Glu Asn Leu Glu	1420	Tyr Tyr Asn Asn Ser	1425	Gly Asn Ser Leu
1430	Ile Leu Pro Tyr Gly Lys	1435	Tyr Thr Val Glu Leu	1440	Leu Thr Tyr Asp
1445	Thr Asn Ala Ala Lys Leu	1450	Glu Ser Asp Lys Ile	1455	Val Ser Phe Thr
1460	Leu Ser Ala Asp Asn Asn	1465	Phe Gln Gln Val Thr	1470	Phe Lys Ile Thr
1475	Met Leu Ala Thr Ser Gln	1480	Ile Thr Ala His Phe	1485	Asp His Leu Leu
1490	Pro Glu Gly Ser Arg Val	1495	Ser Leu Lys Thr Ala	1500	Gln Asp Gln Leu
1505	Ile Pro Leu Glu Gln Ser	1510	Leu Tyr Val Pro Lys	1515	Ala Tyr Gly Lys
1520	Thr Val Gln Glu Gly Thr	1525	Tyr Glu Val Val Val	1530	Ser Leu Pro Lys
1535	Gly Tyr Arg Ile Glu Gly	1540	Asn Thr Lys Val Asn	1545	Thr Leu Pro Asn
1550	Glu Val His Glu Leu Ser	1555	Leu Arg Leu Val Lys	1560	Val Gly Asp Ala
1565	Ser Asp Ser Thr Gly Asp	1570	His Lys Val Met Ser	1575	Lys Asn Asn Ser
1580	Gln Ala Leu Thr Ala Ser	1585	Ala Thr Pro Thr Lys	1590	Ser Thr Thr Ser
1595	Ala Thr Ala Lys Ala Leu	1600	Pro Ser Thr Gly Glu	1605	Lys Met Gly Leu
1610	Lys Leu Arg Ile Val Gly	1615	Leu Val Leu Leu Gly	1620	Leu Thr Cys Val
1625	Phe Ser Arg Lys Lys Ser	1630	Lys Lys Asp	1635	
1640		1645			

<210> SEQ ID NO 81

<211> LENGTH: 846

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 81

```
atgtctttta aaaaatggat tggaatagtc ggaatcgctt tagcatcaac tgtattgggt 60
gcttgttctg aaaaacaaga tgataaaaac actttaacta ttgggggtgat gacaaaaaca 120
gaatctgatac aagcgagatg ggataaagtt gaagaattat tgaaaaaaga caatatcact 180
ttgaagtaca aagaatttac agattactcg caacctaata aggagttgc taatggtgaa 240
gtcgatatta atgccttcca aactataat ttcttaaata actggaataa ggaaaaataag 300
gaacatttgg tggccattgc tgatacctat atcagcccaa ttaacctttt ctctggaacc 360
agtcaagatg gaaaggctaa atacaaatca gtagctgatac tgccaaatgg tactcaaatt 420
gcagtaccaa atgatgagac caatgaaagc cgtgccctct atgtgctgca atcagctggc 480
ctcattaaat tgaatgtgtc tggatgacaa ttagcaacca ttgccaatat ctacagagaac 540
aaaaagaaat tagatatcaa ggaattagat gctagccaaa cggcacgtgc tttagtagtct 600
gctgatgcag ctgttgtaaa taatagttac gctgttctcg caaaaattga ctacaaaacc 660
tctcttttca aagaaaaagc agatgacaat tcaaaacagt ggattaacat tattgcaggt 720
caaaaagatt gggaaaaaatc agagaaggct gatgctatta aaaaactcat caaggcctac 780
caaactgatg aggtgaagaa agtcgtggaa aaaacttcaa atggtataga tgtatccgta 840
tggttaa
```

<210> SEQ ID NO 82

<211> LENGTH: 281

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 82

```
Met Ser Phe Lys Lys Trp Ile Gly Ile Val Gly Ile Ala Leu Ala Ser
1      5      10      15
Thr Val Leu Val Ala Cys Ser Glu Lys Gln Asp Asp Lys Asn Thr Leu
20     25     30
Thr Ile Gly Val Met Thr Lys Thr Glu Ser Asp Gln Ala Arg Trp Asp
35     40     45
Lys Val Glu Glu Leu Leu Lys Lys Asp Asn Ile Thr Leu Lys Tyr Lys
50     55     60
Glu Phe Thr Asp Tyr Ser Gln Pro Asn Lys Ala Val Ala Asn Gly Glu
65     70     75     80
Val Asp Ile Asn Ala Phe Gln His Tyr Asn Phe Leu Asn Asn Trp Asn
85     90     95
Lys Glu Asn Lys Glu His Leu Val Ala Ile Ala Asp Thr Tyr Ile Ser
100    105    110
Pro Ile Asn Leu Phe Ser Gly Thr Ser Gln Asp Gly Lys Ala Lys Tyr
115    120    125
Lys Ser Val Ala Asp Leu Pro Asn Gly Thr Gln Ile Ala Val Pro Asn
130    135    140
Asp Ala Thr Asn Glu Ser Arg Ala Leu Tyr Val Leu Gln Ser Ala Gly
145    150    155    160
Leu Ile Lys Leu Asn Val Ser Gly Asp Gln Leu Ala Thr Ile Ala Asn
165    170    175
Ile Ser Glu Asn Lys Lys Lys Leu Asp Ile Lys Glu Leu Asp Ala Ser
180    185    190
Gln Thr Ala Arg Ala Leu Val Ser Ala Asp Ala Ala Val Val Asn Asn
195    200    205
Ser Tyr Ala Val Pro Ala Lys Ile Asp Tyr Lys Thr Ser Leu Phe Lys
210    215    220
Glu Lys Ala Asp Asp Asn Ser Lys Gln Trp Ile Asn Ile Ile Ala Gly
225    230    235    240
Gln Lys Asp Trp Glu Lys Ser Glu Lys Ala Asp Ala Ile Lys Lys Leu
245    250    255
Ile Lys Ala Tyr Gln Thr Asp Glu Val Lys Lys Val Val Glu Lys Thr
260    265    270
```

Ser Asn Gly Ile Asp Val Ser Val Trp
275 280

<210> SEQ ID NO 83
<211> LENGTH: 402
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 83
ttgcagctat ttaaaggaat actaatggat aatgatatga ggaataaaaat gaaaaaagaa 60
gaactcttaa aaattgttgt ggaagcaact gaggaaaagc gtgctaaaga tatttttagcc 120
ttggatttag aggggttaac tagtttgacc gattattttg tgattgcgag tgcaacaaac 180
agtcgtcaat tagaggctat tgcggataat attcgtgaaa aggtaaaaga ggctggtgga 240
gatgctagcc atggtgaagg taatagccaa gcaggctggg tcttgcttga tttgaccgat 300
gtggtggtac atcttttttt agaagacgag cgttaccact ataatcttga aaaattgtgg 360
catgaagcgc ctgctgtggc tctagatgcc tatttagctt aa 402

<210> SEQ ID NO 84
<211> LENGTH: 133
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 84
Met Gln Leu Phe Lys Gly Ile Leu Met Asp Asn Asp Met Arg Asn Lys
1 5 10 15
Met Lys Lys Glu Glu Leu Leu Lys Ile Val Val Glu Ala Thr Glu Glu
20 25 30
Lys Arg Ala Lys Asp Ile Leu Ala Leu Asp Leu Glu Gly Leu Thr Ser
35 40 45
Leu Thr Asp Tyr Phe Val Ile Ala Ser Ala Thr Asn Ser Arg Gln Leu
50 55 60
Glu Ala Ile Ala Asp Asn Ile Arg Glu Lys Val Lys Glu Ala Gly Gly
65 70 75 80
Asp Ala Ser His Val Glu Gly Asn Ser Gln Ala Gly Trp Val Leu Leu
85 90 95
Asp Leu Thr Asp Val Val Val His Leu Phe Leu Glu Asp Glu Arg Tyr
100 105 110
His Tyr Asn Leu Glu Lys Leu Trp His Glu Ala Pro Ala Val Ala Leu
115 120 125
Asp Ala Tyr Leu Ala
130

<210> SEQ ID NO 85
<211> LENGTH: 1515
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 85
ttgaggacaa ctatgaaaaa atatattttta aaccgtatca tgcgatcggt agtgtcggta 60
gttctggttaa cggctttaac atacaccatc gtatatactc tagtacctac cagccttatc 120
tttaaacaag accctaatta taataaaatg acaacaacac cagataaaaa agtagcgtat 180
gaaaatctaa cttttcaacg tatgggttat gtcaattatt tttcaagcaa agaattaaaa 240
gataatgctt cttaaagtaga tagtagtgta acgacagaag caactagtgc taacaaagct 300
atctatgaga agtatattga ttctcttggc aatggctggc agctaaaacg cttccccact 360
agcaaacagt tttatgcaat tcgcaatatt cctattttacg aacgtgtttg gaactttttc 420
tcaaacttag ttgttattga tcacccttgg aagatttcagg ataaagataa tccaaaatta 480
gttaggtata ttcgtctaga aaaagataaa tcagttggct ggtcacttgt tgggttcgggg 540
acaaaacata agtatctcct ctatactaac ggaaaatttc cttatcttca ccaaaacttt 600
gttaccttaa acttagggac atcttatcca acatacagca atattcctgt tcttcaggtc 660
atttcacaag ggcaaggacg aacagctctt caagatgtga ccttcccatc aggtgtcact 720

aagaaatcgt	cagtggatat	ctatagccgt	agctacaaaa	atccaaaatc	attggatgat	780
atcaccaagg	taaactatgg	taagggagat	tcctacacta	aaaccatcaa	taattatgtc	840
gacccatcaa	tgattcacaa	ttcttttgta	attgggtttt	ttgggtgttat	gttttcctat	900
atcgttgggt	tgctctctgg	tttatttatg	gctcgggtta	aaaataccta	ttttgacagt	960
ttctcaacag	cgaccatgac	cttcattgctt	gctttaccaa	gtattgctgt	tatctatgtt	1020
gttcgcttcc	taggtggcat	ggttgggtta	ccagatagtt	tcccaatgct	gggggcatct	1080
gacctaataa	cttatatttt	accagccctt	attttaggaa	ttttaaatat	tccaactacg	1140
ggtatctggg	tccgtcgcta	tcttggtgac	cttcaggcca	gcgattgggt	acgttttgcg	1200
cgttcaaaaag	gattatcaga	atctgaaatt	tacagagggc	atctcttcaa	aaatgccatg	1260
gtcccaattg	tgtcaggggt	tcctgcaagt	attatccttg	ctattgggtg	tgcaacatta	1320
acagagactg	tctttgcctt	cccgggtatg	ggtaaaatgt	taattgattc	tattaaatct	1380
gctaacaatt	ctatgattgt	tggattaacc	tttatcttca	ctgtcttgct	aattgtttca	1440
cttttactag	gagatattgt	catgaccctt	gtcgatccac	gtattaaatt	gtcaacaaaa	1500
aaaggaggta	agtaa					1515

<210> SEQ ID NO 86

<211> LENGTH: 504

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 86

Met	Arg	Thr	Thr	Met	Lys	Lys	Tyr	Ile	Leu	Asn	Arg	Ile	Met	Arg	Ser
1				5					10				15		
Leu	Val	Ser	Val	Val	Leu	Val	Thr	Ala	Leu	Thr	Tyr	Thr	Ile	Val	Tyr
			20					25					30		
Thr	Leu	Val	Pro	Thr	Ser	Leu	Ile	Phe	Lys	Gln	Asp	Pro	Asn	Tyr	Asn
			35				40					45			
Lys	Met	Thr	Thr	Thr	Pro	Asp	Lys	Lys	Val	Ala	Tyr	Glu	Asn	Leu	Thr
	50					55					60				
Phe	Gln	Arg	Met	Gly	Tyr	Val	Asn	Tyr	Phe	Ser	Ser	Lys	Glu	Leu	Lys
65					70					75				80	
Asp	Asn	Ala	Ser	Lys	Val	Asp	Ser	Ser	Val	Thr	Thr	Glu	Ala	Thr	Ser
				85					90					95	
Ala	Asn	Lys	Ala	Ile	Tyr	Glu	Lys	Tyr	Ile	Asp	Ser	Leu	Gly	Asn	Gly
			100					105					110		
Trp	Gln	Leu	Lys	Arg	Phe	Pro	Thr	Ser	Lys	Gln	Phe	Tyr	Ala	Ile	Arg
	115						120					125			
Asn	Ile	Pro	Ile	Tyr	Glu	Arg	Val	Trp	Asn	Phe	Phe	Ser	Asn	Leu	Val
	130					135					140				
Val	Ile	Asp	His	Pro	Trp	Lys	Ile	Gln	Asp	Lys	Asp	Asn	Pro	Lys	Leu
145					150					155				160	
Ala	Arg	Tyr	Ile	Arg	Leu	Glu	Lys	Asp	Lys	Ser	Val	Gly	Trp	Ser	Leu
				165					170					175	
Val	Gly	Ser	Gly	Thr	Lys	His	Lys	Tyr	Leu	Leu	Tyr	Thr	Asn	Gly	Lys
			180					185					190		
Phe	Pro	Tyr	Leu	His	Gln	Asn	Phe	Val	Thr	Leu	Asn	Leu	Gly	Thr	Ser
	195						200					205			
Tyr	Pro	Thr	Tyr	Ser	Asn	Ile	Pro	Val	Leu	Gln	Val	Ile	Ser	Gln	Gly
	210					215					220				
Gln	Gly	Arg	Thr	Ala	Leu	Gln	Asp	Val	Thr	Phe	Pro	Ser	Gly	Val	Thr
225					230					235				240	
Lys	Lys	Ser	Ser	Val	Asp	Ile	Tyr	Ser	Arg	Ser	Tyr	Lys	Asn	Pro	Lys
				245					250					255	
Ser	Leu	Asp	Asp	Ile	Thr	Lys	Val	Asn	Tyr	Gly	Lys	Gly	Asp	Ser	Tyr
			260					265					270		
Thr	Lys	Thr	Ile	Asn	Asn	Tyr	Val	Asp	Pro	Ser	Met	Ile	His	Asn	Ser
	275						280					285			
Phe	Val	Ile	Gly	Phe	Phe	Gly	Val	Met	Phe	Ser	Tyr	Ile	Val	Gly	Leu

290	295	300
Pro Leu Gly Leu Phe Met	Ala Arg Phe Lys Asn	Thr Tyr Phe Asp Ser
305	310	315
Phe Ser Thr Ala Thr Met	Thr Phe Met Leu Ala	Leu Pro Ser Ile Ala
	325	330
Val Ile Tyr Val Val Arg	Phe Leu Gly Gly Met	Val Gly Leu Pro Asp
	340	345
Ser Phe Pro Met Leu Gly	Ala Ser Asp Pro Lys	Ser Tyr Ile Leu Pro
	355	360
Ala Leu Ile Leu Gly Ile	Leu Asn Ile Pro Thr	Thr Val Ile Trp Phe
	370	375
Arg Arg Tyr Leu Val Asp	Leu Gln Ala Ser Asp	Trp Val Arg Phe Ala
385	390	395
Arg Ser Lys Gly Leu Ser	Glu Ser Glu Ile Tyr	Arg Gly His Leu Phe
	405	410
Lys Asn Ala Met Val Pro	Ile Val Ser Gly Val	Pro Ala Ser Ile Ile
	420	425
Leu Ala Ile Gly Gly Ala	Thr Leu Thr Glu Thr	Val Phe Ala Phe Pro
	435	440
Gly Met Gly Lys Met Leu	Ile Asp Ser Ile Lys	Ser Ala Asn Asn Ser
	450	455
Met Ile Val Gly Leu Thr	Phe Ile Phe Thr Val	Leu Ser Ile Val Ser
465	470	475
Leu Leu Leu Gly Asp Ile	Val Met Thr Leu Val	Asp Pro Arg Ile Lys
	485	490
Leu Ser Thr Lys Lys Gly	Gly Gly Lys	
	500	

<210> SEQ ID NO 87

<211> LENGTH: 1980

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 87

gtgacttttta	tgaagaaaag	taaatgggtt	gcagctgtaa	gtggttgcgat	cttgctcagta	60
tccgcttttgg	cagcttggtg	taataaaaaat	gcttcagggtg	gctcagaagc	tacaaaaaacc	120
tacaagtacg	tttttggttaa	cgatccaaaa	tcattgggatt	atatttttgac	taatggcggt	180
ggaacgactg	atgtgataac	acaaatgggt	gatggctctt	tggaaaacga	tgagtatggt	240
aatttagtac	catcacttgc	taaagattgg	aaggtttcaa	aagacgggtct	gacttatact	300
tatactcttc	gcgatgggtg	ctcttggtat	acggctgatg	gtgaagaata	tgccccagta	360
acagcagaag	atthttgtgac	tggtttgaag	cacgcgggtg	acgataaatc	agatgctctt	420
tacgttggtg	aagattcaat	aaaaaactta	aaggcttacc	aaaatgggtga	agtagatttt	480
aaagaagttg	gtgtcaaagc	ccttgacgat	aaaactgttc	agtatacttt	gaacaagcct	540
gaaagctact	ggaattcaaa	aacaacttat	agtgtgcttt	tcccagttaa	tgcgaaattt	600
ttgaagtcaa	aaggtaaaga	ttttggtaca	accgatccat	catcaatcct	tgtaaatggt	660
gcttacttct	tgagcgcctt	cacctcaaaa	tcatctatgg	aattccataa	aaatgaaaac	720
tactgggatg	ctaagaatgt	tgggatagaa	tctgttaaata	tgacttactc	agatgggttca	780
gacccagggt	cgttctacaa	gaactttgac	aagggtgagt	tcagcggttg	acgactttac	840
ccaaatgacc	ctacctacaa	atcagctaag	aaaaactatg	ctgataacat	tacttacgga	900
atgttgactg	gagatatccg	tcatttaaca	tgggaatttga	accgtacttc	tttcaaaaac	960
actaagaaaag	accctgcaca	acaagatgcc	ggtaagaaaag	ctcttaacaa	caaggatttt	1020
cgtcaagcta	ttcagtttgc	ttttgaccga	gcgtcattcc	aagcacaaac	tgcagggtcaa	1080
gatgccaaaa	caaaagcctt	acgtaacatg	cttgctccac	caacatttgt	gaccattgga	1140
gaaagtgatt	ttggttcaga	agttgaaaag	gaaatggcaa	aacttggtga	tgaatggaaa	1200
gacgttaact	tagctgatgc	tcaagatggt	ttctataatc	ctgaaaaagc	aaaagctgag	1260
tttgcaaaaag	ccaaagaagc	tttaacagct	gaaggtgtaa	ccttcccagt	tcaattagat	1320
taccctgttg	accaagcaaa	cgcagcaact	gttcagggaag	cccagtcctt	caaacaatct	1380
gttgaagcat	ctcttggtaa	agagaatgtc	attgtcaatg	ttcttgaaac	agaaacatca	1440

actcacgaag	cccaaggctt	ctatgctgag	accccagaac	aacaagacta	cgatatcatt	1500
tcatcatggt	ggggaccaga	ctatcaagat	ccacggacct	accttgacat	catgagtcca	1560
gtaggtggtg	gatctgttat	ccaaaaactt	ggaatcaaag	caggtcaaaa	taaggatggt	1620
gtggcagctg	caggccttga	tacctaccaa	actcttcttg	atgaagcagc	agcaattaca	1680
gacgacaacg	atgcgcgcta	taaagcttac	gcaaaaagcac	aagcctacct	tacagataat	1740
gccgtagata	ttccagttgt	ggcattgggt	ggcactccac	gagttactaa	agccgttcca	1800
tttagcgggg	gcttctcttg	ggcaggggtc	aaagggtcctc	tagcatataa	aggaatgaaa	1860
cttcaagaca	aacctgtcac	agtaaaaacaa	tacgaaaaag	caaaagaaaa	atggatgaaa	1920
gcaaaggcta	agtcaaattgc	aaaatatgct	gagaagttag	ctgatcacgt	tgaaaaataa	1980

<210> SEQ ID NO 88

<211> LENGTH: 659

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 88

Met	Thr	Phe	Met	Lys	Lys	Ser	Lys	Trp	Leu	Ala	Ala	Val	Ser	Val	Ala	
1				5					10					15		
Ile	Leu	Ser	Val	Ser	Ala	Leu	Ala	Ala	Cys	Gly	Asn	Lys	Asn	Ala	Ser	
			20					25					30			
Gly	Gly	Ser	Glu	Ala	Thr	Lys	Thr	Tyr	Lys	Tyr	Val	Phe	Val	Asn	Asp	
		35					40					45				
Pro	Lys	Ser	Leu	Asp	Tyr	Ile	Leu	Thr	Asn	Gly	Gly	Gly	Thr	Thr	Asp	
	50					55					60					
Val	Ile	Thr	Gln	Met	Val	Asp	Gly	Leu	Leu	Glu	Asn	Asp	Glu	Tyr	Gly	
65					70					75					80	
Asn	Leu	Val	Pro	Ser	Leu	Ala	Lys	Asp	Trp	Lys	Val	Ser	Lys	Asp	Gly	
				85					90					95		
Leu	Thr	Tyr	Thr	Tyr	Thr	Leu	Arg	Asp	Gly	Val	Ser	Trp	Tyr	Thr	Ala	
			100					105					110			
Asp	Gly	Glu	Glu	Tyr	Ala	Pro	Val	Thr	Ala	Glu	Asp	Phe	Val	Thr	Gly	
		115					120					125				
Leu	Lys	His	Ala	Val	Asp	Asp	Lys	Ser	Asp	Ala	Leu	Tyr	Val	Val	Glu	
	130					135					140					
Asp	Ser	Ile	Lys	Asn	Leu	Lys	Ala	Tyr	Gln	Asn	Gly	Glu	Val	Asp	Phe	
145				150						155					160	
Lys	Glu	Val	Gly	Val	Lys	Ala	Leu	Asp	Asp	Lys	Thr	Val	Gln	Tyr	Thr	
				165					170					175		
Leu	Asn	Lys	Pro	Glu	Ser	Tyr	Trp	Asn	Ser	Lys	Thr	Thr	Tyr	Ser	Val	
			180					185					190			
Leu	Phe	Pro	Val	Asn	Ala	Lys	Phe	Leu	Lys	Ser	Lys	Gly	Lys	Asp	Phe	
	195						200					205				
Gly	Thr	Thr	Asp	Pro	Ser	Ser	Ile	Leu	Val	Asn	Gly	Ala	Tyr	Phe	Leu	
	210					215					220					
Ser	Ala	Phe	Thr	Ser	Lys	Ser	Ser	Met	Glu	Phe	His	Lys	Asn	Glu	Asn	
225					230					235					240	
Tyr	Trp	Asp	Ala	Lys	Asn	Val	Gly	Ile	Glu	Ser	Val	Lys	Leu	Thr	Tyr	
				245					250					255		
Ser	Asp	Gly	Ser	Asp	Pro	Gly	Ser	Phe	Tyr	Lys	Asn	Phe	Asp	Lys	Gly	
			260					265					270			
Glu	Phe	Ser	Val	Ala	Arg	Leu	Tyr	Pro	Asn	Asp	Pro	Thr	Tyr	Lys	Ser	
	275						280					285				
Ala	Lys	Lys	Asn	Tyr	Ala	Asp	Asn	Ile	Thr	Tyr	Gly	Met	Leu	Thr	Gly	
	290					295					300					
Asp	Ile	Arg	His	Leu	Thr	Trp	Asn	Leu	Asn	Arg	Thr	Ser	Phe	Lys	Asn	
305				310						315					320	
Thr	Lys	Lys	Asp	Pro	Ala	Gln	Gln	Asp	Ala	Gly	Lys	Lys	Ala	Leu	Asn	
				325					330					335		


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gaagtactga aattatctag caaatcctcc actatTTTTg ctggacaaac catttacagt 660
tataattaca tgcttaaagg catgccttgt tatcgagaag gcgtggatgg tctTTTTgtt 720
ggttattcta aaaaagccgg tgcttctttt gtagtacta gtgtcgaaaa tcaaagtagg 780
gttattacag tagttttaaa tgctgatcaa agccacgagg atgatttagc tatattttaaa 840
acaaccaatc aattgttgca gtacctttta attaattttc aaaaagtcca gtttaattgaa 900
aataataaac cagtaaaaac gttatatgtc ttagacagtc ctgaaaaaac tgtcaaaactt 960
gtagcccaaa atagtttatt ttttatcaaa ccaatacata caaagaccaa aaataccgtc 1020
catattacta agaaatcatc cacaatgata gcacctctat caaagggaca agtcttaggt 1080
agagcaaccc ttcaagataa acatcttatt ggacaagggt atctggatac tcctccttct 1140
atcaatctta tccttcaaaa aaacatttct aaaagtttct ttttaaagggt ctggtggaac 1200
cgttttgtga ggtatgtcaa tacctcttta tag 1233

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<210> SEQ ID NO 90

<211> LENGTH: 410

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 90

```

Met Ile Lys Arg Leu Ile Ser Leu Val Val Ile Ala Leu Phe Phe Ala
1           5           10          15
Ala Ser Thr Val Ser Gly Glu Glu Tyr Ser Val Thr Ala Lys His Ala
20          25          30
Ile Ala Val Asp Leu Glu Ser Gly Lys Val Leu Tyr Glu Lys Asp Ala
35          40          45
Lys Glu Val Val Pro Val Ala Ser Val Ser Lys Leu Leu Thr Thr Tyr
50          55          60
Leu Val Tyr Lys Glu Val Ser Lys Gly Lys Leu Asn Trp Asp Ser Pro
65          70          75          80
Val Thr Ile Ser Asn Tyr Pro Tyr Glu Leu Thr Thr Asn Tyr Thr Ile
85          90          95
Ser Asn Val Pro Leu Asp Lys Arg Lys Tyr Thr Val Lys Glu Leu Leu
100         105         110
Ser Ala Leu Val Val Asn Asn Ala Asn Ser Pro Ala Ile Ala Leu Ala
115         120         125
Glu Lys Ile Gly Gly Thr Glu Pro Lys Phe Val Asp Lys Met Lys Lys
130         135         140
Gln Leu Arg Gln Trp Gly Ile Ser Asp Ala Lys Val Val Asn Ser Thr
145         150         155         160
Gly Leu Thr Asn His Phe Leu Gly Ala Asn Thr Tyr Pro Asn Thr Glu
165         170         175
Pro Asp Asp Glu Asn Cys Phe Cys Ala Thr Asp Leu Ala Ile Ile Ala
180         185         190
Arg His Leu Leu Leu Glu Phe Pro Glu Val Leu Lys Leu Ser Ser Lys
195         200         205
Ser Ser Thr Ile Phe Ala Gly Gln Thr Ile Tyr Ser Tyr Asn Tyr Met
210         215         220
Leu Lys Gly Met Pro Cys Tyr Arg Glu Gly Val Asp Gly Leu Phe Val
225         230         235         240
Gly Tyr Ser Lys Lys Ala Gly Ala Ser Phe Val Ala Thr Ser Val Glu
245         250         255
Asn Gln Met Arg Val Ile Thr Val Val Leu Asn Ala Asp Gln Ser His
260         265         270
Glu Asp Asp Leu Ala Ile Phe Lys Thr Thr Asn Gln Leu Leu Gln Tyr
275         280         285
Leu Leu Ile Asn Phe Gln Lys Val Gln Leu Ile Glu Asn Asn Lys Pro
290         295         300
Val Lys Thr Leu Tyr Val Leu Asp Ser Pro Glu Lys Thr Val Lys Leu
305         310         315         320

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Val	Ala	Gln	Asn	Ser	Leu	Phe	Phe	Ile	Lys	Pro	Ile	His	Thr	Lys	Thr
				325					330					335	
Lys	Asn	Thr	Val	His	Ile	Thr	Lys	Lys	Ser	Ser	Thr	Met	Ile	Ala	Pro
			340					345					350		
Leu	Ser	Lys	Gly	Gln	Val	Leu	Gly	Arg	Ala	Thr	Leu	Gln	Asp	Lys	His
		355					360					365			
Leu	Ile	Gly	Gln	Gly	Tyr	Leu	Asp	Thr	Pro	Pro	Ser	Ile	Asn	Leu	Ile
	370					375					380				
Leu	Gln	Lys	Asn	Ile	Ser	Lys	Ser	Phe	Phe	Leu	Lys	Val	Trp	Trp	Asn
385					390					395					400
Arg	Phe	Val	Arg	Tyr	Val	Asn	Thr	Ser	Leu						
				405					410						

<210> SEQ ID NO 91

<211> LENGTH: 471

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 91

atgagtcgta	aaaatcaagc	gcctaaacgc	gaagtattac	cagatccatt	atataactca	60
aaaatcgtaa	cacgtcttat	caaccgtgtt	atgcttgacg	gtaaacgtgg	tacagctgct	120
actatcgttt	acgatgcttt	caacgctatc	aaagaagcaa	caggaaatga	cgctcttgaa	180
gtatttgaaa	cagctatgga	caacatcatg	cctgtacttg	aagtacgcgc	acgccgtgct	240
ggtgggttcta	actaccaagt	cccagttgaa	gttcgtccag	aacgtcgtac	aacacttgga	300
cttcggttggt	tggtaaacgc	atcacgtgct	cgtgggtgaac	acactatgaa	agatcgtctt	360
gctaaagaaa	tcatggatgc	tgcaaacaac	acaggtgcat	cagttaagaa	acgtgaagac	420
actcacaanaa	tggctgaagc	taaccgtgcc	tttgctcact	tccgttggtta	a	471

<210> SEQ ID NO 92

<211> LENGTH: 156

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 92

Met	Ser	Arg	Lys	Asn	Gln	Ala	Pro	Lys	Arg	Glu	Val	Leu	Pro	Asp	Pro
1				5					10					15	
Leu	Tyr	Asn	Ser	Lys	Ile	Val	Thr	Arg	Leu	Ile	Asn	Arg	Val	Met	Leu
			20					25				30			
Asp	Gly	Lys	Arg	Gly	Thr	Ala	Ala	Thr	Ile	Val	Tyr	Asp	Ala	Phe	Asn
		35				40					45				
Ala	Ile	Lys	Glu	Ala	Thr	Gly	Asn	Asp	Ala	Leu	Glu	Val	Phe	Glu	Thr
	50					55				60					
Ala	Met	Asp	Asn	Ile	Met	Pro	Val	Leu	Glu	Val	Arg	Ala	Arg	Arg	Val
65				70					75					80	
Gly	Gly	Ser	Asn	Tyr	Gln	Val	Pro	Val	Glu	Val	Arg	Pro	Glu	Arg	Arg
			85					90					95		
Thr	Thr	Leu	Gly	Leu	Arg	Trp	Leu	Val	Asn	Ala	Ser	Arg	Ala	Arg	Gly
		100					105					110			
Glu	His	Thr	Met	Lys	Asp	Arg	Leu	Ala	Lys	Glu	Ile	Met	Asp	Ala	Ala
	115					120						125			
Asn	Asn	Thr	Gly	Ala	Ser	Val	Lys	Lys	Arg	Glu	Asp	Thr	His	Lys	Met
	130					135					140				
Ala	Glu	Ala	Asn	Arg	Ala	Phe	Ala	His	Phe	Arg	Trp				
145				150					155						

<210> SEQ ID NO 93

<211> LENGTH: 2640

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 93

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attgcttttaa cctcaacaat tgctttattg agtgccagtg taggcgtatc tcaccaagtc      120
aaagcagatg atagagcctc aggagaaaagc aaggcgagta atactcacga cgatagttta      180
ccaaaaccag aaacaattca agaggcaaag gcaactattg atgcagttga aaaaactctc      240
agtcaacaaa aagcagaact gacagagctt gctaccgctc tgacaaaaac tactgtctgaa      300
atcaaccact taaaagagca gcaagataat gaacaaaaag cttaaaccctc tgcacaagaa      360
atttacacta atactcttgc aagtagtgag gagacgctat tagcccaagg agccgaacat      420
caaagagagt taacagctac tgaaacagag cttcataatg ctcaagcaga tcaacattca      480
aaagagactg cattgtcaga acaaaaagct agcatttcag cagaaactac tcgagctcaa      540
gatttagtgg aacaagtcaa aacgtctgaa caaaatattg ctaagctcaa tgctatgatt      600
agcaatcctg atgctatcac taaagcagct caaacggcta atgataatac aaaagcatta      660
agctcagaat tggagaaggc taaagctgac ttagaaaatc aaaaagctaa agttaaaaag      720
caattgactg aagagttggc agctcagaaa gctgctctag cagaaaaaga ggcagaactt      780
agtcgtctta aatcctcagc tccgtctact caagatagca ttgtgggtaa taataccatg      840
aaagcaccgc aaggctatcc tcttgaagaa cttaaaaaat tagaagctag tggttatatt      900
ggatcagcta gttacaataa ttattacaaa gagcatgcag atcaaattat tgccaaagct      960
agtccaggta atcaattaaa tcaataccaa gatattccag cagatcgtaa tcgctttgtt     1020
gatcccgata atttgacacc agaagtgcaa aatgagctag cgcagtttgc agctcacatg     1080
attaatagtg taagaagaca attaggtcta ccaccagtta ctgttacagc aggatcacia     1140
gaatttgcaa gattacttag taccagctat aagaaaactc atggtaatac aagaccatca     1200
tttgtctacg gacagccagg ggtatcaggg cattatgggt ttgggcctca tgataaaaact     1260
attattgaag actctgccgg agcgtcaggg ctcattcgaa atgatgataa catgtacgag     1320
aatatcggtg cttttaacga tgtgcatact gtgaatggta ttaaacgtgg tatttatgac     1380
agtatcaagt atatgctctt tacagatcat ttacacggaa atacatacgg ccatgctatt     1440
aactttttac gtgtagataa acataaccct aatgcgcctg tttacctgg attttcaacc     1500
agcaatgtag gatctttgaa tgaacacttt gtaatgttct cagagtctaa cattgctaac     1560
catcaacgct ttaataagac ccctataaaa gccgttgtaa gtacaaaaga ttatgcccaa     1620
agagtaggca ctgtatctga tactattgca gcgatcaaag gaaaagtaag ctcatagaa     1680
aatcgtttgt cggctattca tcaagaagct gatattatgg cagccaagc taaagtaagt     1740
caacttcaag gttaaattagc aagcacactt aagcagtcag acagcttaaa tctccaagtg     1800
agacaattaa atgatactaa aggttctttg agaacagaat tactagcagc taaagcaaaa     1860
caagcacaaac tcgaagctac tcgtgatcaa tcattagcta agctagcatc gttgaaagcc     1920
gcaactgcacc agacagaagc cttagcagag caagccgcag ccagagtgc agcactgggtg     1980
gctaaaaaag ctcatattgca atatctaagg gactttaaat tgaatcctaa ccgccttcaa     2040
gtgatacgtg agcgcattga taatactaag caagatttgg ctaaaactac ctcatctttg     2100
ttaaatgcac aagaagcttt agcagcctta caagctaaac aaagcagtct agaagctact     2160
attgctacca cagaacacca gttgactttg cttaaaacct tagctaacga aaaggaatat     2220
cgccacttag acgaagatat agctactgtg cctgatttgc aagtagctcc acctcttacg     2280
ggcgtaaaac cgctatcata tagtaagata gatactactc cgcttggtca agaaatggtt     2340
aaagaaacga aacaactatt agaagcttca gcaagattag ctgctgaaaa tacaagtctt     2400
gtagcagaag cgcttggtgg ccaaacctct gaaatggtag caagtaatgc cattgtgtct     2460
aaaatcacat cttcgattac tcagccctca tctaagacat cttatggctc aggatcttct     2520
acaacgagca atctcatttc tgatgttgat gaaagtactc aaagagctct taaagcagga     2580
gtcgtcatgt tggcagctgt cggcctcaca ggatttaggt tccgtaagga atctaagtga     2640
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<210> SEQ ID NO 94

<211> LENGTH: 879

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 94

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Met Glu Lys Gly Glu Arg Met Asp Leu Glu Gln Thr Lys Pro Asn Gln
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Val Lys Gln Lys Ile Ala Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala
      20             25             30
Ser Val Gly Val Ser His Gln Val Lys Ala Asp Asp Arg Ala Ser Gly
      35             40             45
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Glu	Thr	Lys	Ala	Ser	Asn	Thr	His	Asp	Asp	Ser	Leu	Pro	Lys	Pro	Glu
50						55					60				
Thr	Ile	Gln	Glu	Ala	Lys	Ala	Thr	Ile	Asp	Ala	Val	Glu	Lys	Thr	Leu
65					70					75					80
Ser	Gln	Gln	Lys	Ala	Glu	Leu	Thr	Glu	Leu	Ala	Thr	Ala	Leu	Thr	Lys
				85					90					95	
Thr	Thr	Ala	Glu	Ile	Asn	His	Leu	Lys	Glu	Gln	Gln	Asp	Asn	Glu	Gln
			100					105					110		
Lys	Ala	Leu	Thr	Ser	Ala	Gln	Glu	Ile	Tyr	Thr	Asn	Thr	Leu	Ala	Ser
		115					120					125			
Ser	Glu	Glu	Thr	Leu	Leu	Ala	Gln	Gly	Ala	Glu	His	Gln	Arg	Glu	Leu
130						135					140				
Thr	Ala	Thr	Glu	Thr	Glu	Leu	His	Asn	Ala	Gln	Ala	Asp	Gln	His	Ser
145					150					155					160
Lys	Glu	Thr	Ala	Leu	Ser	Glu	Gln	Lys	Ala	Ser	Ile	Ser	Ala	Glu	Thr
				165					170					175	
Thr	Arg	Ala	Gln	Asp	Leu	Val	Glu	Gln	Val	Lys	Thr	Ser	Glu	Gln	Asn
			180					185					190		
Ile	Ala	Lys	Leu	Asn	Ala	Met	Ile	Ser	Asn	Pro	Asp	Ala	Ile	Thr	Lys
		195					200					205			
Ala	Ala	Gln	Thr	Ala	Asn	Asp	Asn	Thr	Lys	Ala	Leu	Ser	Ser	Glu	Leu
		210				215					220				
Glu	Lys	Ala	Lys	Ala	Asp	Leu	Glu	Asn	Gln	Lys	Ala	Lys	Val	Lys	Lys
225					230					235					240
Gln	Leu	Thr	Glu	Glu	Leu	Ala	Ala	Gln	Lys	Ala	Ala	Leu	Ala	Glu	Lys
				245					250					255	
Glu	Ala	Glu	Leu	Ser	Arg	Leu	Lys	Ser	Ser	Ala	Pro	Ser	Thr	Gln	Asp
			260					265					270		
Ser	Ile	Val	Gly	Asn	Asn	Thr	Met	Lys	Ala	Pro	Gln	Gly	Tyr	Pro	Leu
		275					280					285			
Glu	Glu	Leu	Lys	Lys	Leu	Glu	Ala	Ser	Gly	Tyr	Ile	Gly	Ser	Ala	Ser
290						295					300				
Tyr	Asn	Asn	Tyr	Tyr	Lys	Glu	His	Ala	Asp	Gln	Ile	Ile	Ala	Lys	Ala
305					310					315					320
Ser	Pro	Gly	Asn	Gln	Leu	Asn	Gln	Tyr	Gln	Asp	Ile	Pro	Ala	Asp	Arg
			325						330					335	
Asn	Arg	Phe	Val	Asp	Pro	Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn	Glu
			340					345					350		
Leu	Ala	Gln	Phe	Ala	Ala	His	Met	Ile	Asn	Ser	Val	Arg	Arg	Gln	Leu
		355					360					365			
Gly	Leu	Pro	Pro	Val	Thr	Val	Thr	Ala	Gly	Ser	Gln	Glu	Phe	Ala	Arg
		370				375					380				
Leu	Leu	Ser	Thr	Ser	Tyr	Lys	Lys	Thr	His	Gly	Asn	Thr	Arg	Pro	Ser
385					390					395					400
Phe	Val	Tyr	Gly	Gln	Pro	Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro
				405					410					415	
His	Asp	Lys	Thr	Ile	Ile	Glu	Asp	Ser	Ala	Gly	Ala	Ser	Gly	Leu	Ile
			420					425					430		
Arg	Asn	Asp	Asp	Asn	Met	Tyr	Glu	Asn	Ile	Gly	Ala	Phe	Asn	Asp	Val
		435					440					445			
His	Thr	Val	Asn	Gly	Ile	Lys	Arg	Gly	Ile	Tyr	Asp	Ser	Ile	Lys	Tyr
		450				455					460				
Met	Leu	Phe	Thr	Asp	His	Leu	His	Gly	Asn	Thr	Tyr	Gly	His	Ala	Ile
465					470					475					480
Asn	Phe	Leu	Arg	Val	Asp	Lys	His	Asn	Pro	Asn	Ala	Pro	Val	Tyr	Leu
				485					490					495	
Gly	Phe	Ser	Thr	Ser	Asn	Val	Gly	Ser	Leu	Asn	Glu	His	Phe	Val	Met

ttggaacca	ttgattttac	atctggtcct	gagaaaatca	caactgctat	tgaagctgga	300
acagctcctg	atgtcctctt	tgatgctcca	ggtcgtatca	ttcaatatgg	taaaaatggg	360
aaattggctg	acttgaatga	cttgttcaca	gaagagttta	ccaaagatgt	taacaatgac	420
aaattgattc	aagcctcaaa	agcaggagat	acagcttaca	tgtatcctat	cagctctgct	480
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aaagaggggtt	ggacaacaga	tgattttgaa	aaagtcttga	aagcattgaa	ggacaaagga	600
tataacccag	gttcttttctt	tgctaattggt	caagggtggtg	accaaggacc	acgtgccttc	660
tttgctaacc	tttatagtag	tcatattacc	gatgacaaag	taaccaaata	caccacagat	720
gatgctaact	ctattaaaagc	catgaccaag	atttccaatt	ggattaaaga	tggtttaagt	780
atgaatggct	ctcagtacga	tggttcagct	gatattcaaa	actttgcgaa	tggccaaact	840
tcctttacca	ttctttgggc	gcctgcacaa	ccaggcatcc	aagctaaatt	gttagaagct	900
agtaaagtgg	attaccttga	aatccccattc	ccatcagatg	atggcaaacc	agaactagaa	960
tacctcgtaa	atggttttgc	ggtctttaat	aacaaagatg	aacaaaaagt	cgctgcctct	1020
aagacattta	tccaatttat	cgctgatgat	aaagaatggg	gacctaaaaa	tgttgttcgt	1080
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aaaattgctg	aatggacaaa	attctactca	ccatactata	acacgattga	tgggtttgct	1200
gaaatgagaa	ctctttgggt	cccaatgggt	caagccgtct	ctaattggtga	tgaaaagcca	1260
gaagatgctt	tgaaagcctt	cactgaaaaa	gcaaacaaga	caatcaaaaa	aacacaataa	1320

<210> SEQ ID NO 96

<211> LENGTH: 439

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 96

Met	Asn	Met	Lys	Lys	Leu	Ala	Ser	Leu	Ala	Met	Leu	Gly	Ala	Ser	Val
1			5					10					15		
Leu	Gly	Leu	Ala	Ala	Cys	Gly	Gly	Lys	Ser	Gln	Lys	Glu	Ala	Gly	Ala
		20						25					30		
Ser	Lys	Ser	Asp	Thr	Ala	Lys	Thr	Glu	Ile	Thr	Trp	Trp	Ala	Phe	Pro
		35					40					45			
Val	Phe	Thr	Gln	Glu	Lys	Ala	Glu	Asp	Gly	Val	Gly	Thr	Tyr	Glu	Lys
	50					55					60				
Lys	Leu	Ile	Ala	Ala	Phe	Glu	Lys	Ala	Asn	Pro	Glu	Ile	Lys	Val	Lys
65					70					75					80
Leu	Glu	Thr	Ile	Asp	Phe	Thr	Ser	Gly	Pro	Glu	Lys	Ile	Thr	Thr	Ala
				85					90					95	
Ile	Glu	Ala	Gly	Thr	Ala	Pro	Asp	Val	Leu	Phe	Asp	Ala	Pro	Gly	Arg
			100						105					110	
Ile	Ile	Gln	Tyr	Gly	Lys	Asn	Gly	Lys	Leu	Ala	Asp	Leu	Asn	Asp	Leu
		115						120					125		
Phe	Thr	Glu	Glu	Phe	Thr	Lys	Asp	Val	Asn	Asn	Asp	Lys	Leu	Ile	Gln
	130					135					140				
Ala	Ser	Lys	Ala	Gly	Asp	Thr	Ala	Tyr	Met	Tyr	Pro	Ile	Ser	Ser	Ala
145					150					155					160
Pro	Phe	Tyr	Met	Ala	Leu	Asn	Lys	Lys	Met	Leu	Lys	Asp	Ala	Gly	Val
			165						170					175	
Leu	Asp	Leu	Val	Lys	Glu	Gly	Trp	Thr	Thr	Asp	Asp	Phe	Glu	Lys	Val
			180						185					190	
Leu	Lys	Ala	Leu	Lys	Asp	Lys	Gly	Tyr	Asn	Pro	Gly	Ser	Phe	Phe	Ala
		195					200					205			
Asn	Gly	Gln	Gly	Gly	Asp	Gln	Gly	Pro	Arg	Ala	Phe	Phe	Ala	Asn	Leu
	210						215					220			
Tyr	Ser	Ser	His	Ile	Thr	Asp	Asp	Lys	Val	Thr	Lys	Tyr	Thr	Thr	Asp
225					230						235				240
Asp	Ala	Asn	Ser	Ile	Lys	Ala	Met	Thr	Lys	Ile	Ser	Asn	Trp	Ile	Lys
				245					250					255	
Asp	Gly	Leu	Met	Met	Asn	Gly	Ser	Gln	Tyr	Asp	Gly	Ser	Ala	Asp	Ile

				260					265					270					
Gln	Asn	Phe	Ala	Asn	Gly	Gln	Thr	Ser	Phe	Thr	Ile	Leu	Trp	Ala	Pro				
		275					280					285							
Ala	Gln	Pro	Gly	Ile	Gln	Ala	Lys	Leu	Leu	Glu	Ala	Ser	Lys	Val	Asp				
	290					295					300								
Tyr	Leu	Glu	Ile	Pro	Phe	Pro	Ser	Asp	Asp	Gly	Lys	Pro	Glu	Leu	Glu				
305					310					315					320				
Tyr	Leu	Val	Asn	Gly	Phe	Ala	Val	Phe	Asn	Asn	Lys	Asp	Glu	Gln	Lys				
			325					330					335						
Val	Ala	Ala	Ser	Lys	Thr	Phe	Ile	Gln	Phe	Ile	Ala	Asp	Asp	Lys	Glu				
		340						345				350							
Trp	Gly	Pro	Lys	Asn	Val	Val	Arg	Thr	Gly	Ala	Phe	Pro	Val	Arg	Thr				
	355						360					365							
Ser	Tyr	Gly	Asp	Leu	Tyr	Lys	Asp	Lys	Arg	Met	Glu	Lys	Ile	Ala	Glu				
	370					375					380								
Trp	Thr	Lys	Phe	Tyr	Ser	Pro	Tyr	Tyr	Asn	Thr	Ile	Asp	Gly	Phe	Ala				
385					390				395						400				
Glu	Met	Arg	Thr	Leu	Trp	Phe	Pro	Met	Val	Gln	Ala	Val	Ser	Asn	Gly				
			405					410						415					
Asp	Glu	Lys	Pro	Glu	Asp	Ala	Leu	Lys	Ala	Phe	Thr	Glu	Lys	Ala	Asn				
		420						425				430							
Lys	Thr	Ile	Lys	Lys	Thr	Gln													
	435																		

<210> SEQ ID NO 97

<211> LENGTH: 1788

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 97

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gtcattgctg	ttgccgttat	cttagcaact	tatttacaag	taaaagctcc	tgtcttctta	120
ggagagtcct	tgactgagtt	gggaaaaatc	ggtcaggctt	attacgttgc	taagatgagt	180
ggccagacac	attttagccc	tgatttatca	gcttttaatg	ccgtgatgtt	taagcttttg	240
atgacttatt	tctttactgt	tttagcta	ctaataata	gtttcttact	tacacgtgtt	300
gtctcacatt	cgactaaccg	catgcgcaag	ggcttatttg	gtaaattaga	acgtttaacc	360
gtcgcctttt	ttgaccgcca	taaagatggg	gagattcttt	ctcgtttcac	gagtgatgtg	420
gataatatcc	aaaactcgct	gaaccaatcc	ttgattcaag	tggtgactaa	tattgccctt	480
tacatcggcc	tggtctggat	gatgtttagg	caagatagcc	gtttagcttt	gttaaccatc	540
gcatcaaccc	cagttgctct	cattttttta	gtgattaaca	tccgtttggc	aagaaaatac	600
accaatatcc	aacagcaaga	agtcagtgtc	ttaaagtctt	ttatggatga	aaccatttca	660
ggacaaaagg	ctattattgt	acaagggtgc	caagaagata	cgatgacagc	ctttttaaag	720
cataatgaaa	gggttcgaca	agccaccttc	aaacgccgtc	tgttctcagg	acaattattt	780
ccagtcatga	atggaatgag	ccttattaac	acggctatcg	tgatttttgt	cggttcaaca	840
attgtcctca	gtgacaaatc	tatgccagca	gcggcagcgc	ttggtttagt	ggttactttt	900
gtacaatatt	cccagcaata	ttaccaaccc	atgatgcaaa	tcgctcttag	ttggggagaa	960
ttgcagctgg	cctttaccgg	tgctcaccgt	attcaagaaa	tgtttgatga	aaccgaagaa	1020
gttcgtccac	aaaatgcacc	agcgttcacc	agcttaaaag	aagcagtggc	gattaaccac	1080
gtcgattttg	ggtatcttcc	tgggcaaaaa	gttttatcag	atgtgtcaat	cgttgcaccc	1140
aagggcaaaa	tgattgccgt	ggttggaccg	acaggttctg	gaaagaccac	tattatgaac	1200
ttgattaacc	gtttctacga	tgtggatgca	ggttcgatta	cctttgatgg	ccgtgatatt	1260
cgtgactacg	atttggtatg	tcttcgtcaa	aaggtagggg	ttgtgttgca	agagtcagtt	1320
cttttttcag	gaaccattac	ggataatatt	cgttttgggt	atcagaccat	tagtcaagac	1380
atggttgaaa	ctgctgcgcg	tgcgacccat	attcatgact	ttatcatgtc	cttaccaaaa	1440
gggtacaata	cctatgtctc	agatgatgac	aatgtctttt	caacagggtc	aaagcagttg	1500
atttctattg	ctaggacgct	actgactgac	cctgaagtgt	tgattttgga	tgaggccact	1560
tcaaatgttg	atacggttac	cgaaagtaaa	attcaacggg	ccatggaagc	tatcgtggca	1620
ggtcgaacta	gctttgtcat	tgctcaccgc	ctcaaaacca	ttttaaatgc	cgatcacatt	1680

attgtgttga aagatggcaa ggtcattgag caaggaaatc atcatgagct attgcatcaa 1740
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<210> SEQ ID NO 98

<211> LENGTH: 595

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 98

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1				5					10					15	
Phe	Ser	Phe	Thr	Val	Ile	Ala	Val	Ala	Val	Ile	Leu	Ala	Thr	Tyr	Leu
			20					25					30		
Gln	Val	Lys	Ala	Pro	Val	Phe	Leu	Gly	Glu	Ser	Leu	Thr	Glu	Leu	Gly
		35					40					45			
Lys	Ile	Gly	Gln	Ala	Tyr	Tyr	Val	Ala	Lys	Met	Ser	Gly	Gln	Thr	His
	50					55					60				
Phe	Ser	Pro	Asp	Leu	Ser	Ala	Phe	Asn	Ala	Val	Met	Phe	Lys	Leu	Leu
65					70					75				80	
Met	Thr	Tyr	Phe	Phe	Thr	Val	Leu	Ala	Asn	Leu	Ile	Tyr	Ser	Phe	Leu
			85						90					95	
Leu	Thr	Arg	Val	Val	Ser	His	Ser	Thr	Asn	Arg	Met	Arg	Lys	Gly	Leu
			100					105					110		
Phe	Gly	Lys	Leu	Glu	Arg	Leu	Thr	Val	Ala	Phe	Phe	Asp	Arg	His	Lys
		115					120					125			
Asp	Gly	Glu	Ile	Leu	Ser	Arg	Phe	Thr	Ser	Asp	Leu	Asp	Asn	Ile	Gln
	130					135					140				
Asn	Ser	Leu	Asn	Gln	Ser	Leu	Ile	Gln	Val	Val	Thr	Asn	Ile	Ala	Leu
145					150					155				160	
Tyr	Ile	Gly	Leu	Val	Trp	Met	Met	Phe	Arg	Gln	Asp	Ser	Arg	Leu	Ala
			165						170					175	
Leu	Leu	Thr	Ile	Ala	Ser	Thr	Pro	Val	Ala	Leu	Ile	Phe	Leu	Val	Ile
			180					185					190		
Asn	Ile	Arg	Leu	Ala	Arg	Lys	Tyr	Thr	Asn	Ile	Gln	Gln	Gln	Glu	Val
		195					200					205			
Ser	Ala	Leu	Asn	Ala	Phe	Met	Asp	Glu	Thr	Ile	Ser	Gly	Gln	Lys	Ala
	210					215					220				
Ile	Ile	Val	Gln	Gly	Val	Gln	Glu	Asp	Thr	Met	Thr	Ala	Phe	Leu	Lys
225					230					235				240	
His	Asn	Glu	Arg	Val	Arg	Gln	Ala	Thr	Phe	Lys	Arg	Arg	Leu	Phe	Ser
			245						250				255		
Gly	Gln	Leu	Phe	Pro	Val	Met	Asn	Gly	Met	Ser	Leu	Ile	Asn	Thr	Ala
			260					265					270		
Ile	Val	Ile	Phe	Val	Gly	Ser	Thr	Ile	Val	Leu	Ser	Asp	Lys	Ser	Met
		275					280					285			
Pro	Ala	Ala	Ala	Ala	Leu	Gly	Leu	Val	Val	Thr	Phe	Val	Gln	Tyr	Ser
	290					295					300				
Gln	Gln	Tyr	Tyr	Gln	Pro	Met	Met	Gln	Ile	Ala	Ser	Ser	Trp	Gly	Glu
305					310					315				320	
Leu	Gln	Leu	Ala	Phe	Thr	Gly	Ala	His	Arg	Ile	Gln	Glu	Met	Phe	Asp
			325						330				335		
Glu	Thr	Glu	Glu	Val	Arg	Pro	Gln	Asn	Ala	Pro	Ala	Phe	Thr	Ser	Leu
			340					345					350		
Lys	Glu	Ala	Val	Ala	Ile	Asn	His	Val	Asp	Phe	Gly	Tyr	Leu	Pro	Gly
		355					360					365			
Gln	Lys	Val	Leu	Ser	Asp	Val	Ser	Ile	Val	Ala	Pro	Lys	Gly	Lys	Met
	370						375				380				
Ile	Ala	Val	Val	Gly	Pro	Thr	Gly	Ser	Gly	Lys	Thr	Thr	Ile	Met	Asn

385		390		395		400									
Leu	Ile	Asn	Arg	Phe	Tyr	Asp	Val	Asp	Ala	Gly	Ser	Ile	Thr	Phe	Asp
				405					410					415	
Gly	Arg	Asp	Ile	Arg	Asp	Tyr	Asp	Leu	Asp	Ser	Leu	Arg	Gln	Lys	Val
			420					425					430		
Gly	Ile	Val	Leu	Gln	Glu	Ser	Val	Leu	Phe	Ser	Gly	Thr	Ile	Thr	Asp
		435					440					445			
Asn	Ile	Arg	Phe	Gly	Asp	Gln	Thr	Ile	Ser	Gln	Asp	Met	Val	Glu	Thr
	450				455					460					
Ala	Ala	Arg	Ala	Thr	His	Ile	His	Asp	Phe	Ile	Met	Ser	Leu	Pro	Lys
465				470					475					480	
Gly	Tyr	Asn	Thr	Tyr	Val	Ser	Asp	Asp	Asp	Asn	Val	Phe	Ser	Thr	Gly
			485					490						495	
Gln	Lys	Gln	Leu	Ile	Ser	Ile	Ala	Arg	Thr	Leu	Leu	Thr	Asp	Pro	Glu
		500						505					510		
Val	Leu	Ile	Leu	Asp	Glu	Ala	Thr	Ser	Asn	Val	Asp	Thr	Val	Thr	Glu
	515						520					525			
Ser	Lys	Ile	Gln	Arg	Ala	Met	Glu	Ala	Ile	Val	Ala	Gly	Arg	Thr	Ser
	530				535					540					
Phe	Val	Ile	Ala	His	Arg	Leu	Lys	Thr	Ile	Leu	Asn	Ala	Asp	His	Ile
545				550					555					560	
Ile	Val	Leu	Lys	Asp	Gly	Lys	Val	Ile	Glu	Gln	Gly	Asn	His	His	Glu
			565					570					575		
Leu	Leu	His	Gln	Lys	Gly	Phe	Tyr	Ala	Glu	Leu	Tyr	His	Asn	Gln	Phe
		580						585					590		
Val	Phe	Glu													
	595														

<210> SEQ ID NO 99

<211> LENGTH: 1728

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 99

ttggaaacga	tattacaaac	aaaattacca	gtagctcaac	tggtggagca	gctaacggag	60
tggctaacta	aaactttctc	aggctctattt	gatattatgc	aagtagttgg	tagctttttg	120
atggattgga	tgaccaaaaac	actttttattt	atccaccctg	tactttttat	tgttctagta	180
acagcagggga	tgtttttctc	tgctaagaaa	aaatggcctt	tgccaacctt	taccttgtta	240
ggattgctct	ttattttacaa	tcaaggggta	tggaagcagc	taatgaatac	ctttactctg	300
gtgttagtag	ctagtttgat	ttcggctactt	attgggtattc	cgctggggat	ttggatggct	360
aaaaatgcca	ctgtccgtca	gattgtgaat	cctatttttg	actttatgca	aaccatgccg	420
gcttttgttt	acttgattcc	tgccgttgcc	ttttttggta	ttggtagtgt	gcctggagta	480
tttgcttcag	tcattctttgc	cttaccacca	acggttcgtt	tcacaaattt	ggccattcgt	540
gacattccaa	cagaattgat	tgaggcctca	gatgcctttg	ggtcaactgg	gaaacaaaag	600
ctctttaaag	tggaattgcc	tttagctaaa	aatactatta	tggcaggtgt	taatcagacc	660
atgatgttag	ccctttccat	ggtagtaaca	ggctccatga	ttggtgctcc	tggttttagga	720
cgtgaagtct	tgtcagccct	tcaacacgct	gatattggta	gtggatttgt	cagtggctct	780
gccttggtta	tcttggcgat	tgtgcttgac	cgtagacac	agttgttcaa	tagcaaacct	840
caagaaaaag	ccaaagctgg	caaaaccaat	aaatggattg	gtttagcagc	ccttgctgtc	900
tttttgatag	ctgcttttagg	acgcggtatt	atggctatga	cttctgggtat	ggcagataag	960
ggtgaaactg	ttaacatcgc	ttacgtgcag	tgggattctg	aggttgcctc	aactcatgtg	1020
attgcagaag	ttttgaaaaa	cgaaggttac	catgtgacct	tgactccgct	tgacaatgcc	1080
gttatgtggc	aaaccgttgc	aaatgggaac	gctgattttt	caactagtgc	ttggttgcca	1140
gtcaccatg	gccaacaata	tcagaaatac	aagtcaaaat	tagatgattt	aggacctaac	1200
ctaaaagggg	ccaaacttgg	tttagctgtt	ccaaaataca	tgacagatgt	caatagtatt	1260
gaggacttaa	gcaaaccaagc	cgatcaaaaa	atcacaggga	tcgaaccagg	tgagggtatc	1320
atggcagcag	cccaaaaagac	tctaaaaagag	tatcataatc	tatctagtgt	ggagttagtg	1380
gcggcatcaa	caggagccat	gacgacttcc	ttggatcaag	cgatcaagaa	aaaagatcct	1440

attgttggtga	cagcttggtc	accacactgg	atgtttgccca	agtatgactt	gaagtacctt	1500
aaagatccta	aagaaatctt	tggctcgact	gagaacatca	ataccattgc	tcgtaaaggc	1560
ttgaaaaaag	aacttcctaaa	tgtctacaaa	atcattgata	agttccactg	gacccaaaaa	1620
gatatggaag	cagtcattgct	tgacatcaac	aaaggcatga	gtccagaagc	tgccgcctaaa	1680
aaatgggtag	aggcaaacaa	atctaaagta	tcaagttgga	caaaataa		1728

<210> SEQ ID NO 100

<211> LENGTH: 575

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 100

Met	Glu	Thr	Ile	Leu	Gln	Thr	Lys	Leu	Pro	Val	Ala	Gln	Leu	Val	Glu
1				5					10				15		
Gln	Leu	Thr	Glu	Trp	Leu	Thr	Lys	Thr	Phe	Ser	Gly	Leu	Phe	Asp	Ile
			20					25				30			
Met	Gln	Val	Val	Gly	Ser	Phe	Leu	Met	Asp	Trp	Met	Thr	Lys	Thr	Leu
		35					40					45			
Leu	Phe	Ile	His	Pro	Leu	Leu	Phe	Ile	Val	Leu	Val	Thr	Ala	Gly	Met
	50					55					60				
Phe	Phe	Leu	Ala	Lys	Lys	Lys	Trp	Pro	Leu	Pro	Thr	Phe	Thr	Leu	Leu
65				70						75				80	
Gly	Leu	Leu	Phe	Ile	Tyr	Asn	Gln	Gly	Leu	Trp	Lys	Gln	Leu	Met	Asn
			85					90					95		
Thr	Phe	Thr	Leu	Val	Leu	Val	Ala	Ser	Leu	Ile	Ser	Val	Leu	Ile	Gly
			100					105					110		
Ile	Pro	Leu	Gly	Ile	Trp	Met	Ala	Lys	Asn	Ala	Thr	Val	Arg	Gln	Ile
	115					120						125			
Val	Asn	Pro	Ile	Leu	Asp	Phe	Met	Gln	Thr	Met	Pro	Ala	Phe	Val	Tyr
	130					135					140				
Leu	Ile	Pro	Ala	Val	Ala	Phe	Phe	Gly	Ile	Gly	Met	Val	Pro	Gly	Val
145				150						155				160	
Phe	Ala	Ser	Val	Ile	Phe	Ala	Leu	Pro	Pro	Thr	Val	Arg	Phe	Thr	Asn
			165					170					175		
Leu	Ala	Ile	Arg	Asp	Ile	Pro	Thr	Glu	Leu	Ile	Glu	Ala	Ser	Asp	Ala
		180						185					190		
Phe	Gly	Ser	Thr	Gly	Lys	Gln	Lys	Leu	Phe	Lys	Val	Glu	Leu	Pro	Leu
	195					200						205			
Ala	Lys	Asn	Thr	Ile	Met	Ala	Gly	Val	Asn	Gln	Thr	Met	Met	Leu	Ala
	210					215					220				
Leu	Ser	Met	Val	Val	Thr	Gly	Ser	Met	Ile	Gly	Ala	Pro	Gly	Leu	Gly
225				230						235				240	
Arg	Glu	Val	Leu	Ser	Ala	Leu	Gln	His	Ala	Asp	Ile	Gly	Ser	Gly	Phe
			245					250					255		
Val	Ser	Gly	Leu	Ala	Leu	Val	Ile	Leu	Ala	Ile	Val	Leu	Asp	Arg	Met
		260						265					270		
Thr	Gln	Leu	Phe	Asn	Ser	Lys	Pro	Gln	Glu	Lys	Ala	Lys	Ala	Gly	Lys
	275					280						285			
Thr	Asn	Lys	Trp	Ile	Gly	Leu	Ala	Ala	Leu	Ala	Val	Phe	Leu	Ile	Ala
	290					295					300				
Ala	Leu	Gly	Arg	Gly	Ile	Met	Ala	Met	Thr	Ser	Gly	Met	Ala	Asp	Lys
305				310						315				320	
Gly	Glu	Thr	Val	Asn	Ile	Ala	Tyr	Val	Gln	Trp	Asp	Ser	Glu	Val	Ala
			325					330					335		
Ser	Thr	His	Val	Ile	Ala	Glu	Val	Leu	Lys	Asn	Glu	Gly	Tyr	His	Val
		340						345					350		
Thr	Leu	Thr	Pro	Leu	Asp	Asn	Ala	Val	Met	Trp	Gln	Thr	Val	Ala	Asn
	355						360					365			

Gly	Asn	Ala	Asp	Phe	Ser	Thr	Ser	Ala	Trp	Leu	Pro	Val	Thr	His	Gly
370						375					380				
Gln	Gln	Tyr	Gln	Lys	Tyr	Lys	Ser	Lys	Leu	Asp	Asp	Leu	Gly	Pro	Asn
385					390					395					400
Leu	Lys	Gly	Thr	Lys	Leu	Gly	Leu	Ala	Val	Pro	Lys	Tyr	Met	Thr	Asp
				405					410					415	
Val	Asn	Ser	Ile	Glu	Asp	Leu	Ser	Lys	Gln	Ala	Asp	Gln	Lys	Ile	Thr
			420					425					430		
Gly	Ile	Glu	Pro	Gly	Ala	Gly	Ile	Met	Ala	Ala	Ala	Gln	Lys	Thr	Leu
		435					440						445		
Lys	Glu	Tyr	His	Asn	Leu	Ser	Ser	Trp	Glu	Leu	Val	Ala	Ala	Ser	Thr
	450					455					460				
Gly	Ala	Met	Thr	Thr	Ser	Leu	Asp	Gln	Ala	Ile	Lys	Lys	Lys	Asp	Pro
465					470					475					480
Ile	Val	Val	Thr	Ala	Trp	Ser	Pro	His	Trp	Met	Phe	Ala	Lys	Tyr	Asp
				485					490					495	
Leu	Lys	Tyr	Leu	Lys	Asp	Pro	Lys	Glu	Ile	Phe	Gly	Ser	Thr	Glu	Asn
			500					505						510	
Ile	Asn	Thr	Ile	Ala	Arg	Lys	Gly	Leu	Lys	Lys	Glu	Leu	Pro	Asn	Val
	515						520						525		
Tyr	Lys	Ile	Ile	Asp	Lys	Phe	His	Trp	Thr	Gln	Lys	Asp	Met	Glu	Ala
	530					535					540				
Val	Met	Leu	Asp	Ile	Asn	Lys	Gly	Met	Ser	Pro	Glu	Ala	Ala	Ala	Lys
545					550				555						560
Lys	Trp	Val	Glu	Ala	Asn	Lys	Ser	Lys	Val	Ser	Ser	Trp	Thr	Lys	
				565					570					575	

<210> SEQ ID NO 101

<211> LENGTH: 1725

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 101

atgaaggaca	tgtctaataa	aaaaacattt	aaaaaatata	gtcgcgtcgc	tgggctactg	60
acggcagctc	ttatcattgg	taaccttggt	actgctaata	ctgaatcgaa	caaacaaaaa	120
actgctagta	cagaaaccac	aacgacaaat	gagcaaccaa	agccagaaa	tagtgagcta	180
actactgaaa	aagcagggtc	gaaaacggat	gatatgctta	actctaacga	tatgattaag	240
cttgctccca	aagaaatgcc	actagaatct	gcagaaaaag	aagaaaaaaa	gtcagaagac	300
aaaaaaaaaga	gcgaagaaga	tcacactgaa	gaaatcaatg	acaagattta	ttcactaaat	360
tataatgagc	ttgaagtact	tgctaaaaat	ggtgaaacca	ttgaaaattt	tgttcctaaa	420
gaaggcggtta	agaaagctga	taaattttatt	gtcattgaaa	gaaagaaaaa	aaatatcaac	480
actacaccag	tcgatatttc	cattattgac	tctgtcactg	ataggaccta	tccagcagcc	540
cttcagctgg	ctaataaagg	ttttaccgaa	aacaaaccag	acgcggtagt	caccaagcga	600
aaccacaaaa	aatccatat	tgattttacca	ggtatgggag	acaaagcaac	ggttgaggtc	660
aatgacccta	cctatgccaa	tgttttcaaca	gctattgata	atcttggtta	ccaatggcat	720
gataattatt	ctgggtggtaa	tacgcttcct	gccagaacac	aatatactga	atcaatggta	780
tattctaagt	cacagattga	agcagctcta	aatgttaata	gcaaaatctt	agatgggtact	840
ttaggcattg	atttcaagtc	gattttcaaaa	ggtgaaaaga	aggatgatgat	tgcagcatac	900
aagcaaat	tttacaccgt	atcagcaaac	cttcctaata	atcctgcgga	tgtgtttgat	960
aaatcgggtga	ccttttaaaga	gttgcaacga	aaagggtgtca	gcaatgaagc	tccgccactc	1020
tttgtgagta	acgtagccta	tggtcgaact	gtttttgtca	aactagaaac	aaagttctaaa	1080
agtaatgatg	ttgaagcggc	cttttagtgca	gctctaaaag	gaacagatgt	taaaactaat	1140
ggaaaatatt	ctgatattct	agaaaatagc	tcattttacag	ctgtcgtttt	aggaggagat	1200
gctgcagagc	acaataaggt	agtcacaaaa	gactttgatg	ttattagaaa	cgttatcaaa	1260
gacaatgcta	ccttcagtag	aaaaaaccca	gcttatccta	tttcatacac	cagtgttttc	1320
cttaaaaata	ataaaattgc	gggtgtcaat	aacagaactg	aatacgttga	aacaacatct	1380
accgagtaca	ctagtggaaa	aattaacctg	tctcatcaag	gcgcgtatgt	tgctcaatat	1440
gaaatccttt	gggatgaaat	caattatgat	gacaaaggaa	aagaagtgat	tacaaaacga	1500

cgttgggaca	acaactggta	tagtaagaca	tcaccattta	gcacagttat	cccactagga	1560
gctaattcac	gaaatatccg	tatcatggct	agagagtgc	ctggccttagc	ttgggaatgg	1620
tggcgaaaag	tgatcgacga	aagagatgtg	aaactgtcta	aagaaatcaa	tgtcaatatc	1680
tcaggatcaa	ccttgagccc	atatggttcg	attacttata	agtag		1725

<210> SEQ ID NO 102

<211> LENGTH: 574

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 102

Met	Lys	Asp	Met	Ser	Asn	Lys	Lys	Thr	Phe	Lys	Lys	Tyr	Ser	Arg	Val
1				5					10					15	
Ala	Gly	Leu	Leu	Thr	Ala	Ala	Leu	Ile	Gly	Asn	Leu	Val	Thr	Ala	
		20						25				30			
Asn	Ala	Glu	Ser	Asn	Lys	Gln	Asn	Thr	Ala	Ser	Thr	Glu	Thr	Thr	Thr
		35					40					45			
Thr	Asn	Glu	Gln	Pro	Lys	Pro	Glu	Ser	Ser	Glu	Leu	Thr	Thr	Glu	Lys
	50					55					60				
Ala	Gly	Gln	Lys	Thr	Asp	Asp	Met	Leu	Asn	Ser	Asn	Asp	Met	Ile	Lys
65					70					75				80	
Leu	Ala	Pro	Lys	Glu	Met	Pro	Leu	Glu	Ser	Ala	Glu	Lys	Glu	Glu	Lys
				85					90				95		
Lys	Ser	Glu	Asp	Lys	Lys	Lys	Ser	Glu	Glu	Asp	His	Thr	Glu	Glu	Ile
			100					105					110		
Asn	Asp	Lys	Ile	Tyr	Ser	Leu	Asn	Tyr	Asn	Glu	Leu	Glu	Val	Leu	Ala
		115					120					125			
Lys	Asn	Gly	Glu	Thr	Ile	Glu	Asn	Phe	Val	Pro	Lys	Glu	Gly	Val	Lys
	130					135					140				
Lys	Ala	Asp	Lys	Phe	Ile	Val	Ile	Glu	Arg	Lys	Lys	Lys	Asn	Ile	Asn
145					150					155				160	
Thr	Thr	Pro	Val	Asp	Ile	Ser	Ile	Ile	Asp	Ser	Val	Thr	Asp	Arg	Thr
				165					170					175	
Tyr	Pro	Ala	Ala	Leu	Gln	Leu	Ala	Asn	Lys	Gly	Phe	Thr	Glu	Asn	Lys
			180					185					190		
Pro	Asp	Ala	Val	Val	Thr	Lys	Arg	Asn	Pro	Gln	Lys	Ile	His	Ile	Asp
	195						200					205			
Leu	Pro	Gly	Met	Gly	Asp	Lys	Ala	Thr	Val	Glu	Val	Asn	Asp	Pro	Thr
	210					215						220			
Tyr	Ala	Asn	Val	Ser	Thr	Ala	Ile	Asp	Asn	Leu	Val	Asn	Gln	Trp	His
225					230					235				240	
Asp	Asn	Tyr	Ser	Gly	Gly	Asn	Thr	Leu	Pro	Ala	Arg	Thr	Gln	Tyr	Thr
				245					250				255		
Glu	Ser	Met	Val	Tyr	Ser	Lys	Ser	Gln	Ile	Glu	Ala	Ala	Leu	Asn	Val
			260					265					270		
Asn	Ser	Lys	Ile	Leu	Asp	Gly	Thr	Leu	Gly	Ile	Asp	Phe	Lys	Ser	Ile
		275					280					285			
Ser	Lys	Gly	Glu	Lys	Lys	Val	Met	Ile	Ala	Ala	Tyr	Lys	Gln	Ile	Phe
	290					295					300				
Tyr	Thr	Val	Ser	Ala	Asn	Leu	Pro	Asn	Asn	Pro	Ala	Asp	Val	Phe	Asp
305					310					315				320	
Lys	Ser	Val	Thr	Phe	Lys	Glu	Leu	Gln	Arg	Lys	Gly	Val	Ser	Asn	Glu
				325					330				335		
Ala	Pro	Pro	Leu	Phe	Val	Ser	Asn	Val	Ala	Tyr	Gly	Arg	Thr	Val	Phe
			340					345					350		
Val	Lys	Leu	Glu	Thr	Ser	Ser	Lys	Ser	Asn	Asp	Val	Glu	Ala	Ala	Phe
	355						360					365			
Ser	Ala	Ala	Leu	Lys	Gly	Thr	Asp	Val	Lys	Thr	Asn	Gly	Lys	Tyr	Ser

370	375	380
Asp Ile Leu Glu Asn Ser Ser Phe Thr Ala Val Val Leu Gly Gly Asp		
385	390	395
Ala Ala Glu His Asn Lys Val Val Thr Lys Asp Phe Asp Val Ile Arg		400
	405	410
Asn Val Ile Lys Asp Asn Ala Thr Phe Ser Arg Lys Asn Pro Ala Tyr		415
	420	425
Pro Ile Ser Tyr Thr Ser Val Phe Leu Lys Asn Asn Lys Ile Ala Gly		430
	435	440
Val Asn Asn Arg Thr Glu Tyr Val Glu Thr Thr Ser Thr Glu Tyr Thr		445
	450	455
Ser Gly Lys Ile Asn Leu Ser His Gln Gly Ala Tyr Val Ala Gln Tyr		460
465	470	475
Glu Ile Leu Trp Asp Glu Ile Asn Tyr Asp Asp Lys Gly Lys Glu Val		480
	485	490
Ile Thr Lys Arg Arg Trp Asp Asn Asn Trp Tyr Ser Lys Thr Ser Pro		495
	500	505
Phe Ser Thr Val Ile Pro Leu Gly Ala Asn Ser Arg Asn Ile Arg Ile		510
	515	520
Met Ala Arg Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Lys Val		525
	530	535
Ile Asp Glu Arg Asp Val Lys Leu Ser Lys Glu Ile Asn Val Asn Ile		540
545	550	555
Ser Gly Ser Thr Leu Ser Pro Tyr Gly Ser Ile Thr Tyr Lys		560
	565	570

<210> SEQ ID NO 103

<211> LENGTH: 648

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 103

atgaaaaaat	ctatattaag	aatttttagct	attgggttatt	tacttatgag	tttttgtttg	60
ttagactccg	tagaggcaga	aaacctcact	gcaagcatta	atattgaagt	tattaatcaa	120
gttgatgttg	ctaccaacaa	acaatcctct	gacatagatg	aaacgtttat	gtttgtaatt	180
gaagcgtag	ataaagaaag	tcctttacct	aattcggtaa	ctacttctgt	taagggaaat	240
gggaaaacat	catttgaaca	gttgactttt	tcagaagttg	gacaatatca	ttataaaatt	300
catcaactgt	taggtaagaa	tagtcaatat	cattatgatg	aaacagtata	tgaagttgtt	360
atttacgtat	tgtataatga	gcaaagtggg	gctttagaaa	ctaacctagt	ttctaacaaa	420
cttgagagaaa	ccgaaaaatc	ggagcttatt	tttaaacaag	aatatagtga	aaaaacaccg	480
gaacctcatc	aaccagatac	aactgagaag	gaaaaaacctc	agaaaaaacg	taatgggtatt	540
ttgccatcaa	ctggtgaaat	ggtgagttac	gtatctgctt	taggaattgt	cttagtggct	600
accattactt	tgtattctat	ttataaaaaag	ctaaagacaa	gcaaatag		648

<210> SEQ ID NO 104

<211> LENGTH: 215

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 104

Met Lys Lys Ser Ile Leu Arg Ile Leu Ala Ile Gly Tyr Leu Leu Met	
1	15
Ser Phe Cys Leu Leu Asp Ser Val Glu Ala Glu Asn Leu Thr Ala Ser	
20	30
Ile Asn Ile Glu Val Ile Asn Gln Val Asp Val Ala Thr Asn Lys Gln	
35	45
Ser Ser Asp Ile Asp Glu Thr Phe Met Phe Val Ile Glu Ala Leu Asp	
50	60
Lys Glu Ser Pro Leu Pro Asn Ser Val Thr Thr Ser Val Lys Gly Asn	

65		70		75		80									
Gly	Lys	Thr	Ser	Phe	Glu	Gln	Leu	Thr	Phe	Ser	Glu	Val	Gly	Gln	Tyr
				85					90					95	
His	Tyr	Lys	Ile	His	Gln	Leu	Leu	Gly	Lys	Asn	Ser	Gln	Tyr	His	Tyr
			100					105					110		
Asp	Glu	Thr	Val	Tyr	Glu	Val	Val	Ile	Tyr	Val	Leu	Tyr	Asn	Glu	Gln
		115					120					125			
Ser	Gly	Ala	Leu	Glu	Thr	Asn	Leu	Val	Ser	Asn	Lys	Leu	Gly	Glu	Thr
	130					135					140				
Glu	Lys	Ser	Glu	Leu	Ile	Phe	Lys	Gln	Glu	Tyr	Ser	Glu	Lys	Thr	Pro
145					150					155					160
Glu	Pro	His	Gln	Pro	Asp	Thr	Thr	Glu	Lys	Glu	Lys	Pro	Gln	Lys	Lys
			165					170					175		
Arg	Asn	Gly	Ile	Leu	Pro	Ser	Thr	Gly	Glu	Met	Val	Ser	Tyr	Val	Ser
		180						185					190		
Ala	Leu	Gly	Ile	Val	Leu	Val	Ala	Thr	Ile	Thr	Leu	Tyr	Ser	Ile	Tyr
	195						200					205			
Lys	Lys	Leu	Lys	Thr	Ser	Lys									
	210					215									

<210> SEQ ID NO 105

<211> LENGTH: 2313

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 105

atgaggtatt	ttatggtgaa	atggaacacg	aaacaaaagc	gtataagtca	tcaaagatta	60
ggtctcttgg	atttggggcc	ggtgctatta	cgtacgttga	gactactgtc	taactttttt	120
tatattgtta	tcttcctttt	tggaatgatg	ggatttggta	tggcatttgg	gtatttggct	180
agtcagattg	aatctgttaa	ggtaccaagt	aaagaaaagt	tagtcaaaca	agttgaatca	240
ttaacgatga	tttcgcaa	gaactattct	gataatagtt	taatttctac	tttagatacg	300
gatttacttc	gaacaccagt	agctaata	gcgatttcag	agaatatcaa	aaaagctatt	360
gtatcaacag	aagacgaaca	ttttcaagaa	cataaaggta	tcgtgccaaa	agctgttttt	420
cgggcaacat	tggcttctgt	attgggattt	ggagaagcta	gtggagggtc	gaccttaaca	480
cagcaattag	tcaagcaaca	agttttggga	gacgatccca	catttaagcg	caagtctaag	540
gagatcgttt	acgctcttgc	cttagagcgt	tatatgtcca	aagacaatat	cttatgtgat	600
tatcttaatg	tttcaccttt	tggccgtaac	aacaagggtc	aaaatattgc	tggtgttgaa	660
gaagctgcgc	gtggcatttt	tggcgtttct	gccaaaagatt	taacgggtgcc	acaggcgaca	720
tttttggcgg	gtcttccgca	gagtcctatt	gtttactctc	cttatttgtc	aacgggacaa	780
ctgaaatcag	aaaaggacat	ggcttatggc	atcaagcgtc	agcaaaatgt	tctctttaac	840
atgtaccgta	cagggtgttct	gtctaaaaaa	gaatacgagg	actataaggc	ttatccgatt	900
caaaaggatt	ttattcaacc	gggaagtgca	atagtaaata	atcacgatta	cctttattac	960
acggtgttag	cggatgctaa	gaaagccatg	tatagctatt	tgattaagcg	agataagggtg	1020
tctagtcgtg	acttgaaaaa	tgacgagact	aaggctgctt	atgaagagag	agccttaaca	1080
gaattgcaac	aggggtggcta	taccatcacc	acaaccatta	ataagcctat	ttacaatgcg	1140
atgcagacag	cggcagctca	gtttggtggc	ttgttagatg	atggcactgg	tacagttcaa	1200
atgggaaatg	tcttgacaga	caatgcgact	ggtgctgtgt	taggttttgt	tggtggtaga	1260
gattatgctc	tgaatcaaaa	taatcatgct	ttcaatacag	ttagatcgcc	aggttctagc	1320
attaaaccga	taatcgctta	tggtcctgct	attgatcaag	gtttaatggg	gagtgctagc	1380
gttttgtcta	attaccaaac	aacttactcg	agtggccaaa	aaatcatgca	tgctgatagt	1440
gaaggaacag	ccatgatgcc	acttcaagag	gccctaaata	cttcttggaa	catcccagct	1500
ttttggacac	agaaattact	gcgtgaaaaa	ggtgtcgatg	tcgaaaatta	tatgacaaaa	1560
atgggttata	agattgcaga	ctactcgatt	gaaagtgttac	ctctaggggg	cggatttgaa	1620
gtctcggttg	ctcaacaaaac	caatgcttac	caaagtcttt	caaacaatgg	cttatatcaa	1680
aagcaataata	ttgtagataa	gattactgct	agcgatggta	cagtcgttta	caaacaatgaa	1740
aataagccaa	ttcgtatttt	ttctgcagca	acagctacga	ttttacaaga	attgttgaga	1800
ggtccgatta	cttcaggcgc	tacgactact	ttcaagaacc	gtttggcggc	tattaatccg	1860
tggtttgcta	atgctgattg	gattgggtaag	accggaacaa	ctgagaatta	tacggatggt	1920

tggctagtcc	tgtctactcc	aaaagttact	ttaggcgggtt	gggcaggaca	tgatgacaat	1980
acctcattag	cgccattaac	aggatataac	aataattcta	attatcttgc	ctatttagct	2040
aatgccatta	atcaggccga	tcccaatgtt	attggagtag	ggcaacgctt	caacttagat	2100
ccaggagtca	ttaaggcgaa	tgtcttgaag	tcaacaggtt	tacaaccagg	aactgttaat	2160
gtcaatggac	atactttttc	tgttggtgga	gaaatgacca	ccagtctatg	gtcccaaaaa	2220
ggaccggggg	ctatgactta	ccgatttgct	attggtggca	cggatgccga	ttatcaaaaa	2280
gcctggggga	acttcggggtt	cagaaaaaat	tag			2313

<210> SEQ ID NO 106

<211> LENGTH: 770

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 106

Met	Arg	Tyr	Phe	Met	Val	Lys	Trp	Asn	Thr	Lys	Gln	Lys	Arg	Ile	Ser
1				5					10					15	
His	Gln	Arg	Leu	Gly	Leu	Leu	Asp	Leu	Gly	Pro	Val	Leu	Leu	Arg	Thr
			20					25						30	
Leu	Arg	Leu	Leu	Ser	Asn	Phe	Phe	Tyr	Ile	Val	Ile	Phe	Leu	Phe	Gly
			35				40					45			
Met	Met	Gly	Phe	Gly	Met	Ala	Phe	Gly	Tyr	Leu	Ala	Ser	Gln	Ile	Glu
	50					55					60				
Ser	Val	Lys	Val	Pro	Ser	Lys	Glu	Ser	Leu	Val	Lys	Gln	Val	Glu	Ser
65					70					75				80	
Leu	Thr	Met	Ile	Ser	Gln	Met	Asn	Tyr	Ser	Asp	Asn	Ser	Leu	Ile	Ser
			85						90					95	
Thr	Leu	Asp	Thr	Asp	Leu	Leu	Arg	Thr	Pro	Val	Ala	Asn	Asp	Ala	Ile
			100					105					110		
Ser	Glu	Asn	Ile	Lys	Lys	Ala	Ile	Val	Ser	Thr	Glu	Asp	Glu	His	Phe
		115					120					125			
Gln	Glu	His	Lys	Gly	Ile	Val	Pro	Lys	Ala	Val	Phe	Arg	Ala	Thr	Leu
	130					135					140				
Ala	Ser	Val	Leu	Gly	Phe	Gly	Glu	Ala	Ser	Gly	Gly	Ser	Thr	Leu	Thr
145					150					155				160	
Gln	Gln	Leu	Val	Lys	Gln	Gln	Val	Leu	Gly	Asp	Asp	Pro	Thr	Phe	Lys
			165						170					175	
Arg	Lys	Ser	Lys	Glu	Ile	Val	Tyr	Ala	Leu	Ala	Leu	Glu	Arg	Tyr	Met
			180					185					190		
Ser	Lys	Asp	Asn	Ile	Leu	Cys	Asp	Tyr	Leu	Asn	Val	Ser	Pro	Phe	Gly
		195					200					205			
Arg	Asn	Asn	Lys	Gly	Gln	Asn	Ile	Ala	Gly	Val	Glu	Glu	Ala	Ala	Arg
	210					215					220				
Gly	Ile	Phe	Gly	Val	Ser	Ala	Lys	Asp	Leu	Thr	Val	Pro	Gln	Ala	Ala
225					230					235				240	
Phe	Leu	Ala	Gly	Leu	Pro	Gln	Ser	Pro	Ile	Val	Tyr	Ser	Pro	Tyr	Leu
			245						250					255	
Ser	Thr	Gly	Gln	Leu	Lys	Ser	Glu	Lys	Asp	Met	Ala	Tyr	Gly	Ile	Lys
			260					265					270		
Arg	Gln	Gln	Asn	Val	Leu	Phe	Asn	Met	Tyr	Arg	Thr	Gly	Val	Leu	Ser
		275					280					285			
Lys	Lys	Glu	Tyr	Glu	Asp	Tyr	Lys	Ala	Tyr	Pro	Ile	Gln	Lys	Asp	Phe
	290					295					300				
Ile	Gln	Pro	Gly	Ser	Ala	Ile	Val	Asn	Asn	His	Asp	Tyr	Leu	Tyr	Tyr
305					310					315				320	
Thr	Val	Leu	Ala	Asp	Ala	Lys	Lys	Ala	Met	Tyr	Ser	Tyr	Leu	Ile	Lys
			325						330					335	
Arg	Asp	Lys	Val	Ser	Ser	Arg	Asp	Leu	Lys	Asn	Asp	Glu	Thr	Lys	Ala
			340					345					350		

Ala	Tyr	Glu	Glu	Arg	Ala	Leu	Thr	Glu	Leu	Gln	Gln	Gly	Gly	Tyr	Thr		
		355					360					365					
Ile	Thr	Thr	Thr	Ile	Asn	Lys	Pro	Ile	Tyr	Asn	Ala	Met	Gln	Thr	Ala		
		370				375					380						
Ala	Ala	Gln	Phe	Gly	Gly	Leu	Leu	Asp	Asp	Gly	Thr	Gly	Thr	Val	Gln		
385					390					395					400		
Met	Gly	Asn	Val	Leu	Thr	Asp	Asn	Ala	Thr	Gly	Ala	Val	Leu	Gly	Phe		
			405						410					415			
Val	Gly	Gly	Arg	Asp	Tyr	Ala	Leu	Asn	Gln	Asn	Asn	His	Ala	Phe	Asn		
			420					425					430				
Thr	Val	Arg	Ser	Pro	Gly	Ser	Ser	Ile	Lys	Pro	Ile	Ile	Ala	Tyr	Gly		
		435					440					445					
Pro	Ala	Ile	Asp	Gln	Gly	Leu	Met	Gly	Ser	Ala	Ser	Val	Leu	Ser	Asn		
		450				455					460						
Tyr	Pro	Thr	Thr	Tyr	Ser	Ser	Gly	Gln	Lys	Ile	Met	His	Ala	Asp	Ser		
465				470						475					480		
Glu	Gly	Thr	Ala	Met	Met	Pro	Leu	Gln	Glu	Ala	Leu	Asn	Thr	Ser	Trp		
				485					490						495		
Asn	Ile	Pro	Ala	Phe	Trp	Thr	Gln	Lys	Leu	Leu	Arg	Glu	Lys	Gly	Val		
			500					505					510				
Asp	Val	Glu	Asn	Tyr	Met	Thr	Lys	Met	Gly	Tyr	Lys	Ile	Ala	Asp	Tyr		
		515					520					525					
Ser	Ile	Glu	Ser	Leu	Pro	Leu	Gly	Gly	Gly	Ile	Glu	Val	Ser	Val	Ala		
		530				535					540						
Gln	Gln	Thr	Asn	Ala	Tyr	Gln	Met	Leu	Ser	Asn	Asn	Gly	Leu	Tyr	Gln		
545				550						555					560		
Lys	Gln	Tyr	Ile	Val	Asp	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Thr	Val	Val		
				565					570						575		
Tyr	Lys	His	Glu	Asn	Lys	Pro	Ile	Arg	Ile	Phe	Ser	Ala	Ala	Thr	Ala		
			580					585					590				
Thr	Ile	Leu	Gln	Glu	Leu	Leu	Arg	Gly	Pro	Ile	Thr	Ser	Gly	Ala	Thr		
		595					600					605					
Thr	Thr	Phe	Lys	Asn	Arg	Leu	Ala	Ala	Ile	Asn	Pro	Trp	Leu	Ala	Asn		
		610				615					620						
Ala	Asp	Trp	Ile	Gly	Lys	Thr	Gly	Thr	Thr	Glu	Asn	Tyr	Thr	Asp	Val		
625				630						635					640		
Trp	Leu	Val	Leu	Ser	Thr	Pro	Lys	Val	Thr	Leu	Gly	Gly	Trp	Ala	Gly		
				645					650					655			
His	Asp	Asp	Asn	Thr	Ser	Leu	Ala	Pro	Leu	Thr	Gly	Tyr	Asn	Asn	Asn		
			660				665						670				
Ser	Asn	Tyr	Leu	Ala	Tyr	Leu	Ala	Asn	Ala	Ile	Asn	Gln	Ala	Asp	Pro		
		675					680					685					
Asn	Val	Ile	Gly	Val	Gly	Gln	Arg	Phe	Asn	Leu	Asp	Pro	Gly	Val	Ile		
		690				695					700						
Lys	Ala	Asn	Val	Leu	Lys	Ser	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Val	Asn		
705				710						715					720		
Val	Asn	Gly	His	Thr	Phe	Ser	Val	Gly	Gly	Glu	Met	Thr	Thr	Ser	Leu		
			725					730						735			
Trp	Ser	Gln	Lys	Gly	Pro	Gly	Ala	Met	Thr	Tyr	Arg	Phe	Ala	Ile	Gly		
		740					745					750					
Gly	Thr	Asp	Ala	Asp	Tyr	Gln	Lys	Ala	Trp	Gly	Asn	Phe	Gly	Phe	Arg		
		755				760						765					
Lys	Asn																
		770															

<210> SEQ ID NO 107

<211> LENGTH: 366

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<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 107
atggctcgta ttgctggagt tgatattcca aatgataaac gcgtagtaat ttcacttact      60
tatgttttacg gaattggtct tgcaacatct aaaaaaatct tagcagctgc aggtatttct      120
gaagatatcc gtgttaaaga tttaacatca gatcaagaag atgctatccg tcgtgaagtg      180
gatgcaatca aagttgaagg tgaccttcga cgtgaagtaa acatgaacat taaacgtttg      240
atggaaatcg gttcataccg tggaatccgt catcgtcgtg gacttcctgt ccgtggacaa      300
aatactaaaa acaatgctcg cactcgtaaa gggaaagctg ttgcgattgc aggtaagaaa      360
aaataa

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<210> SEQ ID NO 108
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 108
Met Ala Arg Ile Ala Gly Val Asp Ile Pro Asn Asp Lys Arg Val Val
1           5           10           15
Ile Ser Leu Thr Tyr Val Tyr Gly Ile Gly Leu Ala Thr Ser Lys Lys
20          25          30
Ile Leu Ala Ala Ala Gly Ile Ser Glu Asp Ile Arg Val Lys Asp Leu
35          40          45
Thr Ser Asp Gln Glu Asp Ala Ile Arg Arg Glu Val Asp Ala Ile Lys
50          55          60
Val Glu Gly Asp Leu Arg Arg Glu Val Asn Met Asn Ile Lys Arg Leu
65          70          75          80
Met Glu Ile Gly Ser Tyr Arg Gly Ile Arg His Arg Arg Gly Leu Pro
85          90          95
Val Arg Gly Gln Asn Thr Lys Asn Asn Ala Arg Thr Arg Lys Gly Lys
100         105         110
Ala Val Ala Ile Ala Gly Lys Lys Lys
115         120

```

```

<210> SEQ ID NO 109
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 109
atgattcaac aagaaactcg cttgaaagtt gctgataata gcggtgctcg tgagatcttg      60
actatcaaag tacttggtgg ttcaggacgt aaattcgcta acatcggtga cgtaatcggt      120
gcttctgtaa aacaagctac tcctggtgga gcagttaaaa aaggtgatgt gggttaaagct      180
gttatcgttc gtacaaaaaac tgggtgcacgc cgtccagacg gttcatacat caaatttgac      240
gacaatgctg ctgtaatcat ccgtgatgat aaaactcctc gcggaactcg tatctttggc      300
ccagttgcac gcgaattgcg tgagggtggc tacatgaaga tcgtatcact tgcaccagaa      360
gtacttttaa
369

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<210> SEQ ID NO 110
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 110
Met Ile Gln Gln Glu Thr Arg Leu Lys Val Ala Asp Asn Ser Gly Ala
1           5           10           15
Arg Glu Ile Leu Thr Ile Lys Val Leu Gly Gly Ser Gly Arg Lys Phe
20          25          30
Ala Asn Ile Gly Asp Val Ile Val Ala Ser Val Lys Gln Ala Thr Pro
35          40          45

```

Gly	Gly	Ala	Val	Lys	Lys	Gly	Asp	Val	Val	Lys	Ala	Val	Ile	Val	Arg
50						55					60				
Thr	Lys	Thr	Gly	Ala	Arg	Arg	Pro	Asp	Gly	Ser	Tyr	Ile	Lys	Phe	Asp
65					70					75					80
Asp	Asn	Ala	Ala	Val	Ile	Ile	Arg	Asp	Asp	Lys	Thr	Pro	Arg	Gly	Thr
				85					90					95	
Arg	Ile	Phe	Gly	Pro	Val	Ala	Arg	Glu	Leu	Arg	Glu	Gly	Gly	Tyr	Met
			100					105					110		
Lys	Ile	Val	Ser	Leu	Ala	Pro	Glu	Val	Leu						
		115					120								

<210> SEQ ID NO 111
 <211> LENGTH: 834
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 111

gtgggtatta	aagtttataa	accaacgaca	aatggccgtc	gtaacatgac	ttctttggat	60
ttcgcgga	tcacaacaag	cacgcctgag	aaatcattgc	ttgtttctct	taagagcaaa	120
gctggtcgta	acaacaatgg	tcgcatcaca	gttcgctcacc	aaggtgggtgg	acacaaacgt	180
cattaccgtt	tgatcgactt	caaacgtaac	aaagatggcg	ttgaagcagt	tgtaaaaca	240
atcgaatacg	atccaaaccg	tactgcaaac	atcgcaacttg	tacattacac	tgacgggtgtg	300
aaagcttaca	tcattgcacc	taaaggtctt	gaagtaggtc	aacgtattgt	ttctgggtcca	360
gatgcagata	tcaaagttgg	taacgcactt	ccattagcaa	acattcctgt	cggtagagtt	420
gttcacaata	ttgagttgaa	acctggtaaa	ggtggagaac	ttgttcgtgc	agctggagct	480
tctgctcaag	tacttgggtca	agaaggtaaa	tacgttcttg	ttcgtcttca	atcaggcgaa	540
gttcgtatga	ttcttgggtac	atgccgtgca	actatcggtg	ctggttggtaa	cgaacaacaa	600
tcatttggtta	acattgggtaa	agcaggacgt	agccgttgga	aaggtatccg	cccaacagtt	660
cgtgggttctg	taatgaaccc	taacgatcac	ccacacgggtg	gtggtgaagg	taaagcacca	720
gttgacgta	aagcgccatc	aactccatgg	ggtaaaccag	cgcttggtct	taaaactcgt	780
aacaagaaa	ctaaatcaga	caaacttatc	gttcgtcgtc	gtaacgaaaa	ataa	834

<210> SEQ ID NO 112
 <211> LENGTH: 277
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 112

Met	Gly	Ile	Lys	Val	Tyr	Lys	Pro	Thr	Thr	Asn	Gly	Arg	Arg	Asn	Met
1			5					10						15	
Thr	Ser	Leu	Asp	Phe	Ala	Glu	Ile	Thr	Thr	Ser	Thr	Pro	Glu	Lys	Ser
		20					25					30			
Leu	Leu	Val	Ser	Leu	Lys	Ser	Lys	Ala	Gly	Arg	Asn	Asn	Asn	Gly	Arg
		35				40					45				
Ile	Thr	Val	Arg	His	Gln	Gly	Gly	Gly	His	Lys	Arg	His	Tyr	Arg	Leu
	50				55				60						
Ile	Asp	Phe	Lys	Arg	Asn	Lys	Asp	Gly	Val	Glu	Ala	Val	Val	Lys	Thr
65				70					75					80	
Ile	Glu	Tyr	Asp	Pro	Asn	Arg	Thr	Ala	Asn	Ile	Ala	Leu	Val	His	Tyr
			85				90						95		
Thr	Asp	Gly	Val	Lys	Ala	Tyr	Ile	Ile	Ala	Pro	Lys	Gly	Leu	Glu	Val
		100					105					110			
Gly	Gln	Arg	Ile	Val	Ser	Gly	Pro	Asp	Ala	Asp	Ile	Lys	Val	Gly	Asn
	115					120					125				
Ala	Leu	Pro	Leu	Ala	Asn	Ile	Pro	Val	Gly	Thr	Val	Val	His	Asn	Ile
	130				135						140				
Glu	Leu	Lys	Pro	Gly	Lys	Gly	Gly	Glu	Leu	Val	Arg	Ala	Ala	Gly	Ala
145				150					155					160	
Ser	Ala	Gln	Val	Leu	Gly	Gln	Glu	Gly	Lys	Tyr	Val	Leu	Val	Arg	Leu

				165					170					175			
Gln	Ser	Gly	Glu	Val	Arg	Met	Ile	Leu	Gly	Thr	Cys	Arg	Ala	Thr	Ile		
			180					185					190				
Gly	Thr	Val	Gly	Asn	Glu	Gln	Gln	Ser	Leu	Val	Asn	Ile	Gly	Lys	Ala		
		195					200					205					
Gly	Arg	Ser	Arg	Trp	Lys	Gly	Ile	Arg	Pro	Thr	Val	Arg	Gly	Ser	Val		
	210					215					220						
Met	Asn	Pro	Asn	Asp	His	Pro	His	Gly	Gly	Gly	Glu	Gly	Lys	Ala	Pro		
225				230						235					240		
Val	Gly	Arg	Lys	Ala	Pro	Ser	Thr	Pro	Trp	Gly	Lys	Pro	Ala	Leu	Gly		
			245					250						255			
Leu	Lys	Thr	Arg	Asn	Lys	Lys	Ala	Lys	Ser	Asp	Lys	Leu	Ile	Val	Arg		
		260						265					270				
Arg	Arg	Asn	Glu	Lys													
		275															

<210> SEQ ID NO 113

<211> LENGTH: 627

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 113

atgacaaaag	gaatccttagg	gaaaaaagtg	ggaatgactc	aaattttcac	tgaatcaggc	60
gaattcatcc	ctgttactgt	cattgaagca	actccaaacg	ttgtgcttca	agttaaaact	120
gttgaaacag	acggttatga	agcagttcag	gttggttttg	atgacaaaacg	tgaagtcttg	180
agtaacaaac	ctgccaaaagg	ccatgttgca	aaagcaaaca	cagctcctaa	gcgcttcatt	240
cgtgaattca	aaaacattga	aggcttagaa	gttggtgcag	aattatctgt	agaacaattt	300
gaagctggtg	atgttggtga	cgtcacaggg	atatcaaaaag	gtaaaagggtt	ccaagggtgt	360
atcaaacgcc	atggtcaatc	acgtggctct	atggctcacg	gttctcgtta	ccatcgtcgc	420
ccagggttcta	tgggacctgt	tgcgcctaac	cgcgttttca	aaaacaaacg	cttggcagga	480
cgtatgggtg	gtaaccgtgt	aacagttcaa	aaccttgaaa	ttgtacaagt	tatcccagaa	540
aagaacgtta	tccttggttaa	aggtaacgta	ccagggtgcta	agaaatctct	tatcactatc	600
aagtcagcag	ttaaagctgc	taaataa				627

<210> SEQ ID NO 114

<211> LENGTH: 208

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 114

Met	Thr	Lys	Gly	Ile	Leu	Gly	Lys	Lys	Val	Gly	Met	Thr	Gln	Ile	Phe
1			5						10				15		
Thr	Glu	Ser	Gly	Glu	Phe	Ile	Pro	Val	Thr	Val	Ile	Glu	Ala	Thr	Pro
		20					25					30			
Asn	Val	Val	Leu	Gln	Val	Lys	Thr	Val	Glu	Thr	Asp	Gly	Tyr	Glu	Ala
		35				40					45				
Val	Gln	Val	Gly	Phe	Asp	Asp	Lys	Arg	Glu	Val	Leu	Ser	Asn	Lys	Pro
	50				55				60						
Ala	Lys	Gly	His	Val	Ala	Lys	Ala	Asn	Thr	Ala	Pro	Lys	Arg	Phe	Ile
65			70						75				80		
Arg	Glu	Phe	Lys	Asn	Ile	Glu	Gly	Leu	Glu	Val	Gly	Ala	Glu	Leu	Ser
			85				90					95			
Val	Glu	Gln	Phe	Glu	Ala	Gly	Asp	Val	Val	Asp	Val	Thr	Gly	Ile	Ser
		100					105					110			
Lys	Gly	Lys	Gly	Phe	Gln	Gly	Val	Ile	Lys	Arg	His	Gly	Gln	Ser	Arg
		115				120					125				
Gly	Pro	Met	Ala	His	Gly	Ser	Arg	Tyr	His	Arg	Arg	Pro	Gly	Ser	Met
	130					135				140					
Gly	Pro	Val	Ala	Pro	Asn	Arg	Val	Phe	Lys	Asn	Lys	Arg	Leu	Ala	Gly

145		150		155		160									
Arg	Met	Gly	Gly	Asn	Arg	Val	Thr	Val	Gln	Asn	Leu	Glu	Ile	Val	Gln
		165		170		175									
Val	Ile	Pro	Glu	Lys	Asn	Val	Ile	Leu	Val	Lys	Gly	Asn	Val	Pro	Gly
		180		185		190									
Ala	Lys	Lys	Ser	Leu	Ile	Thr	Ile	Lys	Ser	Ala	Val	Lys	Ala	Ala	Lys
		195		200		205									

<210> SEQ ID NO 115
 <211> LENGTH: 309
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 115

atggc	aaaaca	aaaaaatccg	tatccgtttg	aaagcgtacg	aacaccgtac	acttgataca	60
gcggc	cagaaa	aaatcgttga	aactgcaaca	cgtaacaggtg	ctacagttgc	tggaaccagtt	120
ccactt	ccaa	ctgaacgcag	tctttacaca	attattcgtg	cgactcacia	atacaaagat	180
tctcg	cgaac	aatttgaaat	gcgtacacac	aaacgtttgg	tagacatcat	caatccaaca	240
caaaaa	actg	ttgatgcttt	gatgaaactt	gatcttccaa	gtggtgtcaa	cgtagaaatc	300
aaactt	taaa						309

<210> SEQ ID NO 116
 <211> LENGTH: 102
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 116

Met	Ala	Asn	Lys	Lys	Ile	Arg	Ile	Arg	Leu	Lys	Ala	Tyr	Glu	His	Arg
1		5		10		15									
Thr	Leu	Asp	Thr	Ala	Ala	Glu	Lys	Ile	Val	Glu	Thr	Ala	Thr	Arg	Thr
		20		25		30									
Gly	Ala	Thr	Val	Ala	Gly	Pro	Val	Pro	Leu	Pro	Thr	Glu	Arg	Ser	Leu
		35		40		45									
Tyr	Thr	Ile	Ile	Arg	Ala	Thr	His	Lys	Tyr	Lys	Asp	Ser	Arg	Glu	Gln
		50		55		60									
Phe	Glu	Met	Arg	Thr	His	Lys	Arg	Leu	Val	Asp	Ile	Ile	Asn	Pro	Thr
65		70		75		80									
Gln	Lys	Thr	Val	Asp	Ala	Leu	Met	Lys	Leu	Asp	Leu	Pro	Ser	Gly	Val
		85		90		95									
Asn	Val	Glu	Ile	Lys	Leu										
		100													

<210> SEQ ID NO 117
 <211> LENGTH: 372
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 117

atgaagaagc	ctagtattgt	tcaattaaat	aatcattata	ttaagaaaga	gaatctcaaa	60
aaaaaatttg	aagaagaaga	atctcaaaaa	agaaatcggt	ttatgggatg	gatccttgta	120
agtatgatgt	ttttatttat	tttgccaact	tataatcttg	tcaaaagtta	tggttgatttt	180
gaaaagcaaa	atcaacaggt	ggttaaaatta	aaaaaaagag	ataatgaatt	gtcagagagt	240
acaaaaaaag	aaaaacaatt	agcagaacga	ctaaaagatg	ataattttgt	caaaaaatat	300
gctagggcaa	aatactat	ttt atcgcgtgaa	ggagaaatga	tttatcctat	tccaggacta	360
ttaccaaaat	ga					372

<210> SEQ ID NO 118
 <211> LENGTH: 123
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 118

```
Met Lys Lys Pro Ser Ile Val Gln Leu Asn Asn His Tyr Ile Lys Lys
 1           5           10           15
Glu Asn Leu Lys Lys Lys Phe Glu Glu Glu Glu Ser Gln Lys Arg Asn
          20           25           30
Arg Phe Met Gly Trp Ile Leu Val Ser Met Met Phe Leu Phe Ile Leu
          35           40           45
Pro Thr Tyr Asn Leu Val Lys Ser Tyr Val Asp Phe Glu Lys Gln Asn
          50           55           60
Gln Gln Val Val Lys Leu Lys Lys Glu Tyr Asn Glu Leu Ser Glu Ser
65           70           75           80
Thr Lys Lys Glu Lys Gln Leu Ala Glu Arg Leu Lys Asp Asp Asn Phe
          85           90           95
Val Lys Lys Tyr Ala Arg Ala Lys Tyr Tyr Leu Ser Arg Glu Gly Glu
          100          105          110
Met Ile Tyr Pro Ile Pro Gly Leu Leu Pro Lys
          115          120
```

<210> SEQ ID NO 119

<211> LENGTH: 1224

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 119

```
atgccaaagta tgaaacatat cttaaaatcc ttaagtattt tactaattgg atttttagga      60
ggattaatag caattattac attcaataat ctctaccac attctccatc aaaaataaat      120
tcaggtaagg caacaactag taatatgggtt ttaacaaca caaccaatac tactaaagct      180
gtcaaagctg ttcaaaatgc agttgtatca gttattaatt atcaagataa cccttcttca      240
tcccttttcta acccttatac aaaactcttt ggagaagggc gttcaaaaga gaataaggat      300
gctgaattat ctatttttag tgaaggatct ggggtcattt atcgaaaaga tggcaactcc      360
gcttacgttg ttactaataa ccatgttatc gacggagcta aacgaattga aattcttatg      420
gcagacggat ctaaagttgt tgggtgaatta gttggagctg atacttattc ggatttagct      480
gttgtaaga tctcttcaga taagataaaa acagtagctg aatttgcaga ttctacaaaa      540
ctaaatgttg gagaagttgc tattgctatc ggcagcccac taggaacaca atacgctaata      600
tctgttactc aaggaaatcgt ctctagttta agtcgtactg taacttttaa aaacgagaat      660
ggtgagactg tctcaacaaa tgctattcag acagatgctg ctattaaccc tggaaactct      720
ggtggaccac taattaatat tgagggggcaa gtaatcggaa ttaattcaag taaaatttct      780
tctaccccaa ctggtagcaa cggtaatagt ggtgctgttg aaggaattgg ttttgctatc      840
ccatctactg atgttattaa aattattaaa caactagaaa ctaatggtga agttatcaga      900
cctgctcttg gaatatccat ggtcaattta aatgacttat ccacaaatgc tcttagtcaa      960
attaatattc caactagtgt aactggtggt attgtagtag cagaagttaa ggaaggaatg     1020
ccggcatctg gcaaacttgc tcagtacgat gtgattacag aaattgatgg caaaacagtt     1080
aattcaatta gtgatttaca aagtagtcta tacggacacg atattaatga tactattaaa     1140
gtaacttttt atagaggaac tacaaagaaa aaagcagata tcaaattaac aaaaactact     1200
caagatttga ctaaaacgca gtaa                                     1224
```

<210> SEQ ID NO 120

<211> LENGTH: 407

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 120

```
Met Pro Ser Met Lys His Ile Leu Lys Ser Leu Ser Ile Leu Leu Ile
 1           5           10           15
Gly Phe Leu Gly Gly Leu Ile Ala Ile Thr Phe Asn Asn Leu Tyr
          20           25           30
Pro His Ser Pro Ser Lys Ile Asn Ser Gly Lys Ala Thr Thr Ser Asn
          35           40           45
Met Val Phe Asn Asn Thr Thr Asn Thr Thr Lys Ala Val Lys Ala Val
```

50		55		60
Gln Asn Ala Val Val Ser Val Ile Asn Tyr Gln Asp Asn Pro Ser Ser				
65		70		75
Ser Leu Ser Asn Pro Tyr Thr Lys Leu Phe Gly Glu Gly Arg Ser Lys				80
		85		90
Glu Asn Lys Asp Ala Glu Leu Ser Ile Phe Ser Glu Gly Ser Gly Val				95
		100		105
Ile Tyr Arg Lys Asp Gly Asn Ser Ala Tyr Val Val Thr Asn Asn His				110
		115		120
Val Ile Asp Gly Ala Lys Arg Ile Glu Ile Leu Met Ala Asp Gly Ser				125
		130		135
Lys Val Val Gly Glu Leu Val Gly Ala Asp Thr Tyr Ser Asp Leu Ala				140
		145		150
Val Val Lys Ile Ser Ser Asp Lys Ile Lys Thr Val Ala Glu Phe Ala				155
		165		170
Asp Ser Thr Lys Leu Asn Val Gly Glu Val Ala Ile Ala Ile Gly Ser				175
		180		185
Pro Leu Gly Thr Gln Tyr Ala Asn Ser Val Thr Gln Gly Ile Val Ser				190
		195		200
Ser Leu Ser Arg Thr Val Thr Leu Lys Asn Glu Asn Gly Glu Thr Val				205
		210		215
Ser Thr Asn Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn Ser				220
		225		230
Gly Gly Pro Leu Ile Asn Ile Glu Gly Gln Val Ile Gly Ile Asn Ser				235
		245		250
Ser Lys Ile Ser Ser Thr Pro Thr Gly Ser Asn Gly Asn Ser Gly Ala				255
		260		265
Val Glu Gly Ile Gly Phe Ala Ile Pro Ser Thr Asp Val Ile Lys Ile				270
		275		280
Ile Lys Gln Leu Glu Thr Asn Gly Glu Val Ile Arg Pro Ala Leu Gly				285
		290		295
Ile Ser Met Val Asn Leu Asn Asp Leu Ser Thr Asn Ala Leu Ser Gln				300
		305		310
Ile Asn Ile Pro Thr Ser Val Thr Gly Gly Ile Val Val Ala Glu Val				315
		325		330
Lys Glu Gly Met Pro Ala Ser Gly Lys Leu Ala Gln Tyr Asp Val Ile				335
		340		345
Thr Glu Ile Asp Gly Lys Thr Val Asn Ser Ile Ser Asp Leu Gln Ser				350
		355		360
Ser Leu Tyr Gly His Asp Ile Asn Asp Thr Ile Lys Val Thr Phe Tyr				365
		370		375
Arg Gly Thr Thr Lys Lys Lys Ala Asp Ile Lys Leu Thr Lys Thr Thr				380
		385		390
Gln Asp Leu Thr Lys Thr Gln				395
		405		400

<210> SEQ ID NO 121

<211> LENGTH: 1560

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 121

gtgatcgagt taaacgatga attcatccga aaagagacga tagaactggc caacgatggc	60
ccacgagtac acaccactca atatgaaact aaagtacctc ggcttcataa atgctatctg	120
cttttcttta gcattattat cagttcttta acaattgcag tacctttttt aacagatgca	180
gccaatgggc ttcagtccca aaacttatat ataggaatga tgtaacgaa ggggcaactt	240
ccctatagtg ctgctttttac aacaggaggg ctcttttact ttgttatcat tgcattaagt	300
tattatttgg gatcgacact ttggctagtc tttgttcagg tgttttgttt ttacttatct	360


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ggtttatatc tttataaaact cattaattat atgacaggct ttcaaaaagt ggctttaact 420
ttttcaatta gctactatctt attatctggt agtcttggtt ttggggggatt gtatcctact 480
caactggcta tgccatttat attaatatcg gcttggtttt taactaagta ttttgcctgt 540
ttagtgaaag atgaggcatt tattcttttt ggctttgtag gtgctcttgc aatgctaatt 600
gacccgagta cccttatctt ttggtctttt gcttgtgtga cagttttttc ttataatata 660
agccaaaagc atcttgcaag aggtttttat caactgctag cttcgatttt tggaatgatt 720
ttagtttttt acacagcagg atatttcatt ttgaacttac aagtgcataa tccttattta 780
tcacaaacga tgatttatcc ttttactttt tttaaatcag gaaacttatc gttgcttttt 840
ggactggcta ttcagttggt cttcgctttg gggcttggtc ttttgacggg aatggagaat 900
gtcattaggc gatttaaaaa caattctgat agggtcgtca agtggctatt tgtcatggtc 960
attctagaat ctatacttgt ggctatatatt tcacaagact atcgccccta tcacttttta 1020
cctcttttac cttttggatt aattttgact gctattcctg ttggctatca gtatgggata 1080
ggattaggtc agagtagtca tcgcagacgt catggtaaaa atggtgttgg tcgagtaatg 1140
atgatttatc ttaagagaca cttttatttg ccaattttaa ttgtagggac aatactaata 1200
tgttctactt attgtttcat tagtagtatt cctcttaatc aggagcgtga tcataattgct 1260
agttatttag aacagaaaact aaataaaaact caatctattt atgtttggga tgatacttct 1320
aaaatttatt tggacagtaa agctaaatct gtttctcaat ttagttctcc tgacatcaat 1380
acgcaaaaag agagtcacg aaaaaatatta gaagatgaac tattagaaaa taaggctgct 1440
tatatcgttg ttaatcgcta taaaaacctg cctaaaatca ttcaaaaagt attatctact 1500
aattacaaag tagataaaca gataacgaca aaaagtttta ttgtttatca gaaaaagtaa 1560

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<210> SEQ ID NO 122

<211> LENGTH: 519

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 122

```

Met Ile Glu Leu Asn Asp Glu Phe Ile Arg Lys Glu Thr Ile Glu Leu
1           5           10           15
Ala Asn Asp Gly Pro Arg Val His Thr Thr Gln Tyr Glu Thr Lys Val
20           25           30
Pro Arg Leu His Lys Cys Tyr Leu Phe Phe Ser Ile Ile Ile Ser
35           40           45
Ser Leu Thr Ile Ala Val Pro Phe Leu Thr Asp Ala Ala Asn Gly Leu
50           55           60
Gln Ser Gln Asn Leu Tyr Ile Gly Met Met Leu Thr Lys Gly Gln Leu
65           70           75           80
Pro Tyr Ser Ala Ala Phe Thr Thr Gly Gly Leu Phe Tyr Phe Val Ile
85           90           95
Ile Ala Leu Ser Tyr Tyr Leu Gly Ser Thr Leu Trp Leu Val Phe Val
100          105          110
Gln Val Phe Cys Phe Tyr Leu Ser Gly Leu Tyr Leu Tyr Lys Leu Ile
115          120          125
Asn Tyr Met Thr Gly Phe Gln Lys Val Ala Leu Thr Phe Ser Ile Ser
130          135          140
Tyr Tyr Leu Leu Ser Val Ser Leu Gly Phe Gly Gly Leu Tyr Pro Thr
145          150          155          160
Gln Leu Ala Met Pro Phe Ile Leu Ile Ser Ala Trp Phe Leu Thr Lys
165          170          175
Tyr Phe Ala Cys Leu Val Lys Asp Glu Ala Phe Ile Leu Phe Gly Phe
180          185          190
Val Gly Ala Leu Ala Met Leu Ile Asp Pro Ser Thr Leu Ile Phe Trp
195          200          205
Ser Phe Ala Cys Val Thr Val Phe Ser Tyr Asn Ile Ser Gln Lys His
210          215          220
Leu Ala Arg Gly Phe Tyr Gln Leu Leu Ala Ser Ile Phe Gly Met Ile
225          230          235          240
Leu Val Phe Tyr Thr Ala Gly Tyr Phe Ile Leu Asn Leu Gln Val Leu

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				245					250					255			
Asn	Pro	Tyr	Leu	Ser	Gln	Thr	Met	Ile	Tyr	Pro	Phe	Thr	Phe	Phe	Lys		
			260					265					270				
Ser	Gly	Asn	Leu	Ser	Leu	Leu	Phe	Gly	Leu	Ala	Ile	Gln	Leu	Phe	Phe		
		275					280					285					
Ala	Leu	Gly	Leu	Gly	Leu	Leu	Thr	Gly	Met	Glu	Asn	Val	Ile	Arg	Arg		
	290					295				300							
Phe	Lys	Asn	Asn	Ser	Asp	Arg	Val	Val	Lys	Trp	Leu	Phe	Val	Met	Val		
305				310					315					320			
Ile	Leu	Glu	Ser	Ile	Leu	Val	Ala	Ile	Phe	Ser	Gln	Asp	Tyr	Arg	Pro		
			325					330					335				
Tyr	His	Leu	Leu	Pro	Leu	Leu	Pro	Phe	Gly	Leu	Ile	Leu	Thr	Ala	Ile		
		340						345				350					
Pro	Val	Gly	Tyr	Gln	Tyr	Gly	Ile	Gly	Leu	Gly	Gln	Ser	Ser	His	Arg		
	355					360				365							
Arg	Arg	His	Gly	Lys	Asn	Gly	Val	Gly	Arg	Val	Met	Met	Ile	Tyr	Leu		
	370				375					380							
Lys	Arg	His	Phe	Tyr	Leu	Pro	Ile	Leu	Ile	Val	Gly	Thr	Ile	Leu	Ile		
385				390					395					400			
Cys	Ser	Thr	Tyr	Cys	Phe	Ile	Ser	Ser	Ile	Pro	Leu	Asn	Gln	Glu	Arg		
		405				410							415				
Asp	His	Ile	Ala	Ser	Tyr	Leu	Glu	Gln	Lys	Leu	Asn	Lys	Thr	Gln	Ser		
		420				425						430					
Ile	Tyr	Val	Trp	Asp	Asp	Thr	Ser	Lys	Ile	Tyr	Leu	Asp	Ser	Lys	Ala		
	435					440					445						
Lys	Ser	Val	Ser	Gln	Phe	Ser	Ser	Pro	Asp	Ile	Asn	Thr	Gln	Lys	Glu		
	450					455				460							
Ser	His	Arg	Lys	Ile	Leu	Glu	Asp	Glu	Leu	Leu	Glu	Asn	Lys	Ala	Ala		
465				470					475					480			
Tyr	Ile	Val	Val	Asn	Arg	Tyr	Lys	Asn	Leu	Pro	Lys	Ile	Ile	Gln	Lys		
		485				490							495				
Val	Leu	Ser	Thr	Asn	Tyr	Lys	Val	Asp	Lys	Gln	Ile	Thr	Thr	Lys	Ser		
		500				505						510					
Phe	Ile	Val	Tyr	Gln	Lys	Lys											
		515															

<210> SEQ ID NO 123

<211> LENGTH: 3075

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 123

atgacgaagg	gtattcgatt	tcaattgctt	ggcagtcctt	acatttttct	tgatgacaaa	60
gaacaatttt	ttgcctttgc	caaagcaaat	gctctccttt	attacttagt	ggttaatgga	120
tctgttagcc	gcgaggtggc	ggcgagtcta	ctttgggaaa	ataagaacac	gcaaacagcg	180
aaaaagaatt	tacgaaacgc	tatctaccag	gtcaataaaag	tcttgcaagc	tgatgtgatt	240
atttgtccca	atcgcaacct	gctggttttg	aataaaaacac	ttgatatcaa	aacagatatt	300
aacctttttc	tggctgatcc	gctagctcac	ttagaactct	accaagggga	gtttttgcag	360
ggctttttacc	ttaaaaagtgg	tgaggaattt	gatcctttggg	tttcaaaaat	gcgtatgcag	420
tatgaacagg	tatacctaaa	agcgtgttac	caaaaaattg	aagaaaagct	ctcttttagat	480
gccattgaag	atgtcgagga	acatttataaa	cagcttattg	aacgtgatga	atttgaagag	540
aaaaattatc	agctcttgat	gaggctttat	cagcagggga	attgtcctgg	taaggctcatc	600
gaaacttatt	atcagttggc	taatgtgttg	gataaggagc	tagggattca	gccaaagtttg	660
caaagccaac	agatttatca	ggaagtggtc	gctaaagatc	gtaatgaacg	caaaatcaag	720
catttttttgc	gcaacagtaa	tcattttttg	gggcggattg	atgagattaa	gcagctggaa	780
aactttttttg	ccaactgttt	ggcctgccaa	gaggtaggag	ctctgctctt	aattgggtgat	840
acaggggattg	ggaaacgaac	cctagccaga	caggtcctag	ccaatcaaac	ccaaacgttt	900
caaattgtca	cagctaaatg	ttttcgtgaa	gaggctatgg	attccttatt	gccttggcgt	960

aatatcttag	atggcctggg	agattttggtg	attcaaaacc	gcttattgac	caccaaagct	1020
tggaaggctg	ctcttaaacc	ctgttttcct	gtggcaacca	tttttcaaga	agataacaac	1080
caacccttta	tcaaggacca	caccagcttg	ttggtttcct	ttattgttga	tattttacaa	1140
catttggcag	aaatcaaggc	gctggtaatc	cttattgagg	attgtcactg	gatggatgag	1200
gatagtttga	ccttgttgca	acgggtcatg	aatcaattgg	tccactatcc	gattgctttt	1260
gtcttgacca	agcatctagg	aacgactcct	gagctcggtc	tttgtttgaa	tgctttgatg	1320
agtcaagggc	gttttagaaa	cattttgtttg	gagcctttta	atcggcaaga	aagtttggtt	1380
tatattaaca	gtcaactggg	tagtcagcca	gtgacggcag	aagaaatgga	gcacctctat	1440
caagccagcc	aaggcaaccc	tttctttttg	tcagaataca	ctcaggccct	actgcgtcac	1500
gaaaaatttg	tgcttttaac	gcctgccatt	aaggctaagt	tggttcttaa	actagctaata	1560
ctaagtagtc	gtgatgacgc	attgttaaac	tatttgcctt	gttgcggag	gcctatccct	1620
ataaatcccc	tcgctcaatt	gatgttactg	cctttagaag	aagtgatcga	gatgggtggat	1680
cttctggggc	actactatat	tttggtagaa	gaaagcgtag	gagaggaagt	gttgatttca	1740
tttcgtcagc	ggattattca	actctatagt	tatgaccggt	tatctttgtc	aaaaaggcgt	1800
ttattgcacg	gacaaattgc	caaacggtta	gaagatttac	tgctattttt	gacaccaagc	1860
cctcacttat	tagatgacat	tgcttacctat	tatcaggaat	cacggcaggt	gattaaggct	1920
ttggaataca	accttaacta	tctagatgct	accttgccat	ttcagcatga	gctgtttccc	1980
atattattcaa	agagtattgg	ctccttggaa	aagtcagatc	gtgaccatca	acgcttaatg	2040
gaagagcagt	ttgataagat	tcgtcaaagc	attgcggatt	tggaactgac	ctatgataat	2100
aaccgtgatt	tccagcagtt	gcttattcgt	ttttcttacc	ttgaaggccg	ttatgatatt	2160
cgaacagggg	ggatcaaga	agggattaaa	cacattcaaa	aggtcacgc	tttggcaacc	2220
gagctaaaac	agccctcctt	cttgctagaa	ggctatcgcc	agttaattca	ttactgtatc	2280
caagtggaaa	acaagccaga	aatgcgttat	tacactagtc	tttcattgga	ggcagcgggt	2340
gctgctaata	atcttgaggc	cattgcgatt	agtttgcggt	taaacggtct	ctatcatttg	2400
attattgggg	agttaaatga	ggcagagcgt	ctgcttcaac	agtcgattga	cttcttcaag	2460
gtgacgccag	gcttgcaagc	taactatgcg	attcagattg	ctgctgcctt	agattatttg	2520
ggggagattg	cccagattcg	ctatcagttt	gaaaaggccg	ttgcttatca	aaaacaagcc	2580
attgccttga	ccgaaaacaa	gccagctgag	ttatcggcga	gtatttttta	tattggatta	2640
gggatttcct	acttttattt	agctgatttt	gaacaagctg	agcaaactct	gagtttggct	2700
aagggaagctt	tggtcaatca	tagttatcct	tggaagaaaa	cgcaacttga	aatttacctg	2760
gctatgattc	aatggaaaaa	gggcaattat	cagccagcct	tgaccctact	tgattacaga	2820
gaaaccttga	tgtctaggta	tcgcaatccg	cgtgataaag	gcttggtttt	ctatttgatg	2880
gctgtggtca	agtaccaatt	gatatttcaa	ggagctaccc	taagtcagca	ggaaaaagaa	2940
atggcagacc	acctgttgtc	agaatccttt	gagtattatt	atgagattgc	tagtactaac	3000
ctcaaccctt	accgagattg	tcatttggtg	agtgaagtga	acgatttgcg	tcaacaatta	3060
tctgctaaaa	gctaa					3075

<210> SEQ ID NO 124

<211> LENGTH: 1024

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 124

Met	Thr	Lys	Gly	Ile	Arg	Phe	Gln	Leu	Leu	Gly	Ser	Pro	His	Ile	Phe
1				5				10						15	
Leu	Asp	Asp	Lys	Glu	Gln	Phe	Phe	Ala	Phe	Ala	Lys	Ala	Asn	Ala	Leu
			20					25					30		
Leu	Tyr	Tyr	Leu	Val	Val	Asn	Gly	Ser	Val	Ser	Arg	Glu	Val	Ala	Ala
			35				40						45		
Ser	Leu	Leu	Trp	Glu	Asn	Lys	Asn	Thr	Gln	Thr	Ala	Lys	Lys	Asn	Leu
	50					55					60				
Arg	Asn	Ala	Ile	Tyr	Gln	Val	Asn	Lys	Val	Leu	Gln	Ala	Asp	Val	Ile
65					70					75				80	
Ile	Cys	Pro	Asn	Arg	Asn	Leu	Leu	Val	Leu	Asn	Lys	Thr	Leu	Asp	Ile
			85					90						95	
Lys	Thr	Asp	Ile	Asn	Leu	Phe	Leu	Ala	Asp	Pro	Leu	Ala	His	Leu	Glu
			100					105					110		
Leu	Tyr	Gln	Gly	Glu	Phe	Leu	Gln	Gly	Phe	Tyr	Leu	Lys	Ser	Gly	Glu

		115					120				125						
Glu	Phe	Asp	Leu	Trp	Val	Ser	Lys	Met	Arg	Met	Gln	Tyr	Glu	Gln	Val		
	130						135					140					
Tyr	Leu	Lys	Ala	Cys	Tyr	Gln	Lys	Ile	Glu	Glu	Lys	Leu	Ser	Leu	Asp		
145					150					155					160		
Ala	Ile	Glu	Asp	Val	Glu	Glu	His	Leu	Lys	Gln	Leu	Ile	Glu	Arg	Asp		
			165						170					175			
Glu	Phe	Glu	Glu	Lys	Asn	Tyr	Gln	Leu	Leu	Met	Arg	Leu	Tyr	Gln	Gln		
			180					185					190				
Gly	Asn	Cys	Pro	Gly	Lys	Val	Ile	Glu	Thr	Tyr	Tyr	Gln	Leu	Ala	Asn		
	195						200					205					
Val	Leu	Asp	Lys	Glu	Leu	Gly	Ile	Gln	Pro	Ser	Leu	Gln	Ser	Gln	Gln		
	210					215						220					
Ile	Tyr	Gln	Glu	Val	Val	Ala	Lys	Asp	Arg	Asn	Glu	Arg	Lys	Ile	Lys		
225					230					235					240		
His	Phe	Leu	Arg	Asn	Ser	Asn	His	Phe	Leu	Gly	Arg	Ile	Asp	Glu	Ile		
			245					250					255				
Lys	Gln	Leu	Glu	Asn	Phe	Phe	Ala	Asn	Cys	Leu	Ala	Cys	Gln	Glu	Val		
			260					265					270				
Gly	Ala	Leu	Leu	Leu	Ile	Gly	Asp	Thr	Gly	Ile	Gly	Lys	Arg	Thr	Leu		
	275					280						285					
Ala	Arg	Gln	Val	Leu	Ala	Asn	Gln	Thr	Gln	Thr	Phe	Gln	Ile	Val	Thr		
	290					295					300						
Ala	Lys	Cys	Phe	Arg	Glu	Glu	Ala	Met	Asp	Ser	Leu	Leu	Pro	Trp	Arg		
305					310					315					320		
Asn	Ile	Leu	Asp	Gly	Leu	Gly	Asp	Leu	Val	Ile	Gln	Asn	Arg	Leu	Leu		
			325						330					335			
Thr	Thr	Lys	Ala	Trp	Lys	Ala	Ala	Leu	Lys	Arg	Cys	Phe	Pro	Val	Ala		
		340						345					350				
Thr	Ile	Phe	Gln	Glu	Asp	Asn	Asn	Gln	Pro	Phe	Ile	Lys	Asp	His	Thr		
	355					360						365					
Ser	Leu	Leu	Val	Ser	Phe	Ile	Val	Asp	Ile	Leu	Gln	His	Leu	Ala	Glu		
	370					375					380						
Ile	Lys	Ala	Leu	Val	Ile	Leu	Ile	Glu	Asp	Cys	His	Trp	Met	Asp	Glu		
385					390					395					400		
Asp	Ser	Leu	Thr	Leu	Leu	Gln	Arg	Val	Met	Asn	Gln	Leu	Val	His	Tyr		
			405						410					415			
Pro	Ile	Ala	Phe	Val	Leu	Thr	Lys	His	Leu	Gly	Thr	Thr	Pro	Glu	Leu		
		420						425					430				
Gly	Leu	Cys	Leu	Asn	Ala	Leu	Met	Ser	Gln	Gly	Arg	Leu	Glu	Ser	Ile		
	435					440						445					
Cys	Leu	Glu	Pro	Phe	Asn	Arg	Gln	Glu	Ser	Leu	Val	Tyr	Ile	Asn	Ser		
	450				455						460						
Gln	Leu	Gly	Ser	Gln	Pro	Val	Thr	Ala	Glu	Glu	Met	Glu	His	Leu	Tyr		
465					470					475					480		
Gln	Ala	Ser	Gln	Gly	Asn	Pro	Phe	Phe	Leu	Ser	Glu	Tyr	Thr	Gln	Ala		
			485						490					495			
Leu	Leu	Arg	His	Glu	Lys	Phe	Val	Pro	Leu	Thr	Pro	Ala	Ile	Lys	Ala		
		500						505					510				
Lys	Leu	Gly	Leu	Lys	Leu	Ala	Asn	Leu	Ser	Ser	Arg	Asp	Asp	Ala	Leu		
	515					520						525					
Leu	Asn	Tyr	Leu	Ser	Cys	Cys	Arg	Arg	Pro	Ile	Pro	Leu	Asn	Thr	Leu		
	530					535					540						
Ala	Gln	Leu	Met	Leu	Leu	Pro	Leu	Glu	Glu	Val	Ile	Glu	Met	Val	Asp		
545					550					555					560		
Asn	Leu	Gly	His	Tyr	Tyr	Ile	Leu	Val	Glu	Glu	Ser	Val	Gly	Glu	Glu		
			565						570					575			

Val	Leu	Ile	Ser	Phe	Arg	Gln	Arg	Ile	Gln	Leu	Tyr	Ser	Tyr	Asp
			580					585				590		
Arg	Leu	Ser	Leu	Ser	Lys	Arg	Arg	Leu	Leu	His	Gly	Gln	Ile	Ala
		595					600					605		Lys
Arg	Leu	Glu	Asp	Leu	Leu	Pro	Ile	Leu	Thr	Pro	Ser	Pro	His	Leu
	610					615					620			Leu
Asp	Asp	Ile	Ala	Tyr	His	Tyr	Gln	Glu	Ser	Arg	Gln	Val	Ile	Lys
625					630					635				640
Leu	Glu	Tyr	Asn	Leu	Asn	Tyr	Leu	Asp	Ala	Thr	Leu	Pro	Phe	Gln
			645						650					655
Glu	Leu	Phe	Pro	Ile	Tyr	Ser	Lys	Ser	Ile	Gly	Ser	Leu	Glu	Lys
		660						665				670		Ser
Asp	Arg	Asp	His	Gln	Arg	Leu	Met	Glu	Glu	Gln	Phe	Asp	Lys	Ile
		675					680					685		Arg
Gln	Ser	Ile	Ala	Asp	Leu	Glu	Leu	Thr	Tyr	Asp	Asn	Asn	Arg	Asp
	690					695					700			Phe
Gln	Gln	Leu	Leu	Ile	Arg	Phe	Ser	Tyr	Leu	Glu	Gly	Arg	Tyr	Asp
705				710						715				720
Arg	Thr	Gly	Arg	Tyr	Gln	Glu	Gly	Ile	Lys	His	Ile	Gln	Lys	Val
				725					730					735
Ala	Leu	Ala	Thr	Glu	Leu	Lys	Gln	Pro	Ser	Phe	Leu	Leu	Glu	Gly
			740					745					750	Tyr
Arg	Gln	Leu	Ile	His	Tyr	Cys	Ile	Gln	Val	Glu	Asn	Lys	Pro	Glu
		755					760					765		Met
Arg	Tyr	Tyr	Thr	Ser	Leu	Ser	Leu	Glu	Ala	Ala	Val	Ala	Ala	Asn
	770					775					780			His
Phe	Glu	Ala	Ile	Ala	Ile	Ser	Leu	Arg	Leu	Asn	Gly	Leu	Tyr	His
785					790					795				800
Ile	Ile	Gly	Glu	Leu	Asn	Glu	Ala	Glu	Arg	Leu	Leu	Gln	Gln	Ser
				805					810					815
Asp	Phe	Phe	Lys	Val	Thr	Pro	Gly	Leu	Gln	Ala	Asn	Tyr	Ala	Ile
			820					825					830	Gln
Ile	Ala	Ala	Ala	Leu	Asp	Tyr	Leu	Gly	Glu	Ile	Ala	Gln	Ile	Arg
		835					840					845		Tyr
Gln	Phe	Glu	Lys	Ala	Val	Ala	Tyr	Gln	Lys	Gln	Ala	Ile	Ala	Leu
	850					855					860			Thr
Glu	Asn	Lys	Pro	Ala	Glu	Leu	Ser	Ala	Ser	Ile	Phe	Tyr	Ile	Gly
865					870					875				880
Gly	Ile	Ser	Tyr	Phe	Tyr	Leu	Ala	Asp	Phe	Glu	Gln	Ala	Glu	Gln
				885					890					895
Leu	Ser	Leu	Ala	Lys	Glu	Ala	Leu	Val	Asn	His	Ser	Tyr	Pro	Trp
			900					905					910	Lys
Glu	Thr	Gln	Leu	Glu	Ile	Tyr	Leu	Ala	Met	Ile	Gln	Trp	Lys	Lys
		915					920					925		Gly
Asn	Tyr	Gln	Pro	Ala	Leu	Thr	Leu	Leu	Asp	Tyr	Arg	Glu	Thr	Leu
	930					935					940			Met
Ser	Arg	Tyr	Arg											

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<210> SEQ ID NO 125
<211> LENGTH: 561
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 125
atgtctctaa ttggaaaaga aattgctgaa ttttcagctc aagcttatca cgatggaaaa      60
ttcatcactg ttacaaatga agacgttaaa ggaaaatggg cagttttttg tttctaccca      120
gcgacttttt catttgtttg cccaactgaa ctcggtgacc ttcaagagca atacgaaaca      180
ctgaaatctc ttggtgtaga agtttattct gtctctactg atactcattt tggtcataaa      240
gcttggcatg atgattcaga tgtggttggc actatcacat accctatgat tggtgaccct      300
tcacacctta tttcacaagc ctttgaagtg cttggcgaag acggacttgc tcaacgtgga      360
acatttatcg ttgatccaga tggattatc caaatgatgg aaattaatgc tgatggtatt      420
ggacgtgacg ctagcacctt gattgataaa attcacgctg cccaatacgt ccgtaaacad      480
ccaggtgaag tttgtccagc taaatggaaa gaaggcgtg aaactttgac accaagtctt      540
gatttagttg gtaaaattta a                                     561

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<210> SEQ ID NO 126
<211> LENGTH: 186
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 126
Met Ser Leu Ile Gly Lys Glu Ile Ala Glu Phe Ser Ala Gln Ala Tyr
1      5      10      15
His Asp Gly Lys Phe Ile Thr Val Thr Asn Glu Asp Val Lys Gly Lys
20     25     30
Trp Ala Val Phe Cys Phe Tyr Pro Ala Asp Phe Ser Phe Val Cys Pro
35     40     45
Thr Glu Leu Gly Asp Leu Gln Glu Gln Tyr Glu Thr Leu Lys Ser Leu
50     55     60
Gly Val Glu Val Tyr Ser Val Ser Thr Asp Thr His Phe Val His Lys
65     70     75     80
Ala Trp His Asp Asp Ser Asp Val Val Gly Thr Ile Thr Tyr Pro Met
85     90     95
Ile Gly Asp Pro Ser His Leu Ile Ser Gln Ala Phe Glu Val Leu Gly
100    105    110
Glu Asp Gly Leu Ala Gln Arg Gly Thr Phe Ile Val Asp Pro Asp Gly
115    120    125
Ile Ile Gln Met Met Glu Ile Asn Ala Asp Gly Ile Gly Arg Asp Ala
130    135    140
Ser Thr Leu Ile Asp Lys Ile His Ala Ala Gln Tyr Val Arg Lys His
145    150    155    160
Pro Gly Glu Val Cys Pro Ala Lys Trp Lys Glu Gly Ala Glu Thr Leu
165    170    175
Thr Pro Ser Leu Asp Leu Val Gly Lys Ile
180    185

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<210> SEQ ID NO 127
<211> LENGTH: 2445
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 127
atgattatgt attcaacgaa gatgcaagac attttttagac aggcgcagtt ccaagctgct      60
cgcttttgata gccattgcct ggaaacttgg catgtttttg tagctatggt agctgtagat      120
aattcttttag caaatatgat tttaagtga tatgatgcc aagtcgccat agaagaatat      180
gaagctgcag ctatttttagc catgggcaaa acccctaaag aacagttgtc tcgtgtagac      240
ttcagacctc aatctaaaac tttgactaac ttgttagctt ttgcgcaggc tattagccaa      300

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atcactaggg	atcaagaagt	cggctctgag	catgtcttat	ttgctatttt	attgaatcca	360
gatattatgg	cgagtcgttt	gttagaaaata	gctgggctatc	agataaaaaga	taacggcaat	420
gggcagccgc	gattagctga	cttgcgaaaa	gcaatagaac	gtcatgcagg	ttacagtaag	480
gaaatgatca	aggctattca	cgaactacgt	aagcctaaaa	aaacgaaaac	acaagggacc	540
ttttcagata	tgatgaagcc	accaagtaca	gctgggtgagt	tgagtgattt	cacaagagat	600
ttgactgaaa	tggcaagaca	aggtttgta	gaatcgggtga	ttggacgtga	ccaagaagta	660
tctcgtatga	ttcagggtact	aagtcgtaaa	acgaaaaaca	atcctgtctt	ggtaggtgat	720
gcagggtgttg	gtaaaactgc	gcttgcttat	ggccttgctc	aacggattgc	aaatggcgct	780
attccttatg	aacttaagga	gatgcgtgtc	ctagaattag	acatgatgag	tgtggttagca	840
ggaacccggt	ttcgtgggga	ttttgaagag	cgcatgaatc	aaatcattga	tgatattgaa	900
gctgatggtc	agattattct	ttttgttgat	gaactacata	ctattatggg	ttctggcagt	960
ggtattgaca	gtacacttga	tgcggctaac	attttaaaac	cagcattatc	gcgcggcact	1020
cttcatatgg	ttggagcaac	aactcaagaa	gaataccaaa	aacatattga	aaaagatgca	1080
gctctttcgc	gtcgttttgc	taaaatatta	attgaagaac	ctaatacaga	agatgcttat	1140
cagattttga	tgggcctaaa	attatcttat	gagacctacc	ataatgtctc	gatatcaaat	1200
gaggcagtta	aaacagctgt	aaaaatggca	caccgttatt	taaccagtaa	aaatctccct	1260
gattcagcta	tcgatttact	agatgaagct	agtgcgtgctg	tgcaaaacat	ggtgaaaaaa	1320
tcagcacctg	agactttaac	accaatagac	caagctctta	tcaatgggtga	tatgaaaaaa	1380
gtatctcgcc	tcttagctaa	agaagcaaaa	ggtcagatga	gaaaaccaac	accggtgaca	1440
gaagatgata	ttttggcaac	cttgagtaag	ttatcgggaa	ttccacttga	aaaactgacg	1500
caagctgata	gtaaaaaata	cctcaattta	gaaaaagaac	tgcataagcg	tgtgattggt	1560
caggatgctg	ctgttacggc	tatttcaaga	gccattcgtc	gtaatcagtc	aggtaattcg	1620
acaggaaaac	gtcctatttg	atcattttatg	tttcttggcc	caacaggagt	aggtaagaca	1680
gaactagcaa	aggcccttgc	agaagttctc	tttgatgatg	aagcagcgct	tattcgtttt	1740
gatatgtctg	agtacatgga	aaaattcgca	gcgtctaggc	ttaatggagc	acctcctggt	1800
tatgtcggct	atgatgaagg	aggatgaactg	acacagaaag	ttagaaataa	accttattca	1860
gtcttgcttt	ttgatgaagt	ggaaaaagca	catcctgata	tttttaacgt	tctccttcaa	1920
gtattagatg	atggtatat	gactgatagt	cgtgggcgta	aggtcgattt	ttcaaatact	1980
attattatca	tgaccagcaa	tcttggcgca	acagccctgc	gcgatgataa	aacggtcggt	2040
tttgggggtca	aagacattca	ccaagaccat	caagctatgg	agaaacgtat	tttagaagaa	2100
ttaagaaaaa	cttaccgccc	agaatttatc	aatcgtattg	atgaaaaagt	ggtctttcat	2160
agtctgaccc	aagataacat	gcgcgatgtg	gttaaaatca	tggtacagcc	cctgattact	2220
acattggcag	aaaaaggtat	tacccttaaa	attcagcctt	tggccttgaa	acatttgtcc	2280
gaggtcggct	atgatgagca	tatgggggca	agaccattac	gtcgaacgct	gcaaactgag	2340
atagaagata	agctatcaga	gcttattctt	tctcgagaat	tgacaagtgg	gcatacgcta	2400
aaaattggat	tatcacatgg	caaattaacg	tttcacatag	cttaa		2445

<210> SEQ ID NO 128

<211> LENGTH: 814

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 128

Met	Ile	Met	Tyr	Ser	Thr	Lys	Met	Gln	Asp	Ile	Phe	Arg	Gln	Ala	Gln
1				5				10						15	
Phe	Gln	Ala	Ala	Arg	Phe	Asp	Ser	His	Cys	Leu	Glu	Thr	Trp	His	Val
		20						25					30		
Leu	Leu	Ala	Met	Val	Ala	Val	Asp	Asn	Ser	Leu	Ala	Asn	Met	Ile	Leu
		35					40					45			
Ser	Glu	Tyr	Asp	Ala	Gln	Val	Ala	Ile	Glu	Glu	Tyr	Glu	Ala	Ala	Ala
	50					55					60				
Ile	Leu	Ala	Met	Gly	Lys	Thr	Pro	Lys	Glu	Gln	Leu	Ser	Arg	Val	Asp
65				70					75					80	
Phe	Arg	Pro	Gln	Ser	Lys	Thr	Leu	Thr	Asn	Leu	Leu	Ala	Phe	Ala	Gln
			85					90						95	
Ala	Ile	Ser	Gln	Ile	Thr	Arg	Asp	Gln	Glu	Val	Gly	Ser	Glu	His	Val
			100					105					110		
Leu	Phe	Ala	Ile	Leu	Leu	Asn	Pro	Asp	Ile	Met	Ala	Ser	Arg	Leu	Leu

		115					120				125				
Glu	Ile	Ala	Gly	Tyr	Gln	Ile	Lys	Asp	Asn	Gly	Asn	Gly	Gln	Pro	Arg
	130						135					140			
Leu	Ala	Asp	Leu	Arg	Lys	Ala	Ile	Glu	Arg	His	Ala	Gly	Tyr	Ser	Lys
145					150					155					160
Glu	Met	Ile	Lys	Ala	Ile	His	Glu	Leu	Arg	Lys	Pro	Lys	Lys	Thr	Lys
			165						170						175
Thr	Gln	Gly	Thr	Phe	Ser	Asp	Met	Met	Lys	Pro	Pro	Ser	Thr	Ala	Gly
		180						185					190		
Glu	Leu	Ser	Asp	Phe	Thr	Arg	Asp	Leu	Thr	Glu	Met	Ala	Arg	Gln	Gly
	195						200					205			
Leu	Leu	Glu	Ser	Val	Ile	Gly	Arg	Asp	Gln	Glu	Val	Ser	Arg	Met	Ile
	210					215					220				
Gln	Val	Leu	Ser	Arg	Lys	Thr	Lys	Asn	Asn	Pro	Val	Leu	Val	Gly	Asp
225					230					235					240
Ala	Gly	Val	Gly	Lys	Thr	Ala	Leu	Ala	Tyr	Gly	Leu	Ala	Gln	Arg	Ile
			245						250					255	
Ala	Asn	Gly	Ala	Ile	Pro	Tyr	Glu	Leu	Lys	Glu	Met	Arg	Val	Leu	Glu
	260							265					270		
Leu	Asp	Met	Met	Ser	Val	Val	Ala	Gly	Thr	Arg	Phe	Arg	Gly	Asp	Phe
	275						280					285			
Glu	Glu	Arg	Met	Asn	Gln	Ile	Ile	Asp	Asp	Ile	Glu	Ala	Asp	Gly	Gln
	290				295					300					
Ile	Ile	Leu	Phe	Val	Asp	Glu	Leu	His	Thr	Ile	Met	Gly	Ser	Gly	Ser
305					310					315					320
Gly	Ile	Asp	Ser	Thr	Leu	Asp	Ala	Ala	Asn	Ile	Leu	Lys	Pro	Ala	Leu
			325						330					335	
Ser	Arg	Gly	Thr	Leu	His	Met	Val	Gly	Ala	Thr	Thr	Gln	Glu	Glu	Tyr
	340							345					350		
Gln	Lys	His	Ile	Glu	Lys	Asp	Ala	Ala	Leu	Ser	Arg	Arg	Phe	Ala	Lys
	355					360						365			
Ile	Leu	Ile	Glu	Glu	Pro	Asn	Thr	Glu	Asp	Ala	Tyr	Gln	Ile	Leu	Met
	370				375					380					
Gly	Leu	Lys	Leu	Ser	Tyr	Glu	Thr	Tyr	His	Asn	Val	Ser	Ile	Ser	Asn
385					390					395					400
Glu	Ala	Val	Lys	Thr	Ala	Val	Lys	Met	Ala	His	Arg	Tyr	Leu	Thr	Ser
			405						410					415	
Lys	Asn	Leu	Pro	Asp	Ser	Ala	Ile	Asp	Leu	Leu	Asp	Glu	Ala	Ser	Ala
	420							425					430		
Ala	Val	Gln	Asn	Met	Val	Lys	Lys	Ser	Ala	Pro	Glu	Thr	Leu	Thr	Pro
	435						440					445			
Ile	Asp	Gln	Ala	Leu	Ile	Asn	Gly	Asp	Met	Lys	Lys	Val	Ser	Arg	Leu
	450				455					460					
Leu	Ala	Lys	Glu	Ala	Lys	Gly	Gln	Met	Arg	Lys	Pro	Thr	Pro	Val	Thr
465					470					475					480
Glu	Asp	Asp	Ile	Leu	Ala	Thr	Leu	Ser	Lys	Leu	Ser	Gly	Ile	Pro	Leu
			485						490					495	
Glu	Lys	Leu	Thr	Gln	Ala	Asp	Ser	Lys	Lys	Tyr	Leu	Asn	Leu	Glu	Lys
	500						505						510		
Glu	Leu	His	Lys	Arg	Val	Ile	Gly	Gln	Asp	Ala	Ala	Val	Thr	Ala	Ile
	515						520					525			
Ser	Arg	Ala	Ile	Arg	Arg	Asn	Gln	Ser	Gly	Ile	Arg	Thr	Gly	Lys	Arg
	530					535				540					
Pro	Ile	Gly	Ser	Phe	Met	Phe	Leu	Gly	Pro	Thr	Gly	Val	Gly	Lys	Thr
545					550					555					560
Glu	Leu	Ala	Lys	Ala	Leu	Ala	Glu	Val	Leu	Phe	Asp	Asp	Glu	Ala	Ala
			565						570					575	

Leu	Ile	Arg	Phe	Asp	Met	Ser	Glu	Tyr	Met	Glu	Lys	Phe	Ala	Ala	Ser		
			580					585					590				
Arg	Leu	Asn	Gly	Ala	Pro	Pro	Gly	Tyr	Val	Gly	Tyr	Asp	Glu	Gly	Gly		
		595					600					605					
Glu	Leu	Thr	Gln	Lys	Val	Arg	Asn	Lys	Pro	Tyr	Ser	Val	Leu	Leu	Phe		
	610					615					620						
Asp	Glu	Val	Glu	Lys	Ala	His	Pro	Asp	Ile	Phe	Asn	Val	Leu	Leu	Gln		
625					630					635					640		
Val	Leu	Asp	Asp	Gly	Ile	Leu	Thr	Asp	Ser	Arg	Gly	Arg	Lys	Val	Asp		
			645					650					655				
Phe	Ser	Asn	Thr	Ile	Ile	Ile	Met	Thr	Ser	Asn	Leu	Gly	Ala	Thr	Ala		
		660					665						670				
Leu	Arg	Asp	Asp	Lys	Thr	Val	Gly	Phe	Gly	Val	Lys	Asp	Ile	His	Gln		
	675						680					685					
Asp	His	Gln	Ala	Met	Glu	Lys	Arg	Ile	Leu	Glu	Glu	Leu	Arg	Lys	Thr		
	690					695					700						
Tyr	Arg	Pro	Glu	Phe	Ile	Asn	Arg	Ile	Asp	Glu	Lys	Val	Val	Phe	His		
705					710				715						720		
Ser	Leu	Thr	Gln	Asp	Asn	Met	Arg	Asp	Val	Val	Lys	Ile	Met	Val	Gln		
			725					730					735				
Pro	Leu	Ile	Thr	Thr	Leu	Ala	Glu	Lys	Gly	Ile	Thr	Leu	Lys	Ile	Gln		
		740					745						750				
Pro	Leu	Ala	Leu	Lys	His	Leu	Ser	Glu	Val	Gly	Tyr	Asp	Glu	His	Met		
	755					760						765					
Gly	Ala	Arg	Pro	Leu	Arg	Arg	Thr	Leu	Gln	Thr	Glu	Ile	Glu	Asp	Lys		
	770				775						780						
Leu	Ser	Glu	Leu	Ile	Leu	Ser	Arg	Glu	Leu	Thr	Ser	Gly	His	Thr	Leu		
785					790					795					800		
Lys	Ile	Gly	Leu	Ser	His	Gly	Lys	Leu	Thr	Phe	His	Ile	Ala				
			805						810								

<210> SEQ ID NO 129

<211> LENGTH: 1725

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 129

gtgaactatc	taggttttctt	cgaaaatcca	ttagccattt	atgatataat	agtaaagaaa	60
aacatagaaa	gttgggggtct	gttgatgacc	aaaccatttc	atcataagaa	actaaaacaa	120
ataactataa	tagctgcaac	tagccttttt	ttattcctga	tcggtggtgc	cttttactac	180
tctaaaaatc	attgtattaa	tgcctatctt	aaagctcgat	cggcccaatc	aggaccagtt	240
tttgagaata	tcaaagcata	tctagtctgg	gatgatacta	atgagcagat	cacaaatgac	300
gaggcgatgt	atactaagtt	tagaagggtat	agtcagaaaag	aattgaggca	aaaaaagcag	360
gattttaaag	ccgctagtca	agatagtgcc	gttcaagtaa	agtctgttgg	tcgtcgtttt	420
tggatttttc	ctgattatcg	gattgccata	aaacccatgg	atttaacgat	aaaaacgaat	480
gtgcctcaag	cagacgttct	tttaaataca	aaaaaagttg	ctgtttctga	ttcagaacag	540
ttctcagtca	agcttgatcg	gctaccaacg	gcagaatata	ccgcaagtat	cagaggcaaa	600
cacaacgggc	gaaacattaa	agtcaacaaa	tcatatgatg	gtgataatcc	cgtgctagat	660
ttgagtgtgt	cttttagaac	tttttttggt	acaagcaatg	ctaagcaagg	agatctttac	720
ttcgatgata	accatattgg	cacattaaaa	gatgggtcaat	tacaagtaga	agattaccct	780
gttacagaaa	acgcacaagc	ttatatgaaa	acaacattcc	cagatggtga	gttaagatca	840
caaaaatatg	ctctagctga	tgttgaagaa	ggagcaaccc	tggagatttt	agttacagat	900
cttttagaag	aggacaaggc	aggggagcta	ttagtatcag	cttttgatca	gctgatgcac	960
tacctcagta	caggtaacga	ctcatctaac	ttacgtagcg	tctttgaggc	agggcttagc	1020
aacgcatttt	ataggggatt	gaaagagtcc	ataaaagcga	aatttcagac	agatacaaga	1080
aaagccagcc	gtctcaatat	tccatctatc	cttttgacaa	caatgactca	agtgggtaaa	1140
acaacttacg	tgcttgattt	cacagctacc	tacgaatttt	tgtatgacaa	gtcaacagat	1200
cctgagcagc	atacctctgg	acatattaat	caagacttga	ctggaaaagt	gactgtaaaa	1260

```

aaagttggac agcattacct tatcagccag tccggctcca aaaatattac tgttgttaaa 1320
gaggacaatc aactcaaagc gccatctgtc tttcctgagt ctattttggg aacgtggaca 1380
ggccaagcca atggtttgag catccatatg tctctagcat cagatggaac aattacgact 1440
aaagttgaag atcaaaaagg caaccgttct aaagaaactc ggacagctaa aattagtaaa 1500
gttgaagaca aaggcaatgg tttttatctt tatacgccag atcctggaag tgacataagc 1560
gccttagttc cagaaggagg attggggggt gcaaagtca aatatgctta tggtttcaaa 1620
atatctggta aaacagcctc tccagtgggtg tggcaggcag cattaacaca tgaatttgat 1680
tataccaagc cactttcggg agtaactttg caaaagcaac cataa 1725

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<210> SEQ ID NO 130
<211> LENGTH: 574
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 130

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```

Met Asn Tyr Leu Gly Phe Phe Glu Asn Pro Leu Ala Ile Tyr Asp Ile
1           5           10          15
Ile Val Lys Lys Asn Ile Glu Ser Trp Gly Leu Leu Met Thr Lys Pro
          20          25          30
Phe His His Lys Lys Leu Lys Gln Ile Thr Ile Ile Ala Ala Thr Ser
          35          40          45
Leu Phe Leu Phe Leu Ile Gly Gly Ala Phe Tyr Tyr Ser Lys Asn His
          50          55          60
Cys Ile Asn Ala Tyr Leu Lys Ala Arg Ser Ala Gln Ser Gly Pro Val
          65          70          75          80
Phe Glu Asn Ile Lys Ala Tyr Leu Val Trp Asp Asp Thr Asn Glu Gln
          85          90          95
Ile Thr Asn Asp Glu Ala Met Tyr Thr Lys Phe Arg Arg Tyr Ser Gln
          100         105         110
Lys Glu Leu Arg Gln Lys Lys Gln Asp Leu Lys Ala Ala Ser Gln Asp
          115         120         125
Ser Ala Val Gln Val Lys Ser Val Gly Arg Arg Phe Trp Ile Phe Pro
          130         135         140
Asp Tyr Arg Ile Ala Ile Lys Pro Met Asp Leu Thr Ile Lys Thr Asn
          145         150         155         160
Val Pro Gln Ala Asp Val Leu Leu Asn Gln Lys Lys Val Ala Val Ser
          165         170         175
Asp Ser Glu Gln Phe Ser Val Lys Leu Asp Arg Leu Pro Thr Ala Glu
          180         185         190
Tyr Thr Ala Ser Ile Arg Gly Lys His Asn Gly Arg Asn Ile Lys Val
          195         200         205
Asn Lys Ser Tyr Asp Gly Asp Asn Pro Val Leu Asp Leu Ser Val Ser
          210         215         220
Phe Arg Thr Phe Leu Val Thr Ser Asn Ala Lys Gln Gly Asp Leu Tyr
          225         230         235         240
Phe Asp Asp Asn His Ile Gly Thr Leu Lys Asp Gly Gln Leu Gln Val
          245         250         255
Glu Asp Tyr Pro Val Thr Glu Asn Ala Gln Ala Tyr Met Lys Thr Thr
          260         265         270
Phe Pro Asp Gly Glu Leu Arg Ser Gln Lys Tyr Ala Leu Ala Asp Val
          275         280         285
Glu Glu Gly Ala Thr Leu Glu Ile Leu Val Thr Asp Leu Leu Glu Glu
          290         295         300
Asp Lys Ala Gly Glu Leu Leu Val Ser Ala Phe Asp Gln Leu Met His
          305         310         315         320
Tyr Leu Ser Thr Gly Gln Asp Ser Ser Asn Leu Arg Ser Val Phe Glu
          325         330         335
Ala Gly Ser Ser Asn Ala Phe Tyr Arg Gly Leu Lys Glu Ser Ile Lys

```

			340					345					350				
Ala	Lys	Phe	Gln	Thr	Asp	Thr	Arg	Lys	Ala	Ser	Arg	Leu	Asn	Ile	Pro		
		355					360					365					
Ser	Ile	Leu	Leu	Thr	Thr	Met	Thr	Gln	Val	Gly	Lys	Thr	Thr	Tyr	Val		
	370					375					380						
Leu	Asp	Phe	Thr	Ala	Thr	Tyr	Glu	Phe	Leu	Tyr	Asp	Lys	Ser	Thr	Asp		
385					390					395					400		
Pro	Glu	Gln	His	Thr	Ser	Gly	His	Ile	Asn	Gln	Asp	Leu	Thr	Gly	Lys		
			405						410					415			
Val	Thr	Val	Lys	Lys	Val	Gly	Gln	His	Tyr	Leu	Ile	Ser	Gln	Ser	Gly		
		420					425						430				
Ser	Lys	Asn	Ile	Thr	Val	Val	Lys	Glu	Asp	Asn	Gln	Leu	Lys	Ala	Pro		
	435					440						445					
Ser	Val	Phe	Pro	Glu	Ser	Ile	Leu	Gly	Thr	Trp	Thr	Gly	Gln	Ala	Asn		
	450					455					460						
Gly	Leu	Ser	Ile	His	Met	Ser	Leu	Ala	Ser	Asp	Gly	Thr	Ile	Thr	Thr		
465				470						475					480		
Lys	Val	Glu	Asp	Gln	Lys	Gly	Asn	Arg	Ser	Lys	Glu	Thr	Arg	Thr	Ala		
			485				490							495			
Lys	Ile	Ser	Lys	Val	Glu	Asp	Lys	Gly	Asn	Gly	Phe	Tyr	Leu	Tyr	Thr		
		500					505						510				
Pro	Asp	Pro	Gly	Ser	Asp	Ile	Ser	Ala	Leu	Val	Pro	Glu	Gly	Gly	Leu		
	515					520						525					
Gly	Gly	Ala	Asn	Val	Lys	Tyr	Ala	Tyr	Gly	Phe	Lys	Ile	Ser	Gly	Lys		
	530				535						540						
Thr	Ala	Ser	Pro	Val	Val	Trp	Gln	Ala	Ala	Leu	Thr	His	Glu	Phe	Asp		
545				550						555					560		
Tyr	Thr	Lys	Pro	Leu	Ser	Gly	Val	Thr	Leu	Gln	Lys	Gln	Pro				
			565						570								

<210> SEQ ID NO 131

<211> LENGTH: 954

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 131

atgagaaaaag	aggctcaaaa	ggacatgaaa	caaatgaata	aactcattac	aggagtggta	60
acgctggcga	cagtcgtgac	cttatcagct	tgtcaatcat	cacacaacaa	caccaaactc	120
gtctcgatga	aaggagacac	catcactgtc	agtgacttct	acaatgagac	caaaaacaca	180
gaactcgcac	aaaaagccat	gttaagcttg	gtgattagcc	gcgtttttga	gacacaatat	240
gccaacaaaag	tctctgacaa	agagggtgaa	aaagcctata	aacaaaccgc	agaccaatac	300
ggtacatcct	ttaagacagt	cctagcacia	tcaggcttaa	cgccagaaac	ctataaaaaa	360
caaattcgcc	tcacaaaatt	agtcgaatat	gccgtcaaaag	aacaagccaa	aaacgaaacc	420
atctcaaaaa	aagactaccg	tcaggcctat	gacgcttata	ccccaacccat	gaccgcagaa	480
atcatgcagt	ttgaaaaaga	agaggatgcc	aaagcagcgc	ttgaagccgt	caaagctgaa	540
ggggcagact	ttgcagctat	tgccaaagaa	aaaaccactg	cagccgataa	aaaaacaacc	600
tatacgtttg	actcaggcga	aacaacccta	ccagcagaag	tagttagagc	tgcatcaggc	660
ctcaaagaag	ggaacagatc	agaaatcatc	acagcgcttg	atccagccac	ctcaaaacgc	720
acctaccata	tcatcaaaag	cacaaaaaaa	gcaactaaaa	aagcagactg	gaaagcgtac	780
caaaaacgct	tgaaagacat	catcgtgact	ggcaaattaa	aagaccctga	cttccaaaac	840
aaagtcatcg	ctaaagctct	tgataaaagca	aatgtcaaaa	tcaaagacaa	agcatttgcc	900
aatatcttag	cccagtttgc	aaaacctaac	caaaaacaac	ctgccccaaa	atag	954

<210> SEQ ID NO 132

<211> LENGTH: 317

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 132

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 134

```
Met Thr Gly Gln Lys Lys Leu Ala Asn Leu Lys Lys Thr Asp Lys Lys
 1          5          10          15
Gln Ile Ile Val Arg Lys Thr Val Asp Ala Ser Val Lys Leu Lys Val
 20          25          30
Ser Lys Gln Lys Glu His Phe Ile Met Lys Phe Lys Lys Val Leu Val
 35          40          45
Ile Pro Ala Leu Ala Leu Ala Ala Thr Cys Phe Leu Thr Ala Cys Gly
 50          55          60
Thr Lys Lys Asp Ser Lys Lys Glu Glu Val Lys Glu Ile Lys Met Ser
 65          70          75          80
Asp Ile Lys Asp Asp Ala Val Ser Lys Lys Thr Lys Val Val Asp Gly
 85          90          95
Glu Glu Val Thr Glu Tyr Thr Thr Lys Asp Gly Asn Val Ile Gln Ile
100          105          110
Pro Ala Gly Asn Glu Glu Gly Met Glu Ser Lys Asp Ala Gly Gly Ser
115          120          125
Gly Ala Pro Ala Lys Asn
130
```

<210> SEQ ID NO 135

<211> LENGTH: 1269

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 135

```
atgtttcagt taagaaaaaa aatgacgcgc aaacaattag ccttggtgag tgctggagtg      60
ttgacctgtg tggttggtgg tagctacttg ataatagaacc atcaacaaca agaaattgtc      120
tctagtgtca acaaagtaaa agccttaacc ataaaaagaag ccatggaaca aggaaaagat      180
atcagcttga ccttagctgg cgaagtaaca gctaacaaca gcagcaaagt caaaatcgac      240
tcaagtaaa gagaagtcaa agaggctctt gttaaaaaag gcgatgttgt caaagtagga      300
caacccttgt ttagctatga aacgtcacag cggttaacgg ctcaaagttc agaatttgat      360
gttcaaacca aagccaatca gctccaagtt gctaaaacca atgcagcatt gaagtgggaa      420
acctacaatc gcaaggtcaa tgaaatcaac accctaaaaa ctcgctacaa cactgcacca      480
gatgagagct tactagagca aattcgcagc gcagaagaca gtgtatccca agcactaagc      540
gatgccaaaa cagcagatag cgatgtcaaa accgctcaaa tcgaactcga taaagctaag      600
gctactgcca caacggaaaa aggtaaaacta gagtatgaca ccgttaagtc agacaccgca      660
ggaaccattg ttagtctaaa tactgatttg ccaaatcaat caaaatccaa aaaagaaaat      720
gaaactttta tggaaattat cgacaaatca aaaatgttag tcaaaggtaa cattagttaa      780
tttgaccgtg acaagttaaa aatcgggtcaa aaagtcgaag tgattgaccg caaagacaac      840
tctaaaaaat ggactggaaa agtaacccaa gttggcaacc tcaaagcaga ggaaaaaggc      900
caaggtcaag gccaaggtgg caatgaccaa caagataatc caaaccaagc aaaattccct      960
tatgttattg aacttgacca atcagacaag cagccactca ttggctcaca cacctatgtt     1020
aatgtgctca acaatgttcc agaagctggc aagatcgtat tgaaagaaac ctttacaatg     1080
gcagaaaatg gaaaaaccta tgtgtggaaa gttgataaaa acaaggtcaa aaaacaagaa     1140
atcaagacta agcccttctc aaaaggttat gttgaggtaa caagtggctt gactatgcaa     1200
gataagattg ctccagccgct tcttgcatg aaagacggtg ttgaggtagg aagtattgtt     1260
aaaccttaa                                     1269
```

<210> SEQ ID NO 136

<211> LENGTH: 422

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 136

```
Met Phe Gln Leu Arg Lys Lys Met Thr Arg Lys Gln Leu Ala Leu Leu
 1          5          10          15
Ser Ala Gly Val Leu Thr Cys Val Val Gly Gly Ser Tyr Leu Ile Met
```

			20					25				30					
Asn	His	Gln	Gln	Gln	Glu	Ile	Val	Ser	Ser	Val	Asn	Lys	Val	Lys	Ala		
		35					40					45					
Leu	Thr	Ile	Lys	Glu	Ala	Met	Glu	Gln	Gly	Lys	Asp	Ile	Ser	Leu	Thr		
	50					55					60						
Leu	Ala	Gly	Glu	Val	Thr	Ala	Asn	Asn	Ser	Ser	Lys	Val	Lys	Ile	Asp		
65					70					75					80		
Ser	Ser	Lys	Gly	Glu	Val	Lys	Glu	Val	Phe	Val	Lys	Lys	Gly	Asp	Val		
			85						90					95			
Val	Lys	Val	Gly	Gln	Pro	Leu	Phe	Ser	Tyr	Glu	Thr	Ser	Gln	Arg	Leu		
			100					105					110				
Thr	Ala	Gln	Ser	Ser	Glu	Phe	Asp	Val	Gln	Thr	Lys	Ala	Asn	Gln	Leu		
		115					120					125					
Gln	Val	Ala	Lys	Thr	Asn	Ala	Ala	Leu	Lys	Trp	Glu	Thr	Tyr	Asn	Arg		
	130				135					140							
Lys	Val	Asn	Glu	Ile	Asn	Thr	Leu	Lys	Ser	Arg	Tyr	Asn	Thr	Ala	Pro		
145					150					155					160		
Asp	Glu	Ser	Leu	Leu	Glu	Gln	Ile	Arg	Ser	Ala	Glu	Asp	Ser	Val	Ser		
			165					170						175			
Gln	Ala	Leu	Ser	Asp	Ala	Lys	Thr	Ala	Asp	Ser	Asp	Val	Lys	Thr	Ala		
		180					185					190					
Gln	Ile	Glu	Leu	Asp	Lys	Ala	Asn	Ala	Thr	Ala	Thr	Thr	Glu	Lys	Gly		
	195						200					205					
Lys	Leu	Glu	Tyr	Asp	Thr	Val	Lys	Ser	Asp	Thr	Ala	Gly	Thr	Ile	Val		
	210				215					220							
Ser	Leu	Asn	Thr	Asp	Leu	Pro	Asn	Gln	Ser	Lys	Ser	Lys	Lys	Glu	Asn		
225					230					235					240		
Glu	Thr	Phe	Met	Glu	Ile	Ile	Asp	Lys	Ser	Lys	Met	Leu	Val	Lys	Gly		
			245					250						255			
Asn	Ile	Ser	Glu	Phe	Asp	Arg	Asp	Lys	Leu	Lys	Ile	Gly	Gln	Lys	Val		
		260					265						270				
Glu	Val	Ile	Asp	Arg	Lys	Asp	Asn	Ser	Lys	Lys	Trp	Thr	Gly	Lys	Val		
	275					280						285					
Thr	Gln	Val	Gly	Asn	Leu	Lys	Ala	Glu	Glu	Lys	Gly	Gln	Gly	Gln	Gly		
	290				295						300						
Gln	Gly	Gly	Asn	Asp	Gln	Gln	Asp	Asn	Pro	Asn	Gln	Ala	Lys	Phe	Pro		
305					310					315					320		
Tyr	Val	Ile	Glu	Leu	Asp	Gln	Ser	Asp	Lys	Gln	Pro	Leu	Ile	Gly	Ser		
			325					330						335			
His	Thr	Tyr	Val	Asn	Val	Leu	Asn	Asn	Val	Pro	Glu	Ala	Gly	Lys	Ile		
		340					345					350					
Val	Leu	Lys	Glu	Thr	Phe	Thr	Met	Ala	Glu	Asn	Gly	Lys	Thr	Tyr	Val		
	355					360					365						
Trp	Lys	Val	Asp	Lys	Asn	Lys	Val	Lys	Lys	Gln	Glu	Ile	Lys	Thr	Lys		
	370				375					380							
Pro	Phe	Ser	Lys	Gly	Tyr	Val	Glu	Val	Thr	Ser	Gly	Leu	Thr	Met	Gln		
385					390					395					400		
Asp	Lys	Ile	Ala	Gln	Pro	Leu	Pro	Gly	Met	Lys	Asp	Gly	Met	Glu	Val		
			405					410						415			
Gly	Ser	Ile	Val	Lys	Pro												
		420															

<210> SEQ ID NO 137
 <211> LENGTH: 1140
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 137

atgcgtagag	cagaaaaataa	caaacacagc	cgctattcca	ttcgcaaact	gagcgttggg	60
gtaacgagta	tagcaattgc	gagtctcttt	ttaggaaagg	ttgcctatgc	cgtagatggc	120
atccctccaa	tctctcttac	tcaaaagact	acagccacta	catcagaaaa	ttggcatcat	180
attgataagg	atggccttat	tccttttaggt	ataagcttag	aagctgccaa	agaggaattt	240
aaaaaagaag	tagaagaatc	acgtttatct	gaagcacaaa	aagaaacgta	taaacaaaaa	300
attaaaactg	caccagacaa	agataagcta	ttattcacgt	atcatagtga	gtatatgaca	360
gccgttaagg	atcttccagc	gtctactgag	tctactactc	agccagttga	ggcaccctg	420
caggagacac	aggcatcagc	ttcagattcg	atggtgacag	gtgattcaac	atcagttacg	480
actgattctc	ctgaggaaac	cccattctcg	gaaagtccag	tggccccagc	tttatctgag	540
gctccagctc	aaccagctga	gagtgaggaa	ccttcagtag	cagcatcttc	tgaggaaacc	600
ccatctccat	caactccagc	ggccccagaa	actcctgaag	aaccagcagc	tccatctcca	660
tcacctgaga	gtgaggaaac	ttcagtagca	gctccttctg	aggaaacccc	atctccagaa	720
actcctgaag	aaccagcagc	tccatctcaa	ccagctgaga	gtgaagaatc	ttcagtagca	780
gctacgacaa	gcccgtctcc	atcaactcca	gctgaatcag	agactcagac	gccaccagct	840
gtttactaaag	actctgataa	gccatcttca	gcagctgaaa	aaccagcagc	ctcttcactt	900
gtttcagaac	aaaccgttca	acaaccaact	tcaaagagat	cttctgataa	aaaagaagag	960
caagaacagt	cttactctcc	aaatcgctca	ttgtcaagac	aggttagggc	ccatgagtca	1020
ggtaagtact	tgcccttcaac	aggtgaaaaa	gcacagccac	tctttatagc	tactatgact	1080
ttgatgtctc	tatttggcag	tcttttagtc	acaaaacgcc	aaaaagaaac	taaaaaatag	1140

<210> SEQ ID NO 138

<211> LENGTH: 379

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 138

Met	Arg	Arg	Ala	Glu	Asn	Asn	Lys	His	Ser	Arg	Tyr	Ser	Ile	Arg	Lys
1				5					10					15	
Leu	Ser	Val	Gly	Val	Thr	Ser	Ile	Ala	Ile	Ala	Ser	Leu	Phe	Leu	Gly
			20					25					30		
Lys	Val	Ala	Tyr	Ala	Val	Asp	Gly	Ile	Pro	Pro	Ile	Ser	Leu	Thr	Gln
			35				40					45			
Lys	Thr	Thr	Ala	Thr	Thr	Ser	Glu	Asn	Trp	His	His	Ile	Asp	Lys	Asp
			50				55				60				
Gly	Leu	Ile	Pro	Leu	Gly	Ile	Ser	Leu	Glu	Ala	Ala	Lys	Glu	Glu	Phe
65					70				75					80	
Lys	Lys	Glu	Val	Glu	Glu	Ser	Arg	Leu	Ser	Glu	Ala	Gln	Lys	Glu	Thr
				85					90					95	
Tyr	Lys	Gln	Lys	Ile	Lys	Thr	Ala	Pro	Asp	Lys	Asp	Lys	Leu	Leu	Phe
			100					105					110		
Thr	Tyr	His	Ser	Glu	Tyr	Met	Thr	Ala	Val	Lys	Asp	Leu	Pro	Ala	Ser
			115				120					125			
Thr	Glu	Ser	Thr	Thr	Gln	Pro	Val	Glu	Ala	Pro	Val	Gln	Glu	Thr	Gln
			130				135					140			
Ala	Ser	Ala	Ser	Asp	Ser	Met	Val	Thr	Gly	Asp	Ser	Thr	Ser	Val	Thr
145					150					155				160	
Thr	Asp	Ser	Pro	Glu	Glu	Thr	Pro	Ser	Ser	Glu	Ser	Pro	Val	Ala	Pro
				165					170					175	
Ala	Leu	Ser	Glu	Ala	Pro	Ala	Gln	Pro	Ala	Glu	Ser	Glu	Glu	Pro	Ser
			180					185					190		
Val	Ala	Ala	Ser	Ser	Glu	Glu	Thr	Pro	Ser	Pro	Ser	Thr	Pro	Ala	Ala
			195				200					205			
Pro	Glu	Thr	Pro	Glu	Glu	Pro	Ala	Ala	Pro	Ser	Pro	Ser	Pro	Glu	Ser
			210				215					220			
Glu	Glu	Pro	Ser	Val	Ala	Ala	Pro	Ser	Glu	Glu	Thr	Pro	Ser	Pro	Glu
225					230					235				240	
Thr	Pro	Glu	Glu	Pro	Ala	Ala	Pro	Ser	Gln	Pro	Ala	Glu	Ser	Glu	Glu
				245					250					255	

Ser	Ser	Val	Ala	Ala	Thr	Thr	Ser	Pro	Ser	Pro	Ser	Thr	Pro	Ala	Glu
			260					265					270		
Ser	Glu	Thr	Gln	Thr	Pro	Pro	Ala	Val	Thr	Lys	Asp	Ser	Asp	Lys	Pro
		275					280					285			
Ser	Ser	Ala	Ala	Glu	Lys	Pro	Ala	Ala	Ser	Ser	Leu	Val	Ser	Glu	Gln
		290				295					300				
Thr	Val	Gln	Gln	Pro	Thr	Ser	Lys	Arg	Ser	Ser	Asp	Lys	Lys	Glu	Glu
305					310					315					320
Gln	Glu	Gln	Ser	Tyr	Ser	Pro	Asn	Arg	Ser	Leu	Ser	Arg	Gln	Val	Arg
				325					330					335	
Ala	His	Glu	Ser	Gly	Lys	Tyr	Leu	Pro	Ser	Thr	Gly	Glu	Lys	Ala	Gln
			340					345					350		
Pro	Leu	Phe	Ile	Ala	Thr	Met	Thr	Leu	Met	Ser	Leu	Phe	Gly	Ser	Leu
		355					360					365			
Leu	Val	Thr	Lys	Arg	Gln	Lys	Glu	Thr	Lys	Lys					
		370				375									

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<210> SEQ ID NO 139
<211> LENGTH: 1635
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 139
ttgattgtgt caaaatacct aaaatacttc tctattatca cggtattttt gactgggctt      60
attttagttg catgtcaaca acaaaagcct caaacaaaag aacgtcagcg caaacaacgt      120
ccaaaagacg aacttgtcgt ttctatgggg gcaaagctcc ctcatgaatt cgatccaaag      180
gaccggttat gagtccacaa tgaaggggaat atcactcata gcactctatt gaaacgttct      240
cctgaactag atataaaaag agagcttgct aaaacatacc atctctctga agatgggctg      300
acttggtcgt ttgacttgca tgatgatttt aaattctcaa atggtgagcc tgttactgct      360
gatgatgtta agtttactta tgatatgttg aaagcagatg gaaaggcttg ggatctaacc      420
ttcattaaga acgttgaagt agttgggaaa aatcaggtca atatccattt gactgaggcg      480
cattcgacat ttacagcaca gttgactgaa atcccaatcg tccctaaaaa acattacaat      540
gataagtata agagcaatcc tatcggttca ggaccttaca tggtaaaaga atataaggct      600
ggagaacaag ctatttttgt tcgtaaccct tattggcatg ggaaaaaacc atactttaa      660
aaatggactt gggcttact tgatgaaaac acagcactag cagctttaga atctggtgat      720
gttgatatga tctacgcaac gccagaactt gctgataaaa aagtcaaagg caccgcctc      780
cttgatattc catcaaatga tgtgcgcggc ttatcattac cttatgtgaa aaagggcgtc      840
atcactgatt ctctgatgg ttatcctgta ggaaatgatg tcactagtga tccagcaatc      900
cgaaaagcct tgactattgg tttaaataag caaaaagttc tcgatacggg tttaaattgg      960
tatggtaaac cagcttattc aattattgat aaacacccat tttggaatcc aaaaacagcc     1020
attaaagata ataaagtagc taaagctaag caattattga caaaagcggg atggaaagaa     1080
caagcagacg gtagccgtaa aaaaggtgac cttgatgcag cgtttgatct gtactaccct     1140
actaatgatc aattgcgagc gaacttagcc gttgaagtag cagagcaagc caaggcccta     1200
gggattacta ttaaaactca agctagtaac tgggatgaaa tggcaacgaa gtcacatgac     1260
tcagccttac tttatgccgg aggacgtcat cacgcgcagc aattttatga atcgcatcat     1320
ccaagcctag cagggaaaag ttggaccaat attacgtttt ataacaatcc taccgtgact     1380
aagtaccttg acaaagcaat gacatcttct gaccttgata aagctaacga atattggaag     1440
ttagcgcagt gggatggcaa aacaggtgct tctactcttg gagatttgcc aaatgtatgg     1500
ttggtgagcc ttaaccatac ttatatgggt gataaacgta tcaatgtagg taaacaaggc     1560
gtccacagtc atggtcatga ttggtcatta ttgactaaca ttgccgagtg gacttgggat     1620
gaatcaacta agtaa                                     1635

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<210> SEQ ID NO 140
<211> LENGTH: 544
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 140
Met Ile Val Ser Lys Tyr Leu Lys Tyr Phe Ser Ile Ile Thr Leu Phe

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1				5					10					15			
Leu	Thr	Gly	Leu	Ile	Leu	Val	Ala	Cys	Gln	Gln	Gln	Lys	Pro	Gln	Thr		
			20					25					30				
Lys	Glu	Arg	Gln	Arg	Lys	Gln	Arg	Pro	Lys	Asp	Glu	Leu	Val	Val	Ser		
		35					40					45					
Met	Gly	Ala	Lys	Leu	Pro	His	Glu	Phe	Asp	Pro	Lys	Asp	Arg	Tyr	Gly		
	50					55					60						
Val	His	Asn	Glu	Gly	Asn	Ile	Thr	His	Ser	Thr	Leu	Leu	Lys	Arg	Ser		
65					70					75					80		
Pro	Glu	Leu	Asp	Ile	Lys	Gly	Glu	Leu	Ala	Lys	Thr	Tyr	His	Leu	Ser		
			85						90					95			
Glu	Asp	Gly	Leu	Thr	Trp	Ser	Phe	Asp	Leu	His	Asp	Asp	Phe	Lys	Phe		
		100						105					110				
Ser	Asn	Gly	Glu	Pro	Val	Thr	Ala	Asp	Asp	Val	Lys	Phe	Thr	Tyr	Asp		
		115					120					125					
Met	Leu	Lys	Ala	Asp	Gly	Lys	Ala	Trp	Asp	Leu	Thr	Phe	Ile	Lys	Asn		
	130				135						140						
Val	Glu	Val	Val	Gly	Lys	Asn	Gln	Val	Asn	Ile	His	Leu	Thr	Glu	Ala		
145				150						155					160		
His	Ser	Thr	Phe	Thr	Ala	Gln	Leu	Thr	Glu	Ile	Pro	Ile	Val	Pro	Lys		
			165						170					175			
Lys	His	Tyr	Asn	Asp	Lys	Tyr	Lys	Ser	Asn	Pro	Ile	Gly	Ser	Gly	Pro		
		180						185					190				
Tyr	Met	Val	Lys	Glu	Tyr	Lys	Ala	Gly	Glu	Gln	Ala	Ile	Phe	Val	Arg		
	195						200					205					
Asn	Pro	Tyr	Trp	His	Gly	Lys	Lys	Pro	Tyr	Phe	Lys	Lys	Trp	Thr	Trp		
	210				215							220					
Val	Leu	Leu	Asp	Glu	Asn	Thr	Ala	Leu	Ala	Ala	Leu	Glu	Ser	Gly	Asp		
225				230					235						240		
Val	Asp	Met	Ile	Tyr	Ala	Thr	Pro	Glu	Leu	Ala	Asp	Lys	Lys	Val	Lys		
		245						250					255				
Gly	Thr	Arg	Leu	Leu	Asp	Ile	Pro	Ser	Asn	Asp	Val	Arg	Gly	Leu	Ser		
		260						265					270				
Leu	Pro	Tyr	Val	Lys	Lys	Gly	Val	Ile	Thr	Asp	Ser	Pro	Asp	Gly	Tyr		
	275					280						285					
Pro	Val	Gly	Asn	Asp	Val	Thr	Ser	Asp	Pro	Ala	Ile	Arg	Lys	Ala	Leu		
	290				295						300						
Thr	Ile	Gly	Leu	Asn	Arg	Gln	Lys	Val	Leu	Asp	Thr	Val	Leu	Asn	Gly		
305				310						315					320		
Tyr	Gly	Lys	Pro	Ala	Tyr	Ser	Ile	Ile	Asp	Lys	Thr	Pro	Phe	Trp	Asn		
		325						330					335				
Pro	Lys	Thr	Ala	Ile	Lys	Asp	Asn	Lys	Val	Ala	Lys	Ala	Lys	Gln	Leu		
		340					345					350					
Leu	Thr	Lys	Ala	Gly	Trp	Lys	Glu	Gln	Ala	Asp	Gly	Ser	Arg	Lys	Lys		
	355					360						365					
Gly	Asp	Leu	Asp	Ala	Ala	Phe	Asp	Leu	Tyr	Tyr	Pro	Thr	Asn	Asp	Gln		
	370				375						380						
Leu	Arg	Ala	Asn	Leu	Ala	Val	Glu	Val	Ala	Glu	Gln	Ala	Lys	Ala	Leu		
385				390					395						400		
Gly	Ile	Thr	Ile	Lys	Leu	Lys	Ala	Ser	Asn	Trp	Asp	Glu	Met	Ala	Thr		
		405						410					415				
Lys	Ser	His	Asp	Ser	Ala	Leu	Leu	Tyr	Ala	Gly	Gly	Arg	His	His	Ala		
		420						425					430				
Gln	Gln	Phe	Tyr	Glu	Ser	His	His	Pro	Ser	Leu	Ala	Gly	Lys	Gly	Trp		
	435					440						445					
Thr	Asn	Ile	Thr	Phe	Tyr	Asn	Asn	Pro	Thr	Val	Thr	Lys	Tyr	Leu	Asp		
	450					455					460						

Lys	Ala	Met	Thr	Ser	Ser	Asp	Leu	Asp	Lys	Ala	Asn	Glu	Tyr	Trp	Lys
465					470					475					480
Leu	Ala	Gln	Trp	Asp	Gly	Lys	Thr	Gly	Ala	Ser	Thr	Leu	Gly	Asp	Leu
				485					490					495	
Pro	Asn	Val	Trp	Leu	Val	Ser	Leu	Asn	His	Thr	Tyr	Ile	Gly	Asp	Lys
			500					505					510		
Arg	Ile	Asn	Val	Gly	Lys	Gln	Gly	Val	His	Ser	His	Gly	His	Asp	Trp
	515						520					525			
Ser	Leu	Leu	Thr	Asn	Ile	Ala	Glu	Trp	Thr	Trp	Asp	Glu	Ser	Thr	Lys
	530					535					540				

<210> SEQ ID NO 141
 <211> LENGTH: 1047
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 141

atgttgacat	caaagcacca	taatctcaac	aaactagtct	ggcgctacgg	gctaacctca	60
gccgctgccg	tccttctagc	ctttggaggc	ggggcaagca	gcgttaaggc	tgaggtttct	120
tctacgacta	tgacgtcgag	tcaaagagag	tcaaaaataa	aagagatcga	agaaagtctt	180
aaaaaatatc	cagaagtgtc	caatgagaaa	ttttgggaaa	gaaagtggta	tggaacctat	240
tttaaagaag	aagattttca	aaaggagcta	aaagatttta	ctgagaagag	gcttaaggag	300
attctagatt	taattggtaa	atctggaatc	aaggagagacc	gtggtgagac	tggtcctgct	360
ggcccagccg	gaccacaagg	taaaactggg	gagagggggc	cccaagggtcc	taaaggtgac	420
cgcggtgagc	aaggaatcca	aggtaaagct	ggtgaaaaag	gtgagcgcgg	tgaaaaaggc	480
gacaaagggtg	aaaccgggtga	acgcggtgaa	aaaggcgaag	ctggaatcca	aggcccacaa	540
ggtgaagctg	gtaaagatgg	cgctccaggt	aaagatggag	ctccaggcga	aaaggggtgaa	600
aaaggtgacc	gcggtgaaac	cggagctcag	ggtccagtag	gcccacaagg	tgaaaaaggt	660
gaaacggggc	cccaaggccc	agcaggccca	caaggtgagg	caggcaaacc	aggtgagcaa	720
ggcccagcag	gcccacaagg	tgaagcaggc	caaccaggcg	aaaaagctcc	agaaaagagc	780
ccagaaggcg	aagcaggcca	accaggcgaa	aaagctccag	aaaagagcaa	agaggttaact	840
ccagctgcag	aaaaacctgc	tgacaaagaa	gctaaccaaa	cgccagaacg	ccgcaatggc	900
aatatggcta	agacacctgt	agccaacaac	cacagacgtc	taccagcaac	tggtgagcaa	960
gccaacccat	tctttacagc	agcagcagta	gcagtgatga	caacagctgg	tgtcctagcc	1020
gttacaaaac	gcaaagaaaa	caactaa				1047

<210> SEQ ID NO 142
 <211> LENGTH: 348
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 142

Met	Leu	Thr	Ser	Lys	His	His	Asn	Leu	Asn	Lys	Leu	Val	Trp	Arg	Tyr
1				5					10					15	
Gly	Leu	Thr	Ser	Ala	Ala	Ala	Val	Leu	Leu	Ala	Phe	Gly	Gly	Gly	Ala
			20					25				30			
Ser	Ser	Val	Lys	Ala	Glu	Val	Ser	Ser	Thr	Thr	Met	Thr	Ser	Ser	Gln
		35					40				45				
Arg	Glu	Ser	Lys	Ile	Lys	Glu	Ile	Glu	Glu	Ser	Leu	Lys	Lys	Tyr	Pro
	50					55					60				
Glu	Val	Ser	Asn	Glu	Lys	Phe	Trp	Glu	Arg	Lys	Trp	Tyr	Gly	Thr	Tyr
65				70						75				80	
Phe	Lys	Glu	Glu	Asp	Phe	Gln	Lys	Glu	Leu	Lys	Asp	Phe	Thr	Glu	Lys
			85					90					95		
Arg	Leu	Lys	Glu	Ile	Leu	Asp	Leu	Ile	Gly	Lys	Ser	Gly	Ile	Lys	Gly
			100					105					110		
Asp	Arg	Gly	Glu	Thr	Gly	Pro	Ala	Gly	Pro	Ala	Gly	Pro	Gln	Gly	Lys
	115						120					125			
Thr	Gly	Glu	Arg	Gly	Ala	Gln	Gly	Pro	Lys	Gly	Asp	Arg	Gly	Glu	Gln

130		135		140
Gly Ile Gln Gly Lys Ala Gly Glu Lys Gly Glu Arg Gly Glu Lys Gly				
145		150		155
Asp Lys Gly Glu Thr Gly Glu Arg Gly Glu Lys Gly Glu Ala Gly Ile				
	165		170	175
Gln Gly Pro Gln Gly Glu Ala Gly Lys Asp Gly Ala Pro Gly Lys Asp				
	180		185	190
Gly Ala Pro Gly Glu Lys Gly Glu Lys Gly Asp Arg Gly Glu Thr Gly				
	195		200	205
Ala Gln Gly Pro Val Gly Pro Gln Gly Glu Lys Gly Glu Thr Gly Ala				
	210		215	220
Gln Gly Pro Ala Gly Pro Gln Gly Glu Ala Gly Lys Pro Gly Glu Gln				
225		230		235
Gly Pro Ala Gly Pro Gln Gly Glu Ala Gly Gln Pro Gly Glu Lys Ala				
	245		250	255
Pro Glu Lys Ser Pro Glu Gly Glu Ala Gly Gln Pro Gly Glu Lys Ala				
	260		265	270
Pro Glu Lys Ser Lys Glu Val Thr Pro Ala Ala Glu Lys Pro Ala Asp				
	275		280	285
Lys Glu Ala Asn Gln Thr Pro Glu Arg Arg Asn Gly Asn Met Ala Lys				
	290		295	300
Thr Pro Val Ala Asn Asn His Arg Arg Leu Pro Ala Thr Gly Glu Gln				
305		310		315
Ala Asn Pro Phe Phe Thr Ala Ala Ala Val Ala Val Met Thr Thr Ala				
	325		330	335
Gly Val Leu Ala Val Thr Lys Arg Lys Glu Asn Asn				
	340		345	

<210> SEQ ID NO 143

<211> LENGTH: 1371

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 143

ttgatttcac	gcataaaaag	ctttaaaaaac	gctttaaatt	atgataaaaat	gaactgtatc	60
gaaattatttt	taaggagaaa	tgacttaatg	tctacatcat	ttgaaaacaa	agctacaaat	120
cgtggcggtga	ttacattttac	aatcagtgcaa	gataaaaataa	aaccagctct	tgataaagct	180
tttaataaaaa	tcaaaaaaga	cttgaatgca	ccagggtttcc	gtaaaggaca	catgcctcgt	240
ccagtcttca	acccaaaaatt	tggtgaagaa	gttctttatg	aagatgcttt	gaatattgta	300
ttgccagaag	cttatgaagc	agctgtgacg	gaacttggtc	ttgatgtggt	tgacacaacca	360
aaaatcgatg	ttgtgtcaat	ggaaaaaggg	aaagagtggg	cactttctgc	tgaagttgtg	420
acaaaacctg	aagtgaacct	tggtgattac	aaaaacctag	ttgtagaagt	tgatgcttca	480
aaagaagttt	cagatgaaga	cgtggatgct	aaaattgagc	gcgaacgtca	aaaccttgcg	540
gaactcatta	ttaaagacgg	tgaagcagct	caaggtgaca	ctgttgatgat	tgactttggt	600
ggttcagttg	atggtgttga	gtttgatggc	ggtaaaggag	ataacttctc	tcttgaactt	660
ggttcaggac	aatttatccc	aggttttgaa	gatcaactag	ttggtgctaa	agctggcgat	720
gaagtagaag	ttaatgtcac	attcccagaa	tcttaccag	cagaagatct	tgacaggtaaa	780
gccgctaaat	ttatgacaac	tattcacgaa	gtcaaaaacaa	aagaagtacc	agagcttgat	840
gatgagcttg	caaaagatat	tgatgaagat	gttgacacac	ttgaagactt	aaaagtaaaa	900
tatcgtaaaag	aacttgaagc	agctcaagaa	actgcttatg	atgatgctgt	tgaaggagct	960
gcgattgaat	tagcagttgc	aaatgctgaa	attggttgatt	taccgaaga	aatgattcat	1020
gaagaagtca	accgttcagt	gaatgaattt	atgggcaaca	tgcaacgtca	aggaatctca	1080
cctgaaatgt	acttccaatt	gactggtaca	actcaagaag	atttacataa	ccaatattca	1140
gctgaagctg	acaaacgtgt	taaaacacac	cttgattattg	aagcaattgc	taaagcagaa	1200
ggtttttgaag	caacagatag	tgaaattgaa	caagaaatta	atgaccttgc	aacagaatat	1260
aacatgccag	ctgaccaagt	tcgttctctt	ctttcagcag	atatgttgaa	acatgatatt	1320
gcaatgaaaa	aagcagttga	agtgattaca	agcacagcaa	gcgttaagta	a	1371

<210> SEQ ID NO 144
 <211> LENGTH: 456
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 144

Met	Ile	Ser	Arg	Ile	Lys	Ser	Phe	Lys	Asn	Ala	Leu	Asn	Tyr	Asp	Lys	1	5	10	15
Met	Asn	Cys	Ile	Glu	Ile	Ile	Leu	Arg	Arg	Asn	Asp	Leu	Met	Ser	Thr	20	25	30	
Ser	Phe	Glu	Asn	Lys	Ala	Thr	Asn	Arg	Gly	Val	Ile	Thr	Phe	Thr	Ile	35	40	45	
Ser	Gln	Asp	Lys	Ile	Lys	Pro	Ala	Leu	Asp	Lys	Ala	Phe	Asn	Lys	Ile	50	55	60	
Lys	Lys	Asp	Leu	Asn	Ala	Pro	Gly	Phe	Arg	Lys	Gly	His	Met	Pro	Arg	65	70	75	80
Pro	Val	Phe	Asn	Gln	Lys	Phe	Gly	Glu	Glu	Val	Leu	Tyr	Glu	Asp	Ala	85	90	95	
Leu	Asn	Ile	Val	Leu	Pro	Glu	Ala	Tyr	Glu	Ala	Ala	Val	Thr	Glu	Leu	100	105	110	
Gly	Leu	Asp	Val	Val	Ala	Gln	Pro	Lys	Ile	Asp	Val	Val	Ser	Met	Glu	115	120	125	
Lys	Gly	Lys	Glu	Trp	Thr	Leu	Ser	Ala	Glu	Val	Val	Thr	Lys	Pro	Glu	130	135	140	
Val	Lys	Leu	Gly	Asp	Tyr	Lys	Asn	Leu	Val	Val	Glu	Val	Asp	Ala	Ser	145	150	155	160
Lys	Glu	Val	Ser	Asp	Glu	Asp	Val	Asp	Ala	Lys	Ile	Glu	Arg	Glu	Arg	165	170	175	
Gln	Asn	Leu	Ala	Glu	Leu	Ile	Ile	Lys	Asp	Gly	Glu	Ala	Ala	Gln	Gly	180	185	190	
Asp	Thr	Val	Val	Ile	Asp	Phe	Val	Gly	Ser	Val	Asp	Gly	Val	Glu	Phe	195	200	205	
Asp	Gly	Lys	Gly	Asp	Asn	Phe	Ser	Leu	Glu	Leu	Gly	Ser	Gly	Gln		210	215	220	
Phe	Ile	Pro	Gly	Phe	Glu	Asp	Gln	Leu	Val	Gly	Ala	Lys	Ala	Gly	Asp	225	230	235	240
Glu	Val	Glu	Val	Asn	Val	Thr	Phe	Pro	Glu	Ser	Tyr	Gln	Ala	Glu	Asp	245	250	255	
Leu	Ala	Gly	Lys	Ala	Ala	Lys	Phe	Met	Thr	Thr	Ile	His	Glu	Val	Lys	260	265	270	
Thr	Lys	Glu	Val	Pro	Glu	Leu	Asp	Asp	Glu	Leu	Ala	Lys	Asp	Ile	Asp	275	280	285	
Glu	Asp	Val	Asp	Thr	Leu	Glu	Asp	Leu	Lys	Val	Lys	Tyr	Arg	Lys	Glu	290	295	300	
Leu	Glu	Ala	Ala	Gln	Glu	Thr	Ala	Tyr	Asp	Asp	Ala	Val	Glu	Gly	Ala	305	310	315	320
Ala	Ile	Glu	Leu	Ala	Val	Ala	Asn	Ala	Glu	Ile	Val	Asp	Leu	Pro	Glu	325	330	335	
Glu	Met	Ile	His	Glu	Glu	Val	Asn	Arg	Ser	Val	Asn	Glu	Phe	Met	Gly	340	345	350	
Asn	Met	Gln	Arg	Gln	Gly	Ile	Ser	Pro	Glu	Met	Tyr	Phe	Gln	Leu	Thr	355	360	365	
Gly	Thr	Gln	Glu	Asp	Leu	His	Asn	Gln	Tyr	Ser	Ala	Glu	Ala	Asp		370	375	380	
Lys	Arg	Val	Lys	Thr	His	Leu	Val	Ile	Glu	Ala	Ile	Ala	Lys	Ala	Glu	385	390	395	400
Gly	Phe	Glu	Ala	Thr	Asp	Ser	Glu	Ile	Glu	Gln	Glu	Ile	Asn	Asp	Leu	405	410	415	

Ala Thr Glu Tyr Asn Met Pro Ala Asp Gln Val Arg Ser Leu Leu Ser
420 425 430
Ala Asp Met Leu Lys His Asp Ile Ala Met Lys Lys Ala Val Glu Val
435 440 445
Ile Thr Ser Thr Ala Ser Val Lys
450 455

<210> SEQ ID NO 145
<211> LENGTH: 927
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 145

atgaaaacta	ttcgaatagc	aaagtattta	ggaattctat	tccttttgat	aactcttatt	60
agcgtaggtg	ctagttttta	tttctttcat	ggtgcacaaa	taagagaaga	gaaatcgttt	120
attaataata	agaaacggag	tacaaataat	ccattatacc	cagctgaaca	gtcttttgac	180
gctttacctt	acgaaaaacg	tcaactaaca	aatcgtgggt	taaaacaagt	ggggtggtac	240
ttaccagctg	ctcaaaaaac	aaaaaagaca	gctattgttg	ttcatgggtt	tacgaatgac	300
aaagaagata	tgaagccata	tgccatgctt	tttcatgatt	tgggctataa	tgtcttaatg	360
ccagacaatg	aggcccatgg	ggaaaagtga	gggaacttga	ttggttatgg	ctggaatgac	420
cgccttaatg	tcatggcttg	gacagaccaa	ctgattaagg	aaaaccctga	aagccaaatc	480
acactctttg	gcttatctat	gggtgctgca	acagtaatga	tggcaagtgg	tgagcgattg	540
cctgcgcaag	tcacctccct	catcgaagat	tgcggttatg	ccagtgtttg	ggacgaattg	600
aagtttcagg	ccaaggctat	gtacaacttg	cctgcctttc	ctttactcta	tgaagtctct	660
gccttatcta	agattcgagc	aggttttagt	tacggagaag	cgagctcagt	gaaacagctg	720
gctaaaaata	aacgtccaac	tttatattatc	cacggtgata	aggatgattt	tgttcctaca	780
aaaatggttt	atgacaatta	taaggccacg	aaaggtccta	aggaaatctt	gattgttaaa	840
ggggcaaaac	acgccaaatc	ctttgaaaaca	aaccagaac	aataaccagaa	aaaaattgcc	900
gcttttttga	aaaaagttga	gaaataa				927

<210> SEQ ID NO 146
<211> LENGTH: 308
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 146

Met	Lys	Thr	Ile	Arg	Ile	Ala	Lys	Tyr	Leu	Gly	Ile	Leu	Phe	Leu	Leu
1				5					10					15	
Ile	Thr	Leu	Ile	Ser	Val	Gly	Ala	Ser	Phe	Tyr	Phe	Phe	His	Val	Ala
			20					25					30		
Gln	Ile	Arg	Glu	Glu	Lys	Ser	Phe	Ile	Asn	Asn	Lys	Lys	Arg	Ser	Thr
		35				40					45				
Asn	Asn	Pro	Leu	Tyr	Pro	Ala	Glu	Gln	Ser	Phe	Asp	Ala	Leu	Pro	Tyr
	50				55					60					
Glu	Lys	Arg	Gln	Leu	Thr	Asn	Arg	Gly	Leu	Lys	Gln	Val	Gly	Trp	Tyr
65				70				75						80	
Leu	Pro	Ala	Ala	Gln	Lys	Thr	Lys	Lys	Thr	Ala	Ile	Val	Val	His	Gly
			85					90					95		
Phe	Thr	Asn	Asp	Lys	Glu	Asp	Met	Lys	Pro	Tyr	Ala	Met	Leu	Phe	His
		100					105					110			
Asp	Leu	Gly	Tyr	Asn	Val	Leu	Met	Pro	Asp	Asn	Glu	Ala	His	Gly	Glu
	115					120					125				
Ser	Glu	Gly	Asn	Leu	Ile	Gly	Tyr	Gly	Trp	Asn	Asp	Arg	Leu	Asn	Val
	130					135				140					
Met	Ala	Trp	Thr	Asp	Gln	Leu	Ile	Lys	Glu	Asn	Pro	Glu	Ser	Gln	Ile
145				150					155					160	
Thr	Leu	Phe	Gly	Leu	Ser	Met	Gly	Ala	Ala	Thr	Val	Met	Met	Ala	Ser
			165					170						175	
Gly	Glu	Arg	Leu	Pro	Ala	Gln	Val	Thr	Ser	Leu	Ile	Glu	Asp	Cys	Gly

			180					185				190					
Tyr	Ala	Ser	Val	Trp	Asp	Glu	Leu	Lys	Phe	Gln	Ala	Lys	Ala	Met	Tyr		
		195					200					205					
Asn	Leu	Pro	Ala	Phe	Pro	Leu	Leu	Tyr	Glu	Val	Ser	Ala	Leu	Ser	Lys		
	210					215					220						
Ile	Arg	Ala	Gly	Phe	Ser	Tyr	Gly	Glu	Ala	Ser	Ser	Val	Lys	Gln	Leu		
225					230					235				240			
Ala	Lys	Asn	Lys	Arg	Pro	Thr	Leu	Phe	Ile	His	Gly	Asp	Lys	Asp	Asp		
			245					250					255				
Phe	Val	Pro	Thr	Lys	Met	Val	Tyr	Asp	Asn	Tyr	Lys	Ala	Thr	Lys	Gly		
		260					265					270					
Pro	Lys	Glu	Ile	Leu	Ile	Val	Lys	Gly	Ala	Lys	His	Ala	Lys	Ser	Phe		
	275					280					285						
Glu	Thr	Asn	Pro	Glu	Gln	Tyr	Gln	Lys	Lys	Ile	Ala	Ala	Phe	Leu	Lys		
	290				295						300						
Lys	Val	Glu	Lys														
305																	

<210> SEQ ID NO 147

<211> LENGTH: 855

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 147

atgaaatcca	aaaaagttgt	tagtggtata	tcacttacct	tatccctttt	tttggtgaca	60
ggttgtgcta	aagttgataa	caacaaatca	gttaatctta	agcctgctac	taaacaaacc	120
tataatagct	atagtgatga	ccaattaaga	tcgcgtgaaa	ataccatgtc	tgttttatgg	180
taccagcgag	ctgcggaaac	tcaagcgctt	tatttacagg	ggtatcagtt	agcaacggat	240
cgttaaaaag	aacaactcaa	taaaccaacg	gataaacctt	attcaattgt	attagatatt	300
gacgaaacag	ttcttgataa	tagcccttat	caagctaaaa	atgttttgga	aggaacagga	360
tttacacctg	aaagctggga	ttattgggta	caaaaagaaag	aagcaaaacc	ggttgctggt	420
gctaaagact	ttttgcaatt	tgcagaccaa	aatgggtgtt	aaatttacta	catttcagac	480
agatcaacta	ctcaagtaga	tgctacaatg	gaaaatctcc	aaaaagaagg	tattccagta	540
caaggtcgtg	atcatcttct	attccttagaa	aaaggcgtaa	aatcaaagga	gagtcgtcgt	600
caaaagggtca	aagaaacaac	taatgtaacg	atgctatttg	gtgataatct	tctagatttt	660
gctgattttt	caaaaaaatc	tcaagaagat	agaacagctt	tattatcaga	tttacaagaa	720
gagtttgga	gacgctttat	cattttccct	aatcctatgt	atggttcatg	ggaaggtgcc	780
atttataaag	gtgaaaagct	ggatgtgctt	aagcaactag	aggaacgccg	taaaagttta	840
aaaagcttta	aataa					855

<210> SEQ ID NO 148

<211> LENGTH: 284

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 148

Met	Lys	Ser	Lys	Lys	Val	Val	Ser	Val	Ile	Ser	Leu	Thr	Leu	Ser	Leu
1			5						10				15		
Phe	Leu	Val	Thr	Gly	Cys	Ala	Lys	Val	Asp	Asn	Asn	Lys	Ser	Val	Asn
		20					25				30				
Leu	Lys	Pro	Ala	Thr	Lys	Gln	Thr	Tyr	Asn	Ser	Tyr	Ser	Asp	Asp	Gln
	35				40				45						
Leu	Arg	Ser	Arg	Glu	Asn	Thr	Met	Ser	Val	Leu	Trp	Tyr	Gln	Arg	Ala
	50				55				60						
Ala	Glu	Thr	Gln	Ala	Leu	Tyr	Leu	Gln	Gly	Tyr	Gln	Leu	Ala	Thr	Asp
65				70				75				80			
Arg	Leu	Lys	Glu	Gln	Leu	Asn	Lys	Pro	Thr	Asp	Lys	Pro	Tyr	Ser	Ile
			85			90					95				
Val	Leu	Asp	Ile	Asp	Glu	Thr	Val	Leu	Asp	Asn	Ser	Pro	Tyr	Gln	Ala

			100					105					110				
Lys	Asn	Val	Leu	Glu	Gly	Thr	Gly	Phe	Thr	Pro	Glu	Ser	Trp	Asp	Tyr		
		115					120					125					
Trp	Val	Gln	Lys	Lys	Glu	Ala	Lys	Pro	Val	Ala	Gly	Ala	Lys	Asp	Phe		
	130					135					140						
Leu	Gln	Phe	Ala	Asp	Gln	Asn	Gly	Val	Gln	Ile	Tyr	Tyr	Ile	Ser	Asp		
145					150					155					160		
Arg	Ser	Thr	Thr	Gln	Val	Asp	Ala	Thr	Met	Glu	Asn	Leu	Gln	Lys	Glu		
				165					170						175		
Gly	Ile	Pro	Val	Gln	Gly	Arg	Asp	His	Leu	Leu	Phe	Leu	Glu	Lys	Gly		
		180					185						190				
Val	Lys	Ser	Lys	Glu	Ser	Arg	Arg	Gln	Lys	Val	Lys	Glu	Thr	Thr	Asn		
	195						200					205					
Val	Thr	Met	Leu	Phe	Gly	Asp	Asn	Leu	Leu	Asp	Phe	Ala	Asp	Phe	Ser		
	210				215						220						
Lys	Lys	Ser	Gln	Glu	Asp	Arg	Thr	Ala	Leu	Leu	Ser	Asp	Leu	Gln	Glu		
225				230					235						240		
Glu	Phe	Gly	Arg	Arg	Phe	Ile	Ile	Phe	Pro	Asn	Pro	Met	Tyr	Gly	Ser		
			245					250						255			
Trp	Glu	Gly	Ala	Ile	Tyr	Lys	Gly	Glu	Lys	Leu	Asp	Val	Leu	Lys	Gln		
		260					265						270				
Leu	Glu	Glu	Arg	Arg	Lys	Ser	Leu	Lys	Ser	Phe	Lys						
		275					280										

<210> SEQ ID NO 149
 <211> LENGTH: 918
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 149

ttgctgtatg	ggtttgaaaa	aagaggaaaa	aaaatgataa	aacgatgtaa	aggaattggt	60
ctagccttaa	tggccttctt	tttggtagct	tgtgtgaatc	agcaccctaa	aacggctaaa	120
gagactgaac	agcagagaat	tgtagccact	tcggttgctg	tggttgatat	ctgtgaccgt	180
ttaaatttag	acctcgttgg	ggtttgtgat	agtaaattat	atacccttcc	taaacgctat	240
gatgctgtta	agcgtgtggg	tttaccatg	aatcctgata	tagagttgat	tgcttctttg	300
aaaccaactt	ggattttgag	tccaattct	ttacaagaag	atttgggaacc	caagtatcaa	360
aaattggata	ctgagtatgg	ttttttgaac	ttacgaagtg	ttgagggcat	gtaccagtcc	420
attgatgatt	tagggaacct	tttccaacgt	caacaagaag	caaaagaatt	gcgccagcaa	480
taccaggact	attatcgtgc	tttccaagct	aaacgtaagg	ggaagaaaaa	gcctaaagtg	540
cttattctta	tgggcttgcc	aggtagttat	ttggtggcga	cgaaccaatc	ttatgtaggg	600
aatcttttgg	acttggcagg	tggtgagaat	gtttatcagt	cagatgagaa	agaatttcta	660
tcagctaata	ctgaagacat	gctggctaag	gagcctgact	tgatttttacg	aacagctcat	720
gccattccag	acaaggtaaa	agtgatgttt	gacaaagaat	ttgctgaaaa	tgatatttgg	780
aaacatttta	cggcagtcaa	ggaagggaaa	gtctatgatt	tggacaatac	cctgtttggc	840
atgagtgcta	aattgaacta	cccagaagcc	ttggacacct	taacacagct	ttttgaccac	900
gtgggagatc	atccgtaa					918

<210> SEQ ID NO 150
 <211> LENGTH: 305
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 150

Met	Leu	Tyr	Gly	Phe	Gly	Lys	Arg	Gly	Lys	Lys	Met	Ile	Lys	Arg	Cys
1				5				10					15		
Lys	Gly	Ile	Gly	Leu	Ala	Leu	Met	Ala	Phe	Phe	Leu	Val	Ala	Cys	Val
		20					25				30				
Asn	Gln	His	Pro	Lys	Thr	Ala	Lys	Glu	Thr	Glu	Gln	Gln	Arg	Ile	Val
		35					40						45		

Ala	Thr	Ser	Val	Ala	Val	Val	Asp	Ile	Cys	Asp	Arg	Leu	Asn	Leu	Asp
50						55					60				
Leu	Val	Gly	Val	Cys	Asp	Ser	Lys	Leu	Tyr	Thr	Leu	Pro	Lys	Arg	Tyr
65				70					75					80	
Asp	Ala	Val	Lys	Arg	Val	Gly	Leu	Pro	Met	Asn	Pro	Asp	Ile	Glu	Leu
			85					90					95		
Ile	Ala	Ser	Leu	Lys	Pro	Thr	Trp	Ile	Leu	Ser	Pro	Asn	Ser	Leu	Gln
		100					105					110			
Glu	Asp	Leu	Glu	Pro	Lys	Tyr	Gln	Lys	Leu	Asp	Thr	Glu	Tyr	Gly	Phe
	115					120					125				
Leu	Asn	Leu	Arg	Ser	Val	Glu	Gly	Met	Tyr	Gln	Ser	Ile	Asp	Asp	Leu
	130				135						140				
Gly	Asn	Leu	Phe	Gln	Arg	Gln	Gln	Glu	Ala	Lys	Glu	Leu	Arg	Gln	Gln
145				150					155					160	
Tyr	Gln	Asp	Tyr	Tyr	Arg	Ala	Phe	Gln	Ala	Lys	Arg	Lys	Gly	Lys	Lys
		165					170						175		
Lys	Pro	Lys	Val	Leu	Ile	Leu	Met	Gly	Leu	Pro	Gly	Ser	Tyr	Leu	Val
		180					185					190			
Ala	Thr	Asn	Gln	Ser	Tyr	Val	Gly	Asn	Leu	Leu	Asp	Leu	Ala	Gly	Gly
	195					200					205				
Glu	Asn	Val	Tyr	Gln	Ser	Asp	Glu	Lys	Glu	Phe	Leu	Ser	Ala	Asn	Pro
	210			215					220						
Glu	Asp	Met	Leu	Ala	Lys	Glu	Pro	Asp	Leu	Ile	Leu	Arg	Thr	Ala	His
225				230					235					240	
Ala	Ile	Pro	Asp	Lys	Val	Lys	Val	Met	Phe	Asp	Lys	Glu	Phe	Ala	Glu
		245					250						255		
Asn	Asp	Ile	Trp	Lys	His	Phe	Thr	Ala	Val	Lys	Glu	Gly	Lys	Val	Tyr
		260					265					270			
Asp	Leu	Asp	Asn	Thr	Leu	Phe	Gly	Met	Ser	Ala	Lys	Leu	Asn	Tyr	Pro
	275					280					285				
Glu	Ala	Leu	Asp	Thr	Leu	Thr	Gln	Leu	Phe	Asp	His	Val	Gly	Asp	His
	290				295					300					
Pro															
305															

<210> SEQ ID NO 151

<211> LENGTH: 1143

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 151

atgaaaaagt	ggcaaaaaat	cgtgtgtgtg	actggaactg	tgcttgcaac	gtctagttta	60
gcagcctgcg	aaagcaagtc	agcatcaaaa	gatagtgatg	tcaaattatt	gatgtaccaa	120
gttggtgaca	aacctgataa	cttcgatgaa	ttgatgacaa	ttgctaacaa	gcgcatcaaa	180
gaaaaaacag	gtgcaacggt	tgaccttcaa	tacatcgggt	ggggggactg	ggatgataaa	240
atgagtacca	tcattgcctc	tggtgaaaac	tacgacattg	cttttgccaa	taattatgtg	300
gtcaatgcac	aaaaaggtgc	ttttgctgat	ttgacaacgt	taatgccaaa	atacgctaag	360
aaaacgtata	aaaacttaga	cccagcctat	attaaaggaa	atactattga	cggtaaactc	420
tatgccttcc	cagtagatgc	caacgtttat	gcccacacaga	tgctttcttt	caataaagaa	480
ctagtggaca	aatatggcct	tgacatttca	aacattaagt	cctatgcaga	tgctgaaaat	540
gtcttgaaac	aattccacga	aaaagaacca	aatacagcag	cttttgctat	tggtcaagtc	600
tttagtatgt	caggtgacta	tgactaccca	ttaacacaaa	cccaaccctt	tgctgtgaaa	660
attgatgaag	gcaagccaac	catcattaat	cagtatgaag	atgagtcctt	taaaaacaat	720
ctccgcttga	tgacacaaatg	gtataaagaa	ggtttgattc	caacagatgc	agcgaccaat	780
acagaagggt	atcccccttga	aggaaacact	tggtttatgc	gtgaagaaac	ccaaggtcct	840
atggactatg	cgatactat	cttgaccaat	gctgcaggaa	aagacatcgt	gtctcgtcca	900
ttgactaaac	gcgtaaaaaac	cacatcacaa	gcacaaatgg	caaactttgt	ggatcaagc	960
gtatctaaaa	acaaagaaaa	agcagttgaa	gtcctttctc	ttcttaatag	cgatcccga	1020

ttgttaaagt	ggcttggtta	tgggtgtcgaa	ggcaaagctt	gggaaaaaat	tggcgacaag	1080
aaaatcaaac	tgctcgatgg	ctatcaacct	aaaaatgcac	atgggtgctt	ggaatactgg	1140
taa						1143

<210> SEQ ID NO 152

<211> LENGTH: 380

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 152

Met	Lys	Lys	Trp	Gln	Lys	Ile	Val	Cys	Val	Thr	Gly	Thr	Val	Leu	Ala
1				5					10					15	
Thr	Ser	Ser	Leu	Ala	Ala	Cys	Glu	Ser	Lys	Ser	Ala	Ser	Lys	Asp	Ser
			20					25					30		
Asp	Val	Lys	Leu	Leu	Met	Tyr	Gln	Val	Gly	Asp	Lys	Pro	Asp	Asn	Phe
		35					40					45			
Asp	Glu	Leu	Met	Thr	Ile	Ala	Asn	Lys	Arg	Ile	Lys	Glu	Lys	Thr	Gly
	50					55					60				
Ala	Thr	Val	Asp	Leu	Gln	Tyr	Ile	Gly	Trp	Gly	Asp	Trp	Asp	Asp	Lys
65					70					75					80
Met	Ser	Thr	Ile	Ile	Ala	Ser	Gly	Glu	Asn	Tyr	Asp	Ile	Ala	Phe	Ala
				85					90					95	
Asn	Asn	Tyr	Val	Val	Asn	Ala	Gln	Lys	Gly	Ala	Phe	Ala	Asp	Leu	Thr
			100					105					110		
Thr	Leu	Met	Pro	Lys	Tyr	Ala	Lys	Lys	Thr	Tyr	Lys	Asn	Leu	Asp	Pro
		115					120					125			
Ala	Tyr	Ile	Lys	Gly	Asn	Thr	Ile	Asp	Gly	Lys	Leu	Tyr	Ala	Phe	Pro
	130					135					140				
Val	Asp	Ala	Asn	Val	Tyr	Ala	Gln	Gln	Met	Leu	Ser	Phe	Asn	Lys	Glu
145					150					155					160
Leu	Val	Asp	Lys	Tyr	Gly	Leu	Asp	Ile	Ser	Asn	Ile	Lys	Ser	Tyr	Ala
			165						170					175	
Asp	Ala	Glu	Asn	Val	Leu	Lys	Gln	Phe	His	Glu	Lys	Glu	Pro	Asn	Thr
			180					185					190		
Ala	Ala	Phe	Ala	Ile	Gly	Gln	Val	Phe	Ser	Met	Ser	Gly	Asp	Tyr	Asp
		195					200						205		
Tyr	Pro	Leu	Thr	Lys	Thr	Gln	Pro	Phe	Ala	Val	Lys	Ile	Asp	Glu	Gly
	210					215						220			
Lys	Pro	Thr	Ile	Ile	Asn	Gln	Tyr	Glu	Asp	Glu	Ser	Phe	Lys	Asn	Asn
225					230					235					240
Leu	Arg	Leu	Met	His	Lys	Trp	Tyr	Lys	Glu	Gly	Leu	Ile	Pro	Thr	Asp
			245						250					255	
Ala	Ala	Thr	Asn	Thr	Glu	Gly	Tyr	Pro	Leu	Glu	Gly	Asn	Thr	Trp	Phe
			260					265					270		
Met	Arg	Glu	Glu	Thr	Gln	Gly	Pro	Met	Asp	Tyr	Gly	Asp	Thr	Ile	Leu
		275				280						285			
Thr	Asn	Ala	Ala	Gly	Lys	Asp	Ile	Val	Ser	Arg	Pro	Leu	Thr	Lys	Pro
	290					295					300				
Leu	Lys	Thr	Thr	Ser	Gln	Ala	Gln	Met	Ala	Asn	Phe	Val	Val	Ser	Ser
305					310					315					320
Val	Ser	Lys	Asn	Lys	Glu	Lys	Ala	Val	Glu	Val	Leu	Ser	Leu	Leu	Asn
			325						330					335	
Ser	Asp	Pro	Glu	Leu	Leu	Asn	Gly	Leu	Val	Tyr	Gly	Val	Glu	Gly	Lys
		340						345					350		
Ala	Trp	Glu	Lys	Ile	Gly	Asp	Lys	Lys	Ile	Lys	Leu	Leu	Asp	Gly	Tyr
		355					360					365			
Gln	Pro	Lys	Asn	Ala	His	Gly	Cys	Leu	Glu	Tyr	Trp				
	370					375					380				

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<210> SEQ ID NO 153
<211> LENGTH: 624
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 153
atgaaaaaag gactattagt aacaactggt ttggcttgtc tcgggctact aactgcttgc      60
tcaacccaag acaatatggc taaaaaggaa ataactcagg acaagatgag catggcagct      120
aaaaagaaaag ataagatgtc aacatcaaag gacaagtcca tgatggcaga taaatcatct      180
gataagaaaa tgaccaatga tggtcctatg gcgcctgatt tcgaactcaa aggcacgat      240
ggtaagacct atcgcttatc agagttcaaa ggtaaaaaag tttatttgaa attttgggcc      300
tcttggtggt caatctgtct atcaaccttg gcagataccg aagacctggc taaaatgtca      360
gataaagact atgtggtcct aacagttgtc tcgccaggtc atcaagggga aaaatcagaa      420
gcgacttta aaaaatggtt ccaaggaaca gactataagg acttaccagt cttgttagat      480
ccggatggca agctattgga agcttacggt gtcagatctt acccaacaga agttttcatt      540
ggaagtgtat gtgttcttgc taaaaaacac attggttatg ccaaaaaatc agacatcaaa      600
aagaccctta aaggtataca ttag

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<210> SEQ ID NO 154
<211> LENGTH: 207
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 154
Met Lys Lys Gly Leu Leu Val Thr Thr Gly Leu Ala Cys Leu Gly Leu
1          5          10          15
Leu Thr Ala Cys Ser Thr Gln Asp Asn Met Ala Lys Lys Glu Ile Thr
20          25          30
Gln Asp Lys Met Ser Met Ala Ala Lys Lys Lys Asp Lys Met Ser Thr
35          40          45
Ser Lys Asp Lys Ser Met Met Ala Asp Lys Ser Ser Asp Lys Lys Met
50          55          60
Thr Asn Asp Gly Pro Met Ala Pro Asp Phe Glu Leu Lys Gly Ile Asp
65          70          75          80
Gly Lys Thr Tyr Arg Leu Ser Glu Phe Lys Gly Lys Lys Val Tyr Leu
85          90          95
Lys Phe Trp Ala Ser Trp Cys Ser Ile Cys Leu Ser Thr Leu Ala Asp
100         105         110
Thr Glu Asp Leu Ala Lys Met Ser Asp Lys Asp Tyr Val Val Leu Thr
115         120         125
Val Val Ser Pro Gly His Gln Gly Glu Lys Ser Glu Ala Asp Phe Lys
130         135         140
Lys Trp Phe Gln Gly Thr Asp Tyr Lys Asp Leu Pro Val Leu Leu Asp
145         150         155         160
Pro Asp Gly Lys Leu Leu Glu Ala Tyr Gly Val Arg Ser Tyr Pro Thr
165         170         175
Glu Val Phe Ile Gly Ser Asp Gly Val Leu Ala Lys Lys His Ile Gly
180         185         190
Tyr Ala Lys Lys Ser Asp Ile Lys Lys Thr Leu Lys Gly Ile His
195         200         205

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<210> SEQ ID NO 155
<211> LENGTH: 228
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 155
gtgttaagaa agaagaaaac taccattgta gggattatth taggaatgat gatagtgacc      60
ttacttgctg gctgtttgac tggtaaaaag aaaggctttc ctcctaaagc aggtgagcgg      120

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```

cagcaaacgg ctgacttaaa aatgaaaaaa agattagaaa aactgttcaa aaaccgttac 180
ctgaaaaaatc taaagaggct aagcaagctg ttatggatgc agatttag 228

```

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<210> SEQ ID NO 156
<211> LENGTH: 75
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 156

```

```

Met Leu Arg Lys Lys Lys Thr Thr Ile Val Gly Ile Ile Leu Gly Met
1          5          10          15
Met Ile Val Thr Leu Leu Val Gly Cys Leu Thr Gly Lys Lys Lys Gly
20          25          30
Phe Pro Pro Lys Ala Gly Glu Arg Gln Gln Thr Ala Asp Leu Lys Met
35          40          45
Lys Lys Arg Leu Glu Lys Leu Phe Lys Asn Arg Tyr Leu Lys Asn Leu
50          55          60
Lys Arg Leu Ser Lys Leu Leu Trp Met Gln Ile
65          70          75

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<210> SEQ ID NO 157
<211> LENGTH: 1032
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 157

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atgaaaacga aaaaagttat tatttttagtt ggtctattgt tatcatctca gttgactttg 60
atagcttgtc aatcacgagg taatggtaca tatcccatta aaacgaaaca atcacgtaag 120
ggaatgacgt caaacaaaat taaaccgatt aaaaaaagca aaaagacaaa caagactcac 180
aaagggtgtg cggtgtgcga ttttcctaca gatgatgggt ttattttaac caaagactca 240
aaaatcttat caaaaacaga tcagggaatc gttgttgacc atgatggtca ttcgcatttt 300
attttttatg ccgatttaaa gggaaagtcca tttgaatacc ttattccaaa aggagcaagt 360
ttagctaagc cagctgttgc tcagcgagca gctagtcaag ggacttctaa agtagcagat 420
cctcatcacc attatgaatt taaccacgag gatattgttg ctgaagatgc tttaggctac 480
acggttcgcc acgatgatca cttccattat attttgaagt caagcttatc aggtcagaca 540
caggcacaag ctaaacaggt tgctactcgc ttgccacaaa ccagtagcct tgtttcaaca 600
gctacagcta atggtattcc aggcttgcat ttcccaacct cagatgggtt tcaatttaac 660
gggtcaaggta ttggtggggg aacaaaagac agtatttttag tggaccacga tgggtcacta 720
catcctattt cttttgcgga ctttcgtcag ggtggctggg cacatgtggc agatcaatac 780
gatcccgcta aaaaagcaga aaagccagca gaaacccatc agacaccaga gctatctgaa 840
cgtgaaaagg aataccaaga aaaattagct tatttggcag aaaaattggg gattgatcca 900
tcaactatta aacgtgtgga aacacaagac ggtaaaacttg gtttgggaata ccctcaccat 960
gaccacgcac acgtattgat gttatctgaa attgaaatcg ggaaaagaca ttccagatcc 1020
acatgctatt ga 1032

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<210> SEQ ID NO 158
<211> LENGTH: 343
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 158

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Met Lys Thr Lys Lys Val Ile Ile Leu Val Gly Leu Leu Leu Ser Ser
1          5          10          15
Gln Leu Thr Leu Ile Ala Cys Gln Ser Arg Gly Asn Gly Thr Tyr Pro
20          25          30
Ile Lys Thr Lys Lys Gln Ser Arg Lys Gly Met Thr Ser Asn Lys Ile Lys
35          40          45
Pro Ile Lys Lys Ser Lys Lys Thr Asn Lys Thr His Lys Gly Val Ala
50          55          60
Gly Val Asp Phe Pro Thr Asp Asp Gly Phe Ile Leu Thr Lys Asp Ser

```

65					70					75					80
Lys	Ile	Leu	Ser	Lys	Thr	Asp	Gln	Gly	Ile	Val	Val	Asp	His	Asp	Gly
				85					90					95	
His	Ser	His	Phe	Ile	Phe	Tyr	Ala	Asp	Leu	Lys	Gly	Ser	Pro	Phe	Glu
			100					105					110		
Tyr	Leu	Ile	Pro	Lys	Gly	Ala	Ser	Leu	Ala	Lys	Pro	Ala	Val	Ala	Gln
		115					120					125			
Arg	Ala	Ala	Ser	Gln	Gly	Thr	Ser	Lys	Val	Ala	Asp	Pro	His	His	His
	130					135					140				
Tyr	Glu	Phe	Asn	Pro	Ala	Asp	Ile	Val	Ala	Glu	Asp	Ala	Leu	Gly	Tyr
145				150						155					160
Thr	Val	Arg	His	Asp	Asp	His	Phe	His	Tyr	Ile	Leu	Lys	Ser	Ser	Leu
			165						170					175	
Ser	Gly	Gln	Thr	Gln	Ala	Gln	Ala	Lys	Gln	Val	Ala	Thr	Arg	Leu	Pro
			180					185					190		
Gln	Thr	Ser	Ser	Leu	Val	Ser	Thr	Ala	Thr	Ala	Asn	Gly	Ile	Pro	Gly
		195					200					205			
Leu	His	Phe	Pro	Thr	Ser	Asp	Gly	Phe	Gln	Phe	Asn	Gly	Gln	Gly	Ile
	210					215					220				
Val	Gly	Val	Thr	Lys	Asp	Ser	Ile	Leu	Val	Asp	His	Asp	Gly	His	Leu
225				230						235					240
His	Pro	Ile	Ser	Phe	Ala	Asp	Leu	Arg	Gln	Gly	Gly	Trp	Ala	His	Val
			245						250					255	
Ala	Asp	Gln	Tyr	Asp	Pro	Ala	Lys	Lys	Ala	Glu	Lys	Pro	Ala	Glu	Thr
			260				265						270		
His	Gln	Thr	Pro	Glu	Leu	Ser	Glu	Arg	Glu	Lys	Glu	Tyr	Gln	Glu	Lys
		275					280					285			
Leu	Ala	Tyr	Leu	Ala	Glu	Lys	Leu	Gly	Ile	Asp	Pro	Ser	Thr	Ile	Lys
	290					295					300				
Arg	Val	Glu	Thr	Gln	Asp	Gly	Lys	Leu	Gly	Leu	Glu	Tyr	Pro	His	His
305				310						315					320
Asp	His	Ala	His	Val	Leu	Met	Leu	Ser	Glu	Ile	Glu	Ile	Gly	Lys	Arg
			325						330					335	
His	Ser	Arg	Ser	Thr	Cys	Tyr									
			340												

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<210> SEQ ID NO 159
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 159
atgtcatgga attggaaaaa aacatctgtg cttggaactt tacccttagc ttcagtgcta      60
cccctaactg cttgcgtaag tgggtggtggt aaaggcgta aggaacaga cggaaagact      120
attgtagtct ctgttgatga gggatatgtt gattacatta agagtattaa gggtagagttt      180
gaaaaagaac ataaagtcac cgtaaagtc aaaaaagaag gtatgatgga tactcttgat      240
aagctatcaa cggatggtcc aacaggagct tcaccagatg tcttttttagc acctttttga      300

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<210> SEQ ID NO 160
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 160
Met Ser Trp Asn Trp Lys Lys Thr Ser Val Leu Gly Thr Leu Ser Leu
1          5          10          15
Ala Ser Val Leu Pro Leu Thr Ala Cys Val Ser Gly Gly Gly Lys Gly
20          25          30
Val Lys Glu Thr Asp Gly Lys Thr Ile Val Val Ser Val Asp Glu Gly

```

	35						40					45					
Tyr	Val	Asp	Tyr	Ile	Lys	Ser	Ile	Lys	Gly	Glu	Phe	Glu	Lys	Glu	His		
	50					55					60						
Lys	Val	Thr	Val	Lys	Val	Lys	Lys	Glu	Gly	Met	Met	Asp	Thr	Leu	Asp		
65					70					75					80		
Lys	Leu	Ser	Thr	Asp	Gly	Pro	Thr	Gly	Ala	Ser	Pro	Asp	Val	Phe	Leu		
				85					90						95		
Ala	Pro	Phe															

<210> SEQ ID NO 161

<211> LENGTH: 621

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 161

atgacaaaaa	aacacttact	aacacttctt	ctcatctctt	tttttactag	cttttttgta	60
gcttggttcaa	caacgaaaga	taaagagcct	caaccgtctg	attcagaaat	cattactccc	120
cgactacacc	aagccgctca	tcaagataaa	cgcgctaact	ttgaaaaaat	taaacttgcg	180
actggtgatt	cctcatttac	aggagggaca	agccttgaag	aacttatctt	actctttgga	240
gagcctagcc	aacatgatcc	aaaaacagca	ggcgaagtaa	caatcgacgc	ttatacttgg	300
cagtttgatc	aagttactct	cactgttaat	ctttatcaaa	atagtagtat	tggtaaaacc	360
atctctaatt	ttacctttgc	aagagagtta	ggcttatcgc	aaaaggaata	ccaacaatta	420
caaaaaggaa	tgtcttatga	agacgttaaa	aagatcttaa	cagaacctga	taattatagc	480
caagcgtcat	ctagtgatca	tcaaactttg	caagcgattt	gggttagtgg	cttaaagaca	540
gatacaagcg	gagctaatat	ttctctcggt	tttgaaaata	atcagttaac	agaaatgtct	600
caggtaggac	ttgaagaata	a				621

<210> SEQ ID NO 162

<211> LENGTH: 206

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 162

Met	Thr	Lys	Lys	His	Leu	Leu	Thr	Leu	Leu	Ile	Ser	Phe	Phe	Thr		
1				5					10				15			
Ser	Phe	Leu	Val	Ala	Cys	Ser	Thr	Thr	Lys	Asp	Lys	Glu	Pro	Gln	Pro	
			20					25				30				
Ser	Asp	Ser	Glu	Ile	Ile	Thr	Pro	Arg	Leu	His	Gln	Ala	Ala	His	Gln	
			35			40					45					
Asp	Lys	Arg	Ala	Asn	Phe	Glu	Lys	Ile	Lys	Leu	Ala	Thr	Val	Asp	Ser	
	50				55				60							
Ser	Phe	Thr	Gly	Gly	Thr	Ser	Leu	Glu	Glu	Leu	Ile	Ser	Leu	Phe	Gly	
65				70					75					80		
Glu	Pro	Ser	Gln	His	Asp	Pro	Lys	Thr	Ala	Gly	Glu	Val	Thr	Ile	Asp	
				85				90					95			
Ala	Tyr	Thr	Trp	Gln	Phe	Asp	Gln	Val	Thr	Leu	Thr	Val	Asn	Leu	Tyr	
			100				105					110				
Gln	Asn	Ser	Ser	Ile	Val	Lys	Thr	Ile	Ser	Asn	Phe	Thr	Phe	Ala	Arg	
	115					120					125					
Glu	Leu	Gly	Leu	Ser	Gln	Lys	Glu	Tyr	Gln	Gln	Leu	Gln	Lys	Gly	Met	
	130					135				140						
Ser	Tyr	Glu	Asp	Val	Lys	Lys	Ile	Leu	Thr	Glu	Pro	Asp	Asn	Tyr	Ser	
145					150				155					160		
Gln	Ala	Ser	Ser	Ser	Asp	His	Gln	Thr	Leu	Gln	Ala	Ile	Trp	Val	Ser	
				165				170					175			
Gly	Leu	Lys	Thr	Asp	Thr	Ser	Gly	Ala	Asn	Ile	Ser	Leu	Val	Phe	Glu	
			180				185					190				
Asn	Asn	Gln	Leu	Thr	Glu	Met	Ser	Gln	Val	Gly	Leu	Glu	Glu			
	195					200					205					

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<210> SEQ ID NO 163
<211> LENGTH: 867
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 163
atgaaaatga aaaaaaaatt ctttttggtta agtcttttgg ccctatcaac tttcttttta      60
tccgcatggt ctagctggat tgataaagggt gagtcaataa ccgctgtagg atcaacagca      120
ctacaaccct tagtagaagc agtagctgat gaatttggaa gcagtaatct aggcaagact      180
gtcaatgttc aaggtggttg ttcagggtaca gggttgtctc aagttcaatc aggagctgtc      240
caaattggaa atagtgatgt ctttgcggaa gaaaaagatg gtattgatgc ttctaaatta      300
gttgatcatc aagtagctgt tgcaggactt gcagttattg ccaatcctaa agtcaagggt      360
tccaatctca gtagtcagca gttgcaaaag attttttcag gagaatatac caattggaaa      420
caagttggag gagaagatct tgcgatttca gtgatcaacc gagcagcaag ttctgggtca      480
cgagcaacct ttgacagtgt tatcatgaaa ggggtcaacg ctaaacaaaag tcaagagcaa      540
gactccaatg ggatgggttaa atcgattggt tcacaaacac caggtgccat ttcttacctt      600
tcctttgcct acgttgattc atctgttaaa tctttgcaat taaatggggt taaggcaaat      660
gctaagaacg tggctacaaa tgattggcca atctggtcct acgaacacat gtataccaaa      720
gataaaccaa cagggttgac caaggaattt cttgattata tgttttcaga tgaagtacaa      780
cagaacattg ttacacatat gggatatatt tcgataaatg atatggaagt ggtcaaatct      840
catgatggaa aagtaacaaa aaggttaa      867

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<210> SEQ ID NO 164
<211> LENGTH: 288
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 164
Met Lys Met Lys Lys Lys Phe Phe Leu Leu Ser Leu Leu Ala Leu Ser
1      5      10      15
Thr Phe Phe Leu Ser Ala Cys Ser Ser Trp Ile Asp Lys Gly Glu Ser
20     25     30
Ile Thr Ala Val Gly Ser Thr Ala Leu Gln Pro Leu Val Glu Ala Val
35     40     45
Ala Asp Glu Phe Gly Ser Ser Asn Leu Gly Lys Thr Val Asn Val Gln
50     55     60
Gly Gly Gly Ser Gly Thr Gly Leu Ser Gln Val Gln Ser Gly Ala Val
65     70     75     80
Gln Ile Gly Asn Ser Asp Val Phe Ala Glu Glu Lys Asp Gly Ile Asp
85     90     95
Ala Ser Lys Leu Val Asp His Gln Val Ala Val Ala Gly Leu Ala Val
100    105    110
Ile Ala Asn Pro Lys Val Lys Val Ser Asn Leu Ser Ser Gln Gln Leu
115    120    125
Gln Lys Ile Phe Ser Gly Glu Tyr Thr Asn Trp Lys Gln Val Gly Gly
130    135    140
Glu Asp Leu Ala Ile Ser Val Ile Asn Arg Ala Ala Ser Ser Gly Ser
145    150    155    160
Arg Ala Thr Phe Asp Ser Val Ile Met Lys Gly Val Asn Ala Lys Gln
165    170    175
Ser Gln Glu Gln Asp Ser Asn Gly Met Val Lys Ser Ile Val Ser Gln
180    185    190
Thr Pro Gly Ala Ile Ser Tyr Leu Ser Phe Ala Tyr Val Asp Ser Ser
195    200    205
Val Lys Ser Leu Gln Leu Asn Gly Phe Lys Ala Asn Ala Lys Asn Val
210    215    220
Ala Thr Asn Asp Trp Pro Ile Trp Ser Tyr Glu His Met Tyr Thr Lys
225    230    235    240

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Asp	Lys	Pro	Thr	Gly	Leu	Thr	Lys	Glu	Phe	Leu	Asp	Tyr	Met	Phe	Ser
				245					250					255	
Asp	Glu	Val	Gln	Gln	Asn	Ile	Val	Thr	His	Met	Gly	Tyr	Ile	Ser	Ile
			260					265					270		
Asn	Asp	Met	Glu	Val	Val	Lys	Ser	His	Asp	Gly	Lys	Val	Thr	Lys	Arg
		275					280						285		

<210> SEQ ID NO 165
 <211> LENGTH: 1053
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 165

atgaacaaga	aattttattgg	tcttggttta	gcgtcagtg	ctgtgctgag	tttagctgct	60
tgtggtaatc	gtggtgcttc	taaaggtggg	gcatcaggaa	aaactgattt	aaaagttgca	120
atgggtaccg	atactggtgg	tgtagatgac	aaatcattca	accaatcagc	atgggaaggc	180
ctgcaatcct	ggggtaaaga	aatgggcctt	caaaaaggaa	caggtttcga	ttattttcaa	240
tctacaagt	aatctgagta	tgcaactaat	ctcgatacag	cagtttcagg	agggtatcaa	300
ctgatttat	gtatcggtt	tgcattgaaa	gatgctattg	ctaaagcagc	tggagataat	360
gaaggagtta	agtttggtat	tatcgatgat	attatcgaag	gaaaagataa	tgtagccagt	420
gttacctttg	ccgaccatga	agctgcttat	cttgcaggaa	ttgcagctgc	aaaaacaaca	480
aaaacaaaaa	cagttgggtt	cgtgggcggt	atggaaggaa	ctgtcataac	tcgatttgaa	540
aaaggttttg	aagcaggagt	taagtctgtt	gacgatacaa	tccaagttaa	agttgattat	600
gctggatcat	ttggtgacgc	tgcaaaaagga	aaaacaatcg	cagcagctca	gtatgcagca	660
ggtgctgatg	ttattttacca	ggcagcagga	ggcactggag	caggtgtatt	taatgaagca	720
aaagctatta	atgaaaaacg	tagtgaagct	gataaagttt	gggttattgg	tgttgaccgt	780
gatcaaaaag	acgaaggaaa	atacacttct	aaagatggca	aagaagcaaa	ctttgtactt	840
gcatcatcaa	tcaaagaagt	cggtaaagct	gttcagttaa	tcaacaagca	agtagcagat	900
aaaaaattcc	ctggaggaaa	aacaactgtc	tatggtctaa	aagatggcgg	tgttgaaatc	960
gcaactacaa	atgtttcaaa	agaagctgtt	aaagctatta	aagaagcgaa	agcaaaaatt	1020
aaatctggtg	acattaaagt	tcctgaaaaa	tag			1053

<210> SEQ ID NO 166
 <211> LENGTH: 350
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 166

Met	Asn	Lys	Lys	Phe	Ile	Gly	Leu	Gly	Leu	Ala	Ser	Val	Ala	Val	Leu
1				5					10					15	
Ser	Leu	Ala	Ala	Cys	Gly	Asn	Arg	Gly	Ala	Ser	Lys	Gly	Gly	Ala	Ser
			20					25					30		
Gly	Lys	Thr	Asp	Leu	Lys	Val	Ala	Met	Val	Thr	Asp	Thr	Gly	Gly	Val
		35				40					45				
Asp	Asp	Lys	Ser	Phe	Asn	Gln	Ser	Ala	Trp	Glu	Gly	Leu	Gln	Ser	Trp
	50				55					60					
Gly	Lys	Glu	Met	Gly	Leu	Gln	Lys	Gly	Thr	Gly	Phe	Asp	Tyr	Phe	Gln
65					70				75					80	
Ser	Thr	Ser	Glu	Ser	Glu	Tyr	Ala	Thr	Asn	Leu	Asp	Thr	Ala	Val	Ser
			85					90					95		
Gly	Gly	Tyr	Gln	Leu	Ile	Tyr	Gly	Ile	Gly	Phe	Ala	Leu	Lys	Asp	Ala
		100					105						110		
Ile	Ala	Lys	Ala	Ala	Gly	Asp	Asn	Glu	Gly	Val	Lys	Phe	Val	Ile	Ile
		115				120						125			
Asp	Asp	Ile	Ile	Glu	Gly	Lys	Asp	Asn	Val	Ala	Ser	Val	Thr	Phe	Ala
	130					135					140				
Asp	His	Glu	Ala	Ala	Tyr	Leu	Ala	Gly	Ile	Ala	Ala	Ala	Lys	Thr	Thr
145					150				155					160	
Lys	Thr	Lys	Thr	Val	Gly	Phe	Val	Gly	Gly	Met	Glu	Gly	Thr	Val	Ile

				165					170					175			
Thr	Arg	Phe	Glu	Lys	Gly	Phe	Glu	Ala	Gly	Val	Lys	Ser	Val	Asp	Asp		
			180					185					190				
Thr	Ile	Gln	Val	Lys	Val	Asp	Tyr	Ala	Gly	Ser	Phe	Gly	Asp	Ala	Ala		
		195					200					205					
Lys	Gly	Lys	Thr	Ile	Ala	Ala	Ala	Gln	Tyr	Ala	Ala	Gly	Ala	Asp	Val		
	210				215						220						
Ile	Tyr	Gln	Ala	Ala	Gly	Gly	Thr	Gly	Ala	Gly	Val	Phe	Asn	Glu	Ala		
225					230				235					240			
Lys	Ala	Ile	Asn	Glu	Lys	Arg	Ser	Glu	Ala	Asp	Lys	Val	Trp	Val	Ile		
			245					250					255				
Gly	Val	Asp	Arg	Asp	Gln	Lys	Asp	Glu	Gly	Lys	Tyr	Thr	Ser	Lys	Asp		
		260						265				270					
Gly	Lys	Glu	Ala	Asn	Phe	Val	Leu	Ala	Ser	Ser	Ile	Lys	Glu	Val	Gly		
	275					280					285						
Lys	Ala	Val	Gln	Leu	Ile	Asn	Lys	Gln	Val	Ala	Asp	Lys	Lys	Phe	Pro		
	290					295				300							
Gly	Gly	Lys	Thr	Thr	Val	Tyr	Gly	Leu	Lys	Asp	Gly	Gly	Val	Glu	Ile		
305					310					315				320			
Ala	Thr	Thr	Asn	Val	Ser	Lys	Glu	Ala	Val	Lys	Ala	Ile	Lys	Glu	Ala		
			325					330					335				
Lys	Ala	Lys	Ile	Lys	Ser	Gly	Asp	Ile	Lys	Val	Pro	Glu	Lys				
		340						345				350					

<210> SEQ ID NO 167

<211> LENGTH: 708

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 167

atgacaaaaa	agaaaggtaa	gcttgacttt	atcagtccttt	ttgttctagc	agcttggtta	60
ggagcttata	gtgcaatgag	acaatctcat	aaaacttcaa	acgtgtcagc	tgagactatc	120
gccagttcct	caacccgaca	ttttattgat	gaaattggtc	caactgctag	tactattggt	180
caagaacgtg	atctttatgc	gtctgttatg	atagcacaag	cgattttaga	atcaagtaat	240
ggtaaatcaa	gtctaagtca	agcaccttat	tataattttt	tcggtattaa	gggtgcctat	300
aacggttcct	ctgtgacgat	gtcaacttgg	gaagatgatg	gtaatggcaa	tacctatacg	360
attgatcaag	ccttttagagc	ttatccaagt	attgcagact	cccttaatga	ctacgcggac	420
ttgctaagtt	ctagcactta	tataggtgct	agaaaatcaa	acacgctatc	gtatcaagat	480
gctacagcag	ctctaactgg	cttatacgct	acagacacca	gttataactt	aaaactaaat	540
aatattattg	caacctatgg	tttgacggct	tatgatgttg	ctaatagctc	agctcaagaa	600
actggtctag	caacttcggg	ttatgtttgg	aatgaatgc	gtcgtaatta	cactgatgcg	660
gagaccctag	cagttgatga	ggcttgggct	aaacgcgatga	cttattaa		708

<210> SEQ ID NO 168

<211> LENGTH: 235

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 168

Met	Thr	Lys	Lys	Lys	Gly	Lys	Leu	Val	Leu	Ile	Ser	Leu	Phe	Val	Leu
1			5					10					15		
Ala	Ala	Cys	Leu	Gly	Ala	Tyr	Ser	Ala	Met	Arg	Gln	Ser	His	Lys	Thr
		20					25					30			
Ser	Asn	Val	Ser	Ala	Glu	Thr	Ile	Ala	Ser	Ser	Ser	Thr	Arg	His	Phe
	35					40					45				
Ile	Asp	Glu	Ile	Gly	Pro	Thr	Ala	Ser	Thr	Ile	Gly	Gln	Glu	Arg	Asp
	50				55				60						
Leu	Tyr	Ala	Ser	Val	Met	Ile	Ala	Gln	Ala	Ile	Leu	Glu	Ser	Ser	Asn
65					70				75						80

Gly	Lys	Ser	Ser	Leu	Ser	Gln	Ala	Pro	Tyr	Tyr	Asn	Phe	Phe	Gly	Ile
				85					90					95	
Lys	Gly	Ala	Tyr	Asn	Gly	Ser	Ser	Val	Thr	Met	Ser	Thr	Trp	Glu	Asp
			100					105					110		
Asp	Gly	Asn	Gly	Asn	Thr	Tyr	Thr	Ile	Asp	Gln	Ala	Phe	Arg	Ala	Tyr
		115					120					125			
Pro	Ser	Ile	Ala	Asp	Ser	Leu	Asn	Asp	Tyr	Ala	Asp	Leu	Leu	Ser	Ser
		130				135					140				
Ser	Thr	Tyr	Ile	Gly	Ala	Arg	Lys	Ser	Asn	Thr	Leu	Ser	Tyr	Gln	Asp
145					150					155					160
Ala	Thr	Ala	Ala	Leu	Thr	Gly	Leu	Tyr	Ala	Thr	Asp	Thr	Ser	Tyr	Asn
				165					170					175	
Leu	Lys	Leu	Asn	Asn	Ile	Ile	Ala	Thr	Tyr	Gly	Leu	Thr	Ala	Tyr	Asp
			180					185					190		
Val	Ala	Asn	Ser	Ser	Ala	Gln	Glu	Thr	Gly	Leu	Ala	Thr	Ser	Gly	Tyr
		195					200					205			
Val	Trp	Asn	Glu	Tyr	Arg	Arg	Asn	Tyr	Thr	Asp	Ala	Glu	Thr	Leu	Ala
	210					215					220				
Val	Asp	Glu	Ala	Trp	Ala	Lys	Arg	Met	Thr	Tyr					
225					230					235					

<210> SEQ ID NO 169
 <211> LENGTH: 549
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 169

atgaaaaaat	taactctact	attaacactc	tgtttgacaa	ctattacctt	aatcgctgt	60
ggtaatcaag	caactaatca	ttctaacacc	gcctcaaaaa	gtttatcgcc	tatgcctcaa	120
attgctggtg	tgacttatta	cggagatatt	cctaaacagc	ctaagcgagt	agtcagtctg	180
gcttcaactt	acactgggta	cctcaaaaaa	ttagatatga	atctagtcgg	ggttacttct	240
tatgacaaga	aaaaccccat	cctagcaaag	actgtaaaaa	aagcaaagca	agttgctgca	300
actgatttag	aagccgttac	aacgccttaag	cctgacctca	ttgttggttg	ctctacagaa	360
gaaaatatta	aacaattggc	agaaattgcg	cctgttatct	cgattgaata	ccgcaaacgt	420
gattatttac	aagtgttatc	tgacttcggc	cgcattctta	acaaagaaga	caaagccaag	480
aagtgggtaa	aagattggaa	aactaaaaca	gcagcttatg	aaaaagaaag	tcaaggccgt	540
tacaggtga						549

<210> SEQ ID NO 170
 <211> LENGTH: 182
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 170

Met	Lys	Lys	Leu	Thr	Leu	Leu	Leu	Thr	Leu	Cys	Leu	Thr	Thr	Ile	Thr
1				5					10					15	
Leu	Ile	Ala	Cys	Gly	Asn	Gln	Ala	Thr	Asn	His	Ser	Asn	Thr	Ala	Ser
			20					25					30		
Lys	Ser	Leu	Ser	Pro	Met	Pro	Gln	Ile	Ala	Gly	Val	Thr	Tyr	Tyr	Gly
		35				40					45				
Asp	Ile	Pro	Lys	Gln	Pro	Lys	Arg	Val	Val	Ser	Leu	Ala	Ser	Thr	Tyr
	50					55				60					
Thr	Gly	Tyr	Leu	Lys	Lys	Leu	Asp	Met	Asn	Leu	Val	Gly	Val	Thr	Ser
65					70					75					80
Tyr	Asp	Lys	Lys	Asn	Pro	Ile	Leu	Ala	Lys	Thr	Val	Lys	Lys	Ala	Lys
			85						90					95	
Gln	Val	Ala	Ala	Thr	Asp	Leu	Glu	Ala	Val	Thr	Thr	Leu	Lys	Pro	Asp
			100					105					110		
Leu	Ile	Val	Val	Gly	Ser	Thr	Glu	Glu	Asn	Ile	Lys	Gln	Leu	Ala	Glu

	115						120					125					
Ile	Ala	Pro	Val	Ile	Ser	Ile	Glu	Tyr	Arg	Lys	Arg	Asp	Tyr	Leu	Gln		
	130						135					140					
Val	Leu	Ser	Asp	Phe	Gly	Arg	Ile	Phe	Asn	Lys	Glu	Asp	Lys	Ala	Lys		
145					150					155					160		
Lys	Trp	Leu	Lys	Asp	Trp	Lys	Thr	Lys	Thr	Ala	Ala	Tyr	Glu	Lys	Glu		
				165					170					175			
Ser	Gln	Gly	Arg	Tyr	Arg												
				180													

<210> SEQ ID NO 171
 <211> LENGTH: 924
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 171

ttgaaactaa	cattaaatcg	catcctcttt	tcaggactag	cactgtcaat	tctactcacc	60
ttgacaggct	gtgtgggaag	agacgctcac	ggaaatccca	aaggtatgat	ttgggaattt	120
cttgaaaaac	ccatgtcata	ctttatcgat	tactttgcaa	acaatgctgg	actaggttat	180
ggactggcta	tcatcatcgt	aaccattatt	gttagaacac	ttatcttacc	actagggtcta	240
tatcaatctt	ggaaagcaag	ttatcaatct	gagaaaaatgg	ccttcttgaa	acctgttttt	300
gaaccaatca	acaaacgtat	caaacaggca	aatagtcagg	aagaaaaaat	ggctgcccac	360
acagaattaa	tggctgctca	gcgtgctcat	gggattaacc	ctcttggagg	tattggatgt	420
ctacctcttc	tcatccagat	gccattcttt	tctgccatgt	atthtgcgcg	tcaatacact	480
aaaggagtat	caacaagcac	ctttatgggt	attgatcttg	gtagccgtag	tttagtggtta	540
acagcaatta	tcgctgctct	ttacttcttc	caatcatggt	tatcaatgat	ggccgtttca	600
gaagaacaac	gtgagcaaat	gaagacgatg	atgtacacca	tgcctatcat	gatgatcttc	660
atgtccttct	cactccctgc	tggtgttggt	ctttactggc	tagttgggtg	tttctttagt	720
attattcaac	agttaatcac	aacctacctc	ttaaaacctc	gattgcataa	gcaaattaaa	780
gaagaatacg	ctaaaaaccc	gcctaaagca	taccaatcaa	cttcttctcg	taaggacgtt	840
acgccttcac	aaaacatgga	acaggctaac	ttgcctaaaa	aaataaaaatc	caatcgtaat	900
gctggaaaaac	agcgaaaagcg	ttaa				924

<210> SEQ ID NO 172
 <211> LENGTH: 307
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 172

Met	Lys	Leu	Thr	Leu	Asn	Arg	Ile	Leu	Phe	Ser	Gly	Leu	Ala	Leu	Ser
1				5					10					15	
Ile	Leu	Leu	Thr	Leu	Thr	Gly	Cys	Val	Gly	Arg	Asp	Ala	His	Gly	Asn
			20				25						30		
Pro	Lys	Gly	Met	Ile	Trp	Glu	Phe	Leu	Gly	Lys	Pro	Met	Ser	Tyr	Phe
		35				40					45				
Ile	Asp	Tyr	Phe	Ala	Asn	Asn	Ala	Gly	Leu	Gly	Tyr	Gly	Leu	Ala	Ile
	50				55				60						
Ile	Ile	Val	Thr	Ile	Ile	Val	Arg	Thr	Leu	Ile	Leu	Pro	Leu	Gly	Leu
65				70					75					80	
Tyr	Gln	Ser	Trp	Lys	Ala	Ser	Tyr	Gln	Ser	Glu	Lys	Met	Ala	Phe	Leu
			85					90					95		
Lys	Pro	Val	Phe	Glu	Pro	Ile	Asn	Lys	Arg	Ile	Lys	Gln	Ala	Asn	Ser
		100					105					110			
Gln	Glu	Glu	Lys	Met	Ala	Ala	Gln	Thr	Glu	Leu	Met	Ala	Gln	Arg	
	115					120				125					
Ala	His	Gly	Ile	Asn	Pro	Leu	Gly	Gly	Ile	Gly	Cys	Leu	Pro	Leu	Leu
	130				135					140					
Ile	Gln	Met	Pro	Phe	Phe	Ser	Ala	Met	Tyr	Phe	Ala	Ala	Gln	Tyr	Thr
145				150					155					160	

actcttagta tttcatttgc tagtaggaac tag

1233

<210> SEQ ID NO 178

<211> LENGTH: 410

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 178

Met	Gly	Val	Met	Met	Lys	Gln	Lys	Ile	Lys	Ile	Leu	Thr	Val	Ile	Gly
1				5					10					15	
Leu	Met	Thr	Val	Gly	Met	Ser	Ala	Cys	His	Asn	Thr	Ser	Lys	Pro	Ser
			20					25					30		
Asn	Thr	Asp	Ser	Val	Phe	Ser	Leu	Thr	Gly	Lys	Lys	Arg	Gln	Gln	Ile
		35					40					45			
Val	Lys	Gln	Val	Arg	Gln	Arg	Tyr	Tyr	Phe	Gln	Gln	Leu	Ser	Lys	Thr
	50					55					60				
Glu	Gln	Glu	Asn	Tyr	Leu	Thr	Leu	Tyr	Asp	Ser	Leu	Ala	Gln	Phe	Arg
65					70					75					80
Glu	Ile	Ile	Ser	Leu	Thr	Pro	Ala	Ser	Lys	Lys	Ser	Leu	Ile	Lys	Thr
			85						90					95	
Ile	Asp	Ala	Phe	Val	Met	Asp	Asn	Pro	Glu	Phe	Tyr	Trp	Ile	Thr	Ser
		100					105						110		
Ala	Asp	Tyr	Arg	Phe	Glu	Phe	Ser	Asp	Gln	Thr	Val	Phe	Val	Thr	Phe
	115						120					125			
Pro	Ile	Pro	Glu	Asp	Ala	Lys	Asn	Ile	Tyr	Gln	Asp	Leu	Gln	Ala	Ile
	130					135						140			
Gly	Asn	Asp	Ile	Val	Ala	Asn	Thr	Pro	Ser	Lys	Asp	Arg	Tyr	Glu	Gln
145					150					155					160
Val	Lys	Tyr	Phe	Tyr	Glu	Val	Ile	Ile	Arg	Asp	Thr	Asp	Tyr	Asn	Lys
			165						170					175	
Lys	Ala	Phe	Glu	Ala	Tyr	Gln	Ser	Gly	Ser	Gln	Ala	Gln	Val	Ala	Ser
		180						185					190		
Asn	Gln	Asp	Ile	Lys	Ser	Val	Phe	Ile	Asp	His	Leu	Ser	Val	Cys	Asn
		195					200					205			
Gly	Tyr	Ala	Gln	Ala	Phe	Gln	Phe	Leu	Cys	Gln	Lys	Ala	Gly	Ile	Pro
	210					215						220			
Val	Ala	Tyr	Ile	Arg	Gly	Thr	Gly	Thr	Ser	Gln	Gln	Pro	Gln	Gln	Ser
225					230					235					240
Phe	Ala	His	Ala	Trp	Asn	Ala	Val	Gln	Ile	Asn	Asn	Thr	Tyr	Tyr	Gly
			245						250					255	
Val	Asp	Val	Thr	Trp	Gly	Asp	Pro	Val	Phe	Asp	Asn	His	Leu	Ser	His
		260						265					270		
Gln	Lys	Gln	Gly	Thr	Ile	Asn	Tyr	Ser	Phe	Leu	Cys	Leu	Pro	Asp	Tyr
		275				280						285			
Leu	Met	Ala	Leu	Ser	His	Gln	Pro	Ser	Lys	Asp	Ile	Ala	Phe	Asn	Thr
	290					295					300				
Lys	Glu	Arg	Phe	Glu	Asn	Val	Trp	Thr	Ile	Pro	Ser	Cys	Thr	Asp	Asp
305					310					315					320
Ser	Leu	Leu	Tyr	Ser	Lys	Arg	His	Gln	Ser	Tyr	Ile	Ser	Thr	Phe	Asp
			325						330					335	
Ser	Asp	Ala	Ile	Leu	Ala	Ser	Leu	Glu	Asn	Gln	Leu	Leu	Asn	Arg	Gln
		340						345					350		
Glu	Pro	Leu	Ser	Leu	Gln	Phe	Ala	His	Gln	Asp	Asp	Tyr	Gln	Gln	Met
		355				360						365			
Val	Thr	Asp	Leu	Thr	Thr	Asn	Gln	Thr	Gly	Tyr	His	Asn	Leu	Phe	Asn
	370					375					380				
Gln	Tyr	Trp	Asn	Asn	Tyr	Thr	Gly	Phe	Thr	Tyr	Gly	Leu	Leu	Pro	Glu
385					390					395					400

Thr Leu Ser Ile Ser Phe Ala Ser Arg Asn
405 410

```
<210> SEQ ID NO 179
<211> LENGTH: 1044
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 179
atgaacaaaa aagtaatgtc acttgggtctt gtttcgactg ccctattcac attaggaggc 60
tgtaccaata actccgctaa acaaacaaact gacaattcat taaaaatcgc tatgattact 120
aatcagacgg gtattgatga caagtcattt aaccagtcag cctgggaagg cttacaagct 180
tggggaaaaa aaaataaaact tgaaaaagga aaaggctatg attattttcca atcagccaat 240
gaatcagagt ttaccacaaa ccttgagtca gcagtaacca atggttataa tcttgttttt 300
gggattggat ttccattaca tgacgctgta gaaaaagtag ccgcaacaa tcctgacaac 360
cattttgcaa ttgtggatga tgtgattaaa ggtcaaaaaa atgttgcaag tatcaccttt 420
tcagaccatg aagcggcata cctagccggt gttgcagcag ctaaaacgac aaaaaccaag 480
caagttgggtt ttgtagggtg tatggaagga gatgttgctca agcgctttga aaaaggtttt 540
gaagctgggtg tgaaatcagt agatgatacc atcaaaagtaa gagttgctta tgcaggctct 600
tttgcagatg ctgccaaaagg caagacgatt gcagctgctc aatacgctga aggcgcagat 660
gttatattatc atgcagcagg aggcacaggg gcggtgtct ttagcgaagc taagtctatc 720
aacgaaaaac gttaaagaaga agataagggtt tgggttattg gtgttgaccg tgaccaaaagt 780
gaagatggaa aatacactac aaaagatggc aagtcagcta attttgtttt gacctcaagt 840
atcaaggaag tcggaaaagc tttagtaaaa gtagccgtaa aaacctcaga agaccaattc 900
ccaggtgggtc aaataaccac ttttggttta aaagaagggtg gtgttagcct tacaacggat 960
gctctgacac aagacactaa aaaagctatt gaggtctgta aaaaagcgat tatcgaagga 1020
accatcacag ttcctgaaaa ctaa 1044
```

```
<210> SEQ ID NO 180
<211> LENGTH: 347
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 180
Met Asn Lys Lys Val Met Ser Leu Gly Leu Val Ser Thr Ala Leu Phe
1 5 10 15
Thr Leu Gly Gly Cys Thr Asn Asn Ser Ala Lys Gln Thr Thr Asp Asn
20 25 30
Ser Leu Lys Ile Ala Met Ile Thr Asn Gln Thr Gly Ile Asp Asp Lys
35 40 45
Ser Phe Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Glu
50 55 60
Asn Lys Leu Glu Lys Gly Lys Gly Tyr Asp Tyr Phe Gln Ser Ala Asn
65 70 75 80
Glu Ser Glu Phe Thr Thr Asn Leu Glu Ser Ala Val Thr Asn Gly Tyr
85 90 95
Asn Leu Val Phe Gly Ile Gly Phe Pro Leu His Asp Ala Val Glu Lys
100 105 110
Val Ala Ala Asn Asn Pro Asp Asn His Phe Ala Ile Val Asp Asp Val
115 120 125
Ile Lys Gly Gln Lys Asn Val Ala Ser Ile Thr Phe Ser Asp His Glu
130 135 140
Ala Ala Tyr Leu Ala Gly Val Ala Ala Ala Lys Thr Thr Lys Thr Lys
145 150 155 160
Gln Val Gly Phe Val Gly Gly Met Glu Gly Asp Val Val Lys Arg Phe
165 170 175
Glu Lys Gly Phe Glu Ala Gly Val Lys Ser Val Asp Asp Thr Ile Lys
180 185 190
Val Arg Val Ala Tyr Ala Gly Ser Phe Ala Asp Ala Ala Lys Gly Lys
```


Ala	Asp	Leu	Phe	Val	Tyr	His	Ser	His	Thr	Leu	Glu	Ala	Trp	Ala	Arg
			85						90					95	
Asp	Leu	Asp	Pro	Asn	Leu	Lys	Lys	Ser	Lys	Val	Asp	Val	Phe	Glu	Ala
			100					105					110		
Ser	Lys	Pro	Leu	Thr	Leu	Asp	Arg	Val	Lys	Gly	Leu	Glu	Asp	Met	Glu
		115					120					125			
Val	Thr	Gln	Gly	Ile	Asp	Pro	Ala	Thr	Leu	Tyr	Asp	Pro	His	Thr	Trp
	130					135					140				
Thr	Asp	Pro	Val	Leu	Ala	Gly	Glu	Glu	Ala	Val	Asn	Ile	Ala	Lys	Glu
145					150					155				160	
Leu	Gly	Arg	Leu	Asp	Pro	Lys	His	Lys	Asp	Ser	Tyr	Thr	Lys	Asn	Ala
			165						170					175	
Lys	Ala	Phe	Lys	Lys	Glu	Ala	Glu	Gln	Leu	Thr	Glu	Glu	Tyr	Thr	Gln
		180						185					190		
Lys	Phe	Lys	Lys	Val	Arg	Ser	Lys	Thr	Phe	Val	Thr	Gln	His	Thr	Ala
	195						200					205			
Phe	Ser	Tyr	Leu	Ala	Lys	Arg	Phe	Gly	Leu	Lys	Gln	Leu	Gly	Ile	Ser
	210					215					220				
Gly	Ile	Ser	Pro	Glu	Gln	Glu	Pro	Ser	Pro	Arg	Gln	Leu	Lys	Glu	Ile
225					230					235				240	
Gln	Asp	Phe	Val	Lys	Glu	Tyr	Asn	Val	Lys	Thr	Ile	Phe	Ala	Glu	Asp
			245						250					255	
Asn	Val	Asn	Pro	Lys	Ile	Ala	His	Ala	Ile	Ala	Lys	Ser	Thr	Gly	Ala
			260					265					270		
Lys	Val	Lys	Thr	Leu	Ser	Pro	Leu	Glu	Ala	Ala	Pro	Ser	Gly	Asn	Lys
	275						280					285			
Thr	Tyr	Leu	Glu	Asn	Leu	Arg	Ala	Asn	Leu	Glu	Val	Leu	Tyr	Gln	Gln
	290					295						300			
Leu	Lys														
305															

<210> SEQ ID NO 183

<211> LENGTH: 942

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 183

atgactagta	aaaaagcgtg	tttatcaagc	atcattgtgt	tagcaagttt	aacgtgtgga	60
aatgatactg	ttagtgccaa	tcatctctca	gcaactggag	ataagtttga	tgattgctca	120
acacttggtg	aaaaagatgt	ggcccctaaa	gatgaacttg	agatgtagc	atggctctcg	180
tctcaaaca	ctgatgatgc	tgacagagac	tatgaagatt	ttctcgatga	tgattctttt	240
atttctcaa	atgaaactga	taagatgttt	gagaatttaa	ctgatgatag	gttattaaat	300
gaattagatg	aattagatga	agaaaatgaa	gaagatgaag	aagatacaat	tgagccagag	360
caaaatgtaa	taatgcctag	tgacgatgag	ctatttgatt	taactgatgc	tggtgagaca	420
cgccttactg	tttctagtgc	tccccattta	gaggctgaat	tgccgaaacc	acatttgagg	480
agcctatcag	atacagcact	gcggtctggt	gaaattagag	gacatttaga	taacaaactg	540
gacgctttgt	ctgtaacagc	tacaaagtta	gcattaacga	tggtcaaaa	atttgatttg	600
acaacgcatg	tctattctat	aggtgaaagc	tttagtgaag	tattagctgc	tcattatgaa	660
gacagaaaag	cagaatcagc	tttttctaag	aaaaagagat	ttcaccttcc	tattgctact	720
ccagatgttg	ttatagagga	gttaaggcgc	ctagtctctt	ctattggaag	ttcaaaagaa	780
gatgtttcag	ttccttatag	tcggaagcta	ggtatggcag	ttgcaaaaag	aaaaatagcc	840
ctgccacaaa	cgggagagag	gttctcttat	tatccagttt	tacttggttt	aatgatatta	900
ggattaacgc	cgattatgat	accaaagaag	ataaataatt	ag		942

<210> SEQ ID NO 184

<211> LENGTH: 313

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 184

```
Met Thr Ser Lys Lys Ala Cys Leu Ser Ser Ile Ile Val Leu Ala Ser
1      5      10      15
Leu Thr Cys Gly Asn Asp Thr Val Ser Ala Asn His Leu Ser Ala Thr
20     25     30
Gly Asp Lys Phe Asp Asp Cys Ser Thr Leu Val Glu Lys Asp Val Ala
35     40     45
Pro Lys Asp Glu Leu Glu Met Leu Ala Trp Ser Ser Ser Gln Thr Thr
50     55     60
Asp Asp Ala Asp Arg Asp Tyr Glu Asp Phe Leu Asp Asp Asp Ser Phe
65     70     75     80
Ile Ser Gln Asn Glu Thr Asp Lys Met Phe Glu Asn Leu Thr Asp Asp
85     90     95
Arg Leu Leu Asn Glu Leu Asp Glu Leu Asp Glu Glu Asn Glu Glu Asp
100    105    110
Glu Glu Asp Thr Ile Glu Pro Glu Gln Asn Val Ile Met Pro Ser Asp
115    120    125
Asp Glu Leu Phe Asp Leu Thr Asp Ala Val Glu Thr Arg Leu Thr Val
130    135    140
Ser Ser Ala Pro His Leu Glu Ala Glu Leu Pro Lys Pro His Leu Arg
145    150    155    160
Ser Leu Ser Asp Thr Ala Leu Arg Ser Gly Glu Ile Arg Gly His Leu
165    170    175
Asp Asn Lys Leu Asp Ala Leu Ser Val Thr Ala Thr Lys Leu Ala Leu
180    185    190
Thr Met Ala Gln Lys Phe Asp Leu Thr Thr His Val Tyr Ser Ile Gly
195    200    205
Glu Ser Phe Ser Glu Val Leu Ala Ala His Tyr Glu Asp Arg Lys Ala
210    215    220
Glu Ser Ala Phe Ser Lys Lys Lys Arg Phe His Leu Pro Ile Ala Thr
225    230    235    240
Pro Asp Val Val Ile Glu Glu Leu Arg Arg Leu Val Ser Ser Ile Gly
245    250    255
Ser Ser Lys Glu Asp Val Ser Val Pro Tyr Ser Arg Lys Leu Gly Met
260    265    270
Ala Val Ala Lys Arg Lys Ile Ala Leu Pro Gln Thr Gly Glu Arg Phe
275    280    285
Ser Tyr Tyr Pro Val Leu Leu Gly Leu Met Ile Leu Gly Leu Thr Pro
290    295    300
Ile Met Ile Pro Lys Lys Ile Asn Asn
305    310
```

<210> SEQ ID NO 185

<211> LENGTH: 882

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 185

```
ttgctgacct ttggaggtgc aagtgcggtt aaggcggaag aaaatgaaaa agtaagagag      60
caagaaaagc tcatacagca actttctgaa aagctagtgg aaattaatga cttacaaact    120
ttaaatggtg ataaagagag tatacagtct ctcgtagatt atctgactcg aagaggaaaa    180
cttgaagaag aatggatgga atatttgaat tctggtattc aacgcaaact ttttgttgggt    240
ccaaaaggac ctgcaggtga aaaaggagaa caaggtccta ctggaaaaca aggcgagcgt    300
ggtgagaccg gccctgcagg tccacgtggt gacaagggcg aaactggtga caaaggagcc    360
caggtgccag taggtcccg c tggcaaggac ggccaaaacg gtaaagatgg tcttccaggt    420
aaagacggca aggacggcca aaacggtaaa gatggtcttc caggtaaaga cggcaaggac    480
ggccaagacg gtaaagatgg cctcccaggt aaagacggta aggatggcca aaatggcaaa    540
gatggtcttc caggtaaaga cggtaacca ggtaaacacg ctctaaaaac accagaggtc    600
```

cctcaaaacc	cagatactgc	accacatact	ccaaaaaccc	ctcggatccc	tggtcaatca	660
aaagacgtga	cacctgctcc	tcaaaaccct	tctaatagag	gtctaaacaa	accacaaaca	720
caaggtggta	atcagctcgc	aaaaacaccg	gcagctcacg	acacacacag	acaattgcca	780
gcaacaggcg	aaacaacca	tccattcttt	acagcagctg	ctgtagctat	catgacgaca	840
gctggagtgtg	tagctgttgc	aaaacgtcaa	gaaaacaact	aa		882

<210> SEQ ID NO 186
 <211> LENGTH: 293
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 186

Met	Leu	Thr	Phe	Gly	Gly	Ala	Ser	Ala	Val	Lys	Ala	Glu	Glu	Asn	Glu
1				5					10					15	
Lys	Val	Arg	Glu	Gln	Glu	Lys	Leu	Ile	Gln	Gln	Leu	Ser	Glu	Lys	Leu
			20					25					30		
Val	Glu	Ile	Asn	Asp	Leu	Gln	Thr	Leu	Asn	Gly	Asp	Lys	Glu	Ser	Ile
			35				40					45			
Gln	Ser	Leu	Val	Asp	Tyr	Leu	Thr	Arg	Arg	Gly	Lys	Leu	Glu	Glu	Glu
	50					55					60				
Trp	Met	Glu	Tyr	Leu	Asn	Ser	Gly	Ile	Gln	Arg	Lys	Leu	Phe	Val	Gly
65					70					75					80
Pro	Lys	Gly	Pro	Ala	Gly	Glu	Lys	Gly	Glu	Gln	Gly	Pro	Thr	Gly	Lys
				85					90					95	
Gln	Gly	Glu	Arg	Gly	Glu	Thr	Gly	Pro	Ala	Gly	Pro	Arg	Gly	Asp	Lys
			100					105					110		
Gly	Glu	Thr	Gly	Asp	Lys	Gly	Ala	Gln	Gly	Pro	Val	Gly	Pro	Ala	Gly
		115					120					125			
Lys	Asp	Gly	Gln	Asn	Gly	Lys	Asp	Gly	Leu	Pro	Gly	Lys	Asp	Gly	Lys
	130					135					140				
Asp	Gly	Gln	Asn	Gly	Lys	Asp	Gly	Leu	Pro	Gly	Lys	Asp	Gly	Lys	Asp
145					150					155					160
Gly	Gln	Asp	Gly	Lys	Asp	Gly	Leu	Pro	Gly	Lys	Asp	Gly	Lys	Asp	Gly
				165					170					175	
Gln	Asn	Gly	Lys	Asp	Gly	Leu	Pro	Gly	Lys	Asp	Gly	Gln	Pro	Gly	Lys
			180					185					190		
Pro	Ala	Pro	Lys	Thr	Pro	Glu	Val	Pro	Gln	Asn	Pro	Asp	Thr	Ala	Pro
			195				200						205		
His	Thr	Pro	Lys	Thr	Pro	Arg	Ile	Pro	Gly	Gln	Ser	Lys	Asp	Val	Thr
	210					215						220			
Pro	Ala	Pro	Gln	Asn	Pro	Ser	Asn	Arg	Gly	Leu	Asn	Lys	Pro	Gln	Thr
225				230						235					240
Gln	Gly	Gly	Asn	Gln	Leu	Ala	Lys	Thr	Pro	Ala	Ala	His	Asp	Thr	His
			245						250					255	
Arg	Gln	Leu	Pro	Ala	Thr	Gly	Glu	Thr	Thr	Asn	Pro	Phe	Phe	Thr	Ala
			260					265					270		
Ala	Ala	Val	Ala	Ile	Met	Thr	Thr	Ala	Gly	Val	Val	Ala	Val	Ala	Lys
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Arg	Gln	Glu	Asn	Asn											
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<210> SEQ ID NO 187
 <211> LENGTH: 3525
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 187

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caatcgggac	actacgataa	cttagctgtc	tggaccttta	aagatgtcaa	aaccccaacg	720
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cagggttttg	tcaaagacac	tgacccaaaa	gtttacaaca	atccttatta	tattgatcag	960
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acggctaatac	cctctcagca	aaagagtcag	acagaccaatc	atcaaaccac	aacaccagat	3360
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aagctcccaa	aaacgggtga	agcctcctca	aaaggcttat	tagcagctgg	aatagctctg	3480
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<210> SEQ ID NO 188

<211> LENGTH: 1174

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 188

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Gly	Ser	Lys	Arg	Tyr	Gln	Tyr	Leu	Leu	Lys	Lys	Trp	Gly	Ile	Gly	Phe
		20					25					30			
Val	Ile	Ala	Ala	Thr	Gly	Thr	Val	Val	Leu	Gly	Cys	Thr	Pro	Ser	Ile
	35					40					45				
Leu	Thr	His	Gln	Val	Ala	Ala	Lys	Thr	Ile	Val	Gly	Leu	Ala	Arg	Asp
	50				55					60					
Glu	Ala	Gln	Gln	Gly	Asp	Gly	Asn	Ala	Lys	Ser	Gly	Asp	Gly	Leu	Gln
65			70						75					80	
Ser	Ser	Ser	Lys	Glu	Ala	Lys	Pro	Val	Leu	Asp	Ser	Ser	Ser	Ala	Asn
			85					90						95	
Pro	Ala	Ser	Ile	Ala	Glu	His	His	Leu	Arg	Met	His	Phe	Lys	Thr	Leu
		100						105					110		
Pro	Ala	Gly	Glu	Ser	Leu	Gly	Ser	Leu	Gly	Leu	Trp	Val	Trp	Gly	Asp
		115				120						125			
Val	Asp	Gln	Pro	Ser	Lys	Asp	Trp	Pro	Asn	Gly	Ala	Ile	Thr	Met	Thr
	130					135					140				
Lys	Ala	Lys	Lys	Asp	Asp	Tyr	Gly	Tyr	Tyr	Leu	Asp	Val	Pro	Leu	Ala
145				150					155					160	
Ala	Lys	His	Arg	Gln	Gln	Val	Ser	Tyr	Leu	Ile	Asn	Asn	Lys	Ala	Gly
			165					170						175	
Glu	Asn	Leu	Ser	Lys	Asp	Gln	His	Ile	Ser	Leu	Leu	Thr	Pro	Lys	Met
		180						185					190		
Asn	Glu	Val	Trp	Ile	Asp	Glu	Asn	Tyr	His	Ala	His	Ala	Tyr	Arg	Pro
	195					200						205			
Leu	Lys	Lys	Gly	Tyr	Leu	Arg	Ile	Asn	Tyr	His	Asn	Gln	Ser	Gly	His
	210				215						220				
Tyr	Asp	Asn	Leu	Ala	Val	Trp	Thr	Phe	Lys	Asp	Val	Lys	Thr	Pro	Thr
225				230						235					240
Thr	Asp	Trp	Pro	Asn	Gly	Leu	Asp	Leu	Ser	His	Lys	Gly	His	Tyr	Gly
			245					250						255	
Ala	Tyr	Val	Asp	Val	Pro	Leu	Lys	Glu	Gly	Ala	Asn	Glu	Ile	Gly	Phe
		260						265					270		
Leu	Ile	Leu	Asp	Lys	Ser	Lys	Thr	Gly	Asp	Ala	Ile	Lys	Val	Gln	Pro
	275						280					285			
Lys	Asp	Tyr	Leu	Phe	Lys	Glu	Leu	Asp	Asn	His	Thr	Gln	Val	Phe	Val
	290					295					300				
Lys	Asp	Thr	Asp	Pro	Lys	Val	Tyr	Asn	Asn	Pro	Tyr	Tyr	Ile	Asp	Gln
305				310					315					320	
Val	Ser	Leu	Lys	Gly	Ala	Glu	Gln	Thr	Thr	Pro	Asn	Glu	Ile	Lys	Ala
			325					330						335	
Ile	Phe	Thr	Thr	Leu	Asp	Gly	Leu	Asp	Glu	Asp	Ala	Val	Lys	Gln	Asn
		340					345						350		
Ile	Lys	Ile	Thr	Asp	Lys	Ala	Gly	Lys	Thr	Val	Ala	Ile	Asp	Glu	Leu
	355					360						365			
Thr	Leu	Asp	Arg	Asp	Lys	Ser	Val	Met	Thr	Leu	Lys	Gly	Asp	Phe	Lys
	370					375					380				
Ala	Gln	Gly	Ala	Val	Tyr	Thr	Val	Thr	Phe	Gly	Glu	Val	Ser	Gln	Val
385				390						395					400
Ala	Arg	Gln	Ser	Trp	Gln	Leu	Lys	Asp	Lys	Leu	Tyr	Ala	Tyr	Asp	Gly

				405					410				415			
Glu	Leu	Gly	Ala	Thr	Leu	Ala	Lys	Asp	Gly	Ser	Val	Asp	Leu	Ala	Leu	
			420					425					430			
Trp	Ser	Pro	Ser	Ala	Asp	Thr	Val	Lys	Val	Val	Val	Tyr	Asp	Lys	Gln	
		435					440					445				
Asp	Gln	Thr	Arg	Val	Val	Gly	Gln	Ala	Asp	Leu	Thr	Lys	Ser	Asp	Lys	
	450					455				460						
Gly	Val	Trp	Arg	Ala	His	Leu	Thr	Ser	Asp	Ser	Val	Lys	Gly	Ile	Ser	
465				470					475					480		
Asp	Tyr	Thr	Gly	Tyr	Tyr	Tyr	Leu	Tyr	Glu	Ile	Thr	Arg	Gly	Gln	Glu	
			485					490					495			
Lys	Val	Met	Val	Leu	Asp	Pro	Tyr	Ala	Lys	Ser	Leu	Ala	Ala	Trp	Asn	
		500						505				510				
Asp	Ala	Thr	Ala	Thr	Asp	Asp	Ile	Lys	Thr	Ala	Lys	Ala	Ala	Phe	Ile	
	515						520					525				
Asp	Pro	Ser	Lys	Leu	Gly	Pro	Thr	Gly	Leu	Asp	Phe	Ala	Lys	Ile	Asn	
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545				550						555					560	
Asp	Phe	Thr	Ser	Asp	Lys	Ala	Leu	Glu	Gly	Lys	Leu	Thr	His	Pro	Phe	
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Gly	Thr	Phe	Ser	Ala	Phe	Val	Glu	Gln	Leu	Asp	Tyr	Leu	Lys	Asp	Leu	
		580					585					590				
Gly	Val	Thr	His	Val	Gln	Leu	Leu	Pro	Val	Leu	Ser	Tyr	Phe	Tyr	Ala	
	595					600					605					
Asn	Glu	Leu	Asp	Lys	Ser	Arg	Ser	Thr	Ala	Tyr	Thr	Ser	Ser	Asp	Asn	
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Asn	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Gln	His	Tyr	Phe	Ala	Leu	Ser	Gly	
625				630						635					640	
Met	Tyr	Ser	Ala	Asn	Pro	Asn	Asp	Pro	Ala	Leu	Arg	Ile	Ala	Glu	Leu	
			645					650					655			
Lys	Asn	Leu	Val	Asn	Glu	Ile	His	Lys	Arg	Gly	Met	Gly	Val	Ile	Phe	
	660							665				670				
Asp	Val	Val	Tyr	Asn	His	Thr	Ala	Arg	Thr	Tyr	Leu	Phe	Glu	Asp	Leu	
	675					680						685				
Glu	Pro	Asn	Tyr	Tyr	His	Phe	Met	Asn	Ala	Asp	Gly	Thr	Ala	Arg	Glu	
	690				695						700					
Ser	Phe	Gly	Gly	Gly	Arg	Leu	Gly	Thr	Thr	His	Ala	Met	Ser	Arg	Arg	
705				710						715					720	
Ile	Leu	Val	Asp	Ser	Ile	Thr	Tyr	Leu	Thr	Arg	Glu	Phe	Lys	Val	Asp	
			725					730					735			
Gly	Phe	Arg	Phe	Asp	Met	Met	Gly	Asp	His	Asp	Ala	Ala	Ala	Ile	Glu	
		740					745					750				
Gln	Ala	Phe	Lys	Ala	Ala	Lys	Ala	Ile	Asn	Pro	Asn	Thr	Ile	Met	Ile	
	755					760					765					
Gly	Glu	Gly	Trp	Arg	Thr	Tyr	Gln	Gly	Asp	Glu	Gly	Lys	Lys	Glu	Ile	
	770				775						780					
Ala	Ala	Asp	Gln	Asp	Trp	Met	Lys	Ala	Thr	Asn	Thr	Val	Gly	Val	Phe	
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Ser	Asp	Asp	Ile	Arg	Asn	Thr	Leu	Lys	Ser	Gly	Phe	Pro	Asn	Glu	Gly	
			805					810					815			
Thr	Ala	Ala	Phe	Ile	Thr	Gly	Gly	Ala	Lys	Asn	Leu	Glu	Gly	Leu	Phe	
		820					825						830			
Lys	Thr	Ile	Lys	Ala	Gln	Pro	Gly	Asn	Phe	Glu	Ala	Asp	Ala	Pro	Gly	
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Asp	Val	Val	Gln	Tyr	Ile	Ala	Ala	His	Asp	Asn	Leu	Thr	Leu	His	Asp	
	850					855					860					

Val	Ile	Ala	Lys	Ser	Ile	Asn	Lys	Asp	Pro	Lys	Val	Ala	Glu	Glu	Glu	
865					870					875					880	
Ile	His	Lys	Arg	Ile	Arg	Leu	Gly	Asn	Thr	Met	Ile	Leu	Thr	Ala	Gln	
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Gly	Thr	Ala	Phe	Ile	His	Ser	Gly	Gln	Glu	Tyr	Gly	Arg	Thr	Lys	Gln	
			900					905						910		
Leu	Leu	Asn	Pro	Asp	Tyr	Lys	Thr	Lys	Ala	Ser	Asp	Asp	Lys	Val	Pro	
		915					920					925				
Asn	Lys	Ala	Thr	Leu	Ile	Asp	Ala	Val	Ala	Gln	Tyr	Pro	Tyr	Phe	Ile	
	930					935					940					
His	Asp	Ser	Tyr	Asp	Ser	Ser	Asp	Ala	Val	Asn	His	Phe	Asp	Trp	Ala	
945				950						955					960	
Lys	Ala	Thr	Asp	Ser	Ile	Ala	His	Pro	Ile	Ser	Asn	Gln	Thr	Lys	Ala	
			965					970						975		
Tyr	Thr	Gln	Gly	Leu	Ile	Ala	Leu	Arg	Arg	Ser	Thr	Asp	Ala	Phe	Thr	
		980						985					990			
Lys	Ala	Thr	Lys	Ala	Glu	Val	Asp	Arg	Asp	Val	Thr	Leu	Ile	Thr	Gln	
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Gln	Thr	Val	Ala	Ser	Asn	Gly	Asp	Arg	Tyr	Ala	Val	Phe	Val	Asn		
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Ala	Asp	Asn	Lys	Thr	Arg	Lys	Val	Val	Leu	Pro	Gln	Ala	Tyr	Arg		
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Tyr	Leu	Leu	Gly	Ala	Gln	Val	Leu	Val	Asp	Ala	Glu	Gln	Ala	Gly		
	1055					1060					1065					
Val	Thr	Ala	Ile	Ala	Lys	Pro	Lys	Gly	Val	Gln	Phe	Thr	Lys	Glu		
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Gly	Leu	Thr	Ile	Glu	Gly	Leu	Thr	Ala	Leu	Val	Leu	Lys	Val	Ser		
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Ser	Lys	Thr	Ala	Asn	Pro	Ser	Gln	Gln	Lys	Ser	Gln	Thr	Asp	Asn		
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His	Gln	Thr	Lys	Thr	Pro	Asp	Gly	Ser	Lys	Asp	Leu	Asp	Lys	Ser		
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Leu	Met	Thr	Arg	Pro	Lys	Arg	Ala	Lys	Thr	Asn	Gln	Lys	Leu	Pro		
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Lys	Thr	Gly	Glu	Ala	Ser	Ser	Lys	Gly	Leu	Leu	Ala	Ala	Gly	Ile		
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Ala	Leu	Leu	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Met	Lys	Arg	Gln	Lys		
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<210> SEQ ID NO 189

<211> LENGTH: 1302

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 189

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gcaggattgg	caacagggat	ttatattcta	gggactttat	tagcccgttt	gatttttgga	300
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attccagctc	gtaaaagagg	agaaggaatt	aatttttatg	gcttgtcaac	cagctagca	540
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<210> SEQ ID NO 190

<211> LENGTH: 433

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 190

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20          25          30
Ser Phe Ser Met Glu Glu Lys Leu Phe Asn Lys His Phe Val Ala Ile
35          40          45
Thr Val Ile Asn Phe Ile Val Tyr Met Val Tyr Tyr Leu Phe Thr Val
50          55          60
Ile Ile Ala Phe Val Ala Thr Arg Glu Leu Gly Ala Gln Thr Ser Gln
65          70          75          80
Ala Gly Leu Ala Thr Gly Ile Tyr Ile Leu Gly Thr Leu Leu Ala Arg
85          90          95
Leu Ile Phe Gly Lys Gln Leu Glu Val Phe Gly Arg Arg Leu Val Leu
100         105         110
Arg Gly Gly Ala Ile Phe Tyr Leu Thr Thr Leu Ala Tyr Phe Tyr
115         120         125
Met Pro Thr Ile Ser Met Met Tyr Leu Val Arg Phe Leu Asn Gly Phe
130         135         140
Gly Tyr Gly Val Val Ser Thr Ala Thr Asn Thr Ile Val Thr Ala Tyr
145         150         155         160
Ile Pro Ala Arg Lys Arg Gly Glu Gly Ile Asn Phe Tyr Gly Leu Ser
165         170         175
Thr Ser Leu Ala Ala Ala Ile Gly Pro Phe Val Gly Thr Phe Met Leu
180         185         190
Asp Asn Leu His Ile Asp Phe Arg Met Ile Ile Val Leu Cys Ser Val
195         200         205
Leu Ile Gly Cys Val Val Val Gly Ala Phe Ala Phe Pro Val Lys Asn
210         215         220
Met Ser Leu Asn Ala Glu Gln Leu Ala Lys Thr Lys Ser Trp Thr Val
225         230         235         240
Asp Ser Phe Ile Glu Lys Lys Ala Leu Phe Ile Thr Ala Ile Ala Phe
245         250         255
Leu Met Gly Ile Ala Tyr Ala Ser Val Leu Gly Phe Gln Lys Leu Tyr
260         265         270
Thr Ser Glu Ile His Leu Thr Thr Val Gly Ala Tyr Phe Phe Val Val
275         280         285
Tyr Ala Leu Ile Ile Thr Ile Thr Arg Pro Ala Met Gly Arg Leu Met
290         295         300
Asp Ala Lys Gly Asp Lys Trp Val Leu Tyr Pro Ser Tyr Leu Phe Leu

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			100					105					110				
Gly	Leu	Phe	Pro	Trp	Ala	His	Val	Leu	Gln	Tyr	Val	Val	Ala	Gln	Leu		
		115						120					125				
Leu	Gly	Ala	Ile	Phe	Gly	Gln	Leu	Val	Val	Val	Met	Val	Tyr	Lys	Pro		
	130					135						140					
Tyr	Phe	Met	Lys	Thr	Glu	Asn	Pro	Asn	His	Val	Leu	Gly	Ser	Phe	Ser		
145					150					155					160		
Thr	Ile	Ser	Ser	Leu	Asp	Asn	Gly	Gln	Lys	Asp	Ser	His	Lys	Ala	Ser		
			165						170					175			
Tyr	Ile	Asn	Gly	Phe	Leu	Asn	Glu	Phe	Val	Gly	Ser	Phe	Val	Leu	Phe		
		180						185					190				
Phe	Gly	Ala	Leu	Ala	Leu	Thr	Lys	Asn	Tyr	Phe	Gly	Val	Glu	Leu	Val		
	195						200					205					
Gly	Lys	Leu	Ile	Glu	Ala	Gly	Tyr	Asp	Gln	Thr	Thr	Ala	Ala	Thr	Gln		
	210					215					220						
Ile	Ser	Pro	Tyr	Val	Thr	Gly	Ser	Leu	Ala	Val	Ala	His	Ile	Gly	Ile		
225					230					235					240		
Gly	Phe	Leu	Val	Met	Val	Leu	Val	Thr	Ser	Leu	Gly	Gly	Pro	Thr	Gly		
			245					250						255			
Pro	Ala	Leu	Asn	Pro	Ala	Arg	Asp	Phe	Gly	Pro	Arg	Leu	Leu	His	His		
		260						265					270				
Phe	Leu	Pro	Lys	Ser	Val	Leu	Gly	Gln	Ala	Lys	Gly	Asp	Ser	Lys	Trp		
	275					280					285						
Trp	Tyr	Ala	Trp	Val	Pro	Val	Val	Ala	Pro	Ile	Leu	Ala	Ala	Ile	Val		
	290				295						300						
Ala	Val	Ala	Ala	Phe	Lys	Tyr	Leu	Tyr	Ile	Arg							
305					310					315							

<210> SEQ ID NO 193

<211> LENGTH: 951

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 193

atgggtttacg	aaatgacttt	ggcggtcatt	aaatgtattg	aaaaccatct	tcacaaaaaa	60
gtatacaaaag	gggccagtct	ggctctcttt	caatctggtc	gatggcaaga	ataccatatac	120
ggaacaattg	atggaagacg	accagttgat	gctaacttag	tttatgactt	ggctagtgtt	180
tcaaaagttg	ttggtgtggc	cacaatatgc	aatattttat	tgaataatgg	tacgttagca	240
ttagatgatac	ccttaaaggt	atattatcct	agtattgctg	atgcgactgt	cactattcga	300
cagttattga	ctcataccag	tggtcttgat	ccttatattc	ctaacagaga	tgttttaaat	360
gcacaacaat	taagaaaagc	acttaatcat	cttactcaaa	aagaaaataa	aaacttttat	420
tacacagatg	tcaatttcct	cttgttaggc	ttcatgttag	aagagctctt	tagtgaatct	480
ttagaccaga	tatttgacaa	gactatcttt	actccctttg	ggatgtatca	tacgtctttt	540
ggccctcgtc	cagaagctgt	accaacatta	aagggtgtga	gtgatggaga	agttcatgat	600
cccaaagcaa	aaatcttaaa	aaaacattct	ggatctgcgg	ggctattttc	aactcttgca	660
gatttagaaa	gttttagcaa	tcattatctt	aatgatccat	tttcagattg	tctgtggcgc	720
aactacagcc	aacaaacaat	tgagcgggtca	ctaggggtgga	atttagatgg	cgattggatt	780
agtcatacag	gttacacagg	gccgtttcta	atgcttaata	aaaaagagca	aacggcagct	840
atTTTTTTTga	ccaaccgtac	ttacgacgag	gatgataaaa	gtaaatgggt	aaaagaacgt	900
cagttgcttt	acaatgcact	aaagcatgat	ctgacaaccc	ccgtatcgta	a	951

<210> SEQ ID NO 194

<211> LENGTH: 316

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 194

Met	Val	Tyr	Glu	Met	Thr	Leu	Ala	Val	Ile	Lys	Cys	Ile	Glu	Asn	His
1					5				10				15		

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 196

```
Met Ile Ser Tyr Glu Lys Val Arg Gln Ala Leu Lys Thr Ser Thr Ile
 1           5           10          15
Ala Ile Ile Ile Leu Asn Gly Leu Gly Val Val Leu Ser Leu Met Gly
 20          25          30
Phe Ala Gly Ile Phe Tyr Leu Gln Ser Gln Leu Lys Asn Glu Ala Phe
 35          40          45
Arg Ala Gln Leu Thr Thr Glu Gln Leu Ala Gln Leu Gln Ser Ser Met
 50          55          60
Thr Pro Phe Met Ile Phe Leu Ser Val Leu Asn Val Leu Ala Ile Ile
 65          70          75          80
Ala Ile Ile Val Phe Cys Ala Gln Asn Leu Ser Lys Leu Lys Gln Gly
 85          90          95
Leu Thr Val Ser Tyr Ile Pro Tyr Ile Leu Gly Leu Ile Leu Ser Val
100         105         110
Ile Gly Leu Val Asn Gln Phe Thr Thr Thr Met Ser Met Val Gly Thr
115         120         125
Ile Leu Ile Leu Ile Gln Ala Ala Leu Tyr Gly Phe Ala Phe Tyr Lys
130         135         140
Ala Lys Thr Leu Asn Glu Lys Gly Asp Asp Thr Asp Gln Ala Met Leu
145         150         155         160
```

<210> SEQ ID NO 197

<211> LENGTH: 2454

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 197

```
atggaatacgt tttttacagg tactgttgat cgtatcattt ttgaaaacca ggctaatttc      60
tttaaaattc tcctccttgc cattgaggat acagacagtg acattgacga ctttgaaatc      120
attatcacag gaacgatggc tgacattatt gaaggagatg actacacctt ttggggggaa      180
ttgaccacgc accctaaata tggacagcaa ctcaaaactaa gccgttacca aaaaatcaaa      240
cctagttcat ctggtttggt taattatttc tctagcgacc attttaaggg gattggtaaa      300
aaaacagcgg agaaaatcat tgcgctatat ggtcataata ccattgacca tatttttagaa      360
gacccaagca aattagaaac tatctctggc ctatctaagg ctaatcgtca agcctttgtc      420
gctaaactaa aattgaatta cggcacagag caactgattg ctggtctcgt cgaacttggc      480
cttagcaacc gttttgccct tcaagcgttt gaaaagtata aagaagaggc tcttgacctt      540
gttaaagaaa atccctatca gttagtgcga gatctacaag gttttgggtt taaaatggca      600
gatgctctcg ctgaaaactt agggattgaa agcgactctc cgaaacgttt tcgtgcagcc      660
ctccttcact gtctcttgga agaatccatc aatcgaggag atacttatgt ccaagcacga      720
caattattag actttgccat cacactcctt gaagatgcac gtcaagtaga atgtgatcct      780
gctgctgtgg ctgaacaact aagcgagtta atcatagagg gcaaaatcaa aaacagtgac      840
accaaactgt ttgatgctag cctttatttt gctgaagaag ggattgctaa caacatctct      900
cgtctcttag atactccttt aagtcagtca tttagtcatg ataccattca aacaaccatc      960
caagccggtt aaaaagactt tgccatcacc tatgaccaag tgcagcaaga agccattact     1020
aaggctttta ccagcaaggc ttttctccta acaggtggtc ccggaacagg aaaaacaact     1080
gttattcgag gcattttgca ggcttacgcg aacctgcata agattgattt ggataaaaaa     1140
gaccttccta tcttgttagc agctccaaca ggtcgggctg cacgtcgcat gaatgagttg     1200
actggacttc ctagcgcaac catccacagg cacttaggcc tcaatggcga caacgattac     1260
caagccatgg aggattatct agactgcgac ctgctgattg tcgatgaatt ttcaatgggtg     1320
gatacctggc ttgccaacca gttgttagga gctattaact caacaactca agtgattatt     1380
gtcggagata gtgaccagct tccttcgggt ggacccggtc aagtcctgtc agatctttta     1440
aaagtcaata gcctgcccc aatcgccttg caaaagatat ttcgtcaatc ccaagaatct     1500
actattgtca atttggcaga ccagatgcgt caaggaatct tagctgctga ctttcgtgat     1560
aaaaaagctg accgttctta ttttgaagcc caagcagcct ttatccctga catgatcaaa     1620
aaaattgtcc tatctgctat taaaagtggc atccctgctg aggaaattca aatttttagca     1680
cctatgtaca aaggacaagc tggcatcaat catcttaatc aactcatgca agaacttctc     1740
```

aatcccttgc	aaggacaaac	agaatttctg	ttcaatgata	cgcatttttcg	taaaggtgat	1800
aaagtcctcc	acttagtcaa	cgatgctcag	ttgaatgtct	ttaacggaga	tattggttat	1860
attacagatt	tgattcctgc	taaatacacc	gaatctaagc	aagacgaatt	aatccttagat	1920
tttgacggta	gcgaagtcac	gtaccctaga	aatgaatggc	taaaattaac	cctggcctat	1980
gccatgagca	ttcataaatc	gcaagggagt	gagtttcaag	tggtgatttt	acctatcaca	2040
cgccaaagcg	gccgactctt	gcaacgaaat	gtgatttaca	cggccattac	tcggtctaaa	2100
agtaagttaa	ttctgttggg	agaatatact	gcctttgagt	atgctattaa	acacgaaggc	2160
gataaacgcc	aaacctactt	gatcgaacgc	ttccaagaac	aatccgactt	agcctcctct	2220
caacctaacc	aagagctaaa	atcaaaaagag	cagacctccc	ttttttctaa	tacggcaacc	2280
cttgaggacg	actctcaaaa	atcttcctct	caatcaacaa	actctaacc	cactgagaac	2340
tctcagtcag	ataatgatga	ttttagggtta	acacctgaga	attattcgac	tatcgattcg	2400
atgatagggc	ttacagaatc	agatattgcc	ctctttttcc	agaaaaaatc	ctag	2454

<210> SEQ ID NO 198

<211> LENGTH: 817

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 198

Met	Glu	Tyr	Val	Phe	Thr	Gly	Thr	Val	Asp	Arg	Ile	Ile	Phe	Glu	Asn	
1				5					10					15		
Gln	Ala	Asn	Phe	Phe	Lys	Ile	Leu	Leu	Leu	Ala	Ile	Glu	Asp	Thr	Asp	
			20					25					30			
Ser	Asp	Ile	Asp	Asp	Phe	Glu	Ile	Ile	Ile	Thr	Gly	Thr	Met	Ala	Asp	
			35					40					45			
Ile	Ile	Glu	Gly	Asp	Asp	Tyr	Thr	Phe	Trp	Gly	Glu	Leu	Thr	Gln	His	
			50				55				60					
Pro	Lys	Tyr	Gly	Gln	Gln	Leu	Lys	Leu	Ser	Arg	Tyr	Gln	Lys	Ile	Lys	
65					70					75				80		
Pro	Ser	Ser	Ser	Gly	Leu	Val	Asn	Tyr	Phe	Ser	Ser	Asp	His	Phe	Lys	
				85					90					95		
Gly	Ile	Gly	Lys	Lys	Thr	Ala	Glu	Lys	Ile	Ile	Ala	Leu	Tyr	Gly	His	
			100					105					110			
Asn	Thr	Ile	Asp	His	Ile	Leu	Glu	Asp	Pro	Ser	Lys	Leu	Glu	Thr	Ile	
			115					120					125			
Ser	Gly	Leu	Ser	Lys	Ala	Asn	Arg	Gln	Ala	Phe	Val	Ala	Lys	Leu	Lys	
			130			135					140					
Leu	Asn	Tyr	Gly	Thr	Glu	Gln	Leu	Ile	Ala	Gly	Leu	Val	Glu	Leu	Gly	
145					150					155					160	
Leu	Ser	Asn	Arg	Phe	Ala	Leu	Gln	Ala	Phe	Glu	Lys	Tyr	Lys	Glu	Glu	
				165					170					175		
Ala	Leu	Asp	Leu	Val	Lys	Glu	Asn	Pro	Tyr	Gln	Leu	Val	Glu	Asp	Leu	
			180					185					190			
Gln	Gly	Phe	Gly	Phe	Lys	Met	Ala	Asp	Ala	Leu	Ala	Glu	Asn	Leu	Gly	
			195				200					205				
Ile	Glu	Ser	Asp	Ser	Pro	Lys	Arg	Phe	Arg	Ala	Ala	Leu	Leu	His	Cys	
			210			215				220						
Leu	Leu	Glu	Glu	Ser	Ile	Asn	Arg	Gly	Asp	Thr	Tyr	Val	Gln	Ala	Arg	
225					230				235						240	
Gln	Leu	Leu	Asp	Phe	Ala	Ile	Thr	Leu	Leu	Glu	Asp	Ala	Arg	Gln	Val	
				245					250					255		
Glu	Cys	Asp	Pro	Ala	Ala	Val	Ala	Glu	Gln	Leu	Ser	Glu	Leu	Ile	Ile	
			260					265					270			
Glu	Gly	Lys	Ile	Lys	Asn	Ser	Asp	Thr	Lys	Leu	Phe	Asp	Ala	Ser	Leu	
			275				280					285				
Tyr	Phe	Ala	Glu	Glu	Gly	Ile	Ala	Asn	Asn	Ile	Ser	Arg	Leu	Leu	Asp	
			290			295				300						
Thr	Pro	Leu	Ser	Gln	Ser	Phe	Ser	His	Asp	Thr	Ile	Gln	Thr	Thr	Ile	

305					310					315				320
Gln	Ala	Val	Gln	Lys	Asp	Phe	Ala	Ile	Thr	Tyr	Asp	Gln	Val	Gln
				325					330					335
Glu	Ala	Ile	Thr	Lys	Ala	Leu	Thr	Ser	Lys	Val	Phe	Leu	Leu	Thr
			340					345					350	
Gly	Pro	Gly	Thr	Gly	Lys	Thr	Thr	Val	Ile	Arg	Gly	Ile	Leu	Gln
		355					360				365			
Tyr	Ala	Asn	Leu	His	Gln	Ile	Asp	Leu	Asp	Lys	Lys	Asp	Leu	Pro
	370					375					380			
Leu	Leu	Ala	Ala	Pro	Thr	Gly	Arg	Ala	Ala	Arg	Arg	Met	Asn	Glu
385					390					395				400
Thr	Gly	Leu	Pro	Ser	Ala	Thr	Ile	His	Arg	His	Leu	Gly	Leu	Asn
				405					410					415
Asp	Asn	Asp	Tyr	Gln	Ala	Met	Glu	Asp	Tyr	Leu	Asp	Cys	Asp	Leu
			420					425				430		
Ile	Val	Asp	Glu	Phe	Ser	Met	Val	Asp	Thr	Trp	Leu	Ala	Asn	Gln
		435					440					445		
Leu	Gly	Ala	Ile	Asn	Ser	Thr	Thr	Gln	Val	Ile	Ile	Val	Gly	Asp
	450					455				460				
Asp	Gln	Leu	Pro	Ser	Val	Gly	Pro	Gly	Gln	Val	Leu	Ser	Asp	Leu
465					470				475					480
Lys	Val	Asn	Ser	Leu	Pro	Gln	Ile	Ala	Leu	Gln	Lys	Ile	Phe	Arg
				485					490					495
Ser	Gln	Glu	Ser	Thr	Ile	Val	Asn	Leu	Ala	Asp	Gln	Met	Arg	Arg
			500					505				510		
Ile	Leu	Ala	Ala	Asp	Phe	Arg	Asp	Lys	Lys	Ala	Asp	Arg	Ser	Tyr
		515					520				525			
Glu	Ala	Gln	Ala	Ala	Phe	Ile	Pro	Asp	Met	Ile	Gln	Lys	Ile	Val
	530					535					540			
Ser	Ala	Ile	Lys	Ser	Gly	Ile	Pro	Ala	Glu	Glu	Ile	Gln	Ile	Leu
545					550				555					560
Pro	Met	Tyr	Lys	Gly	Gln	Ala	Gly	Ile	Asn	His	Leu	Asn	Gln	Leu
				565					570					575
Gln	Glu	Leu	Leu	Asn	Pro	Leu	Gln	Gly	Gln	Thr	Glu	Phe	Leu	Phe
			580				585					590		
Asp	Thr	His	Phe	Arg	Lys	Gly	Asp	Lys	Val	Leu	His	Leu	Val	Asn
		595					600					605		
Ala	Gln	Leu	Asn	Val	Phe	Asn	Gly	Asp	Ile	Gly	Tyr	Ile	Thr	Asp
	610					615					620			
Ile	Pro	Ala	Lys	Tyr	Thr	Glu	Ser	Lys	Gln	Asp	Glu	Leu	Ile	Leu
625					630				635					640
Phe	Asp	Gly	Ser	Glu	Val	Thr	Tyr	Pro	Arg	Asn	Glu	Trp	Leu	Lys
				645					650					655
Thr	Leu	Ala	Tyr	Ala	Met	Ser	Ile	His	Lys	Ser	Gln	Gly	Ser	Glu
			660				665						670	
Gln	Val	Val	Ile	Leu	Pro	Ile	Thr	Arg	Gln	Ser	Gly	Arg	Leu	Leu
		675					680					685		
Arg	Asn	Val	Ile	Tyr	Thr	Ala	Ile	Thr	Arg	Ser	Lys	Ser	Lys	Leu
	690					695					700			
Leu	Leu	Gly	Glu	Tyr	Thr	Ala	Phe	Glu	Tyr	Ala	Ile	Lys	His	Glu
705					710				715					720
Asp	Lys	Arg	Gln	Thr	Tyr	Leu	Ile	Glu	Arg	Phe	Gln	Glu	Gln	Ser
				725					730					735
Leu	Ala	Ser	Ser	Gln	Pro	Asn	Gln	Glu	Leu	Lys	Ser	Lys	Glu	Gln
			740					745					750	
Ser	Leu	Phe	Ser	Asn	Thr	Ala	Thr	Leu	Glu	Asp	Asp	Ser	Gln	Lys
		755					760							

Ser	Ser	Gln	Ser	Thr	Asn	Ser	Asn	Pro	Thr	Glu	Asn	Ser	Gln	Ser	Asp
770						775					780				
Asn	Asp	Asp	Phe	Arg	Leu	Thr	Pro	Glu	Asn	Tyr	Ser	Thr	Ile	Asp	Ser
785					790					795					800
Met	Ile	Gly	Leu	Thr	Glu	Ser	Asp	Ile	Ala	Leu	Phe	Phe	Gln	Lys	Lys
				805					810					815	
Ser															

<210> SEQ ID NO 199

<211> LENGTH: 660

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 199

gtgctaaact	tcacttcgcc	aacactcaca	aagcgcaagc	gcttctcact	aaataaaaagg	60
aatcatatga	aacagtttat	taaagaatgg	ggcccattca	ctctcttttt	aattctcttt	120
gggtctatctc	gtcttttttt	gtggcaggct	gttaaagtag	acggccattc	tatggaccca	180
actctagctc	atggcgaaacg	ccttatcggt	tttaatcaag	ctagaattga	tcgctttgat	240
attgtagttg	ctcaggaaga	agaaaacgga	caaaagaaaag	aaatcgtaaa	aagagttatt	300
ggattgccag	gcgataccat	ttcttataat	gatgacacac	tttatattaa	tggtaaaaaaa	360
acagttgagc	cgtatttggc	tgagtatcta	aaacaattta	aaaacgataa	actccaaaaa	420
acttacgcct	ataataccct	attccaacag	ttagcagaaa	catctgatgc	ttttacaact	480
aattctgagg	gacaaacacg	ctttgagatg	agtgttccaa	aaggagaata	ccttcttctt	540
gggtgatgac	gtattgtttc	cagggatagt	cgcgaagtgt	gtagtttcaa	aaaagaaaac	600
cttatcggtg	aagtgaaagc	tcgttttttg	ccactcaata	aatgaccgt	ttttaattag	660

<210> SEQ ID NO 200

<211> LENGTH: 219

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 200

Met	Leu	Asn	Phe	Thr	Ser	Pro	Thr	Leu	Thr	Lys	Arg	Lys	Arg	Phe	Ser
1			5						10					15	
Leu	Asn	Lys	Arg	Asn	His	Met	Lys	Gln	Phe	Ile	Lys	Glu	Trp	Gly	Pro
		20						25					30		
Phe	Thr	Leu	Phe	Leu	Ile	Leu	Phe	Gly	Leu	Ser	Arg	Leu	Phe	Leu	Trp
		35					40					45			
Gln	Ala	Val	Lys	Val	Asp	Gly	His	Ser	Met	Asp	Pro	Thr	Leu	Ala	His
	50					55				60					
Gly	Glu	Arg	Leu	Ile	Val	Phe	Asn	Gln	Ala	Arg	Ile	Asp	Arg	Phe	Asp
65				70					75					80	
Ile	Val	Val	Ala	Gln	Glu	Glu	Glu	Asn	Gly	Gln	Lys	Lys	Glu	Ile	Val
			85					90					95		
Lys	Arg	Val	Ile	Gly	Leu	Pro	Gly	Asp	Thr	Ile	Ser	Tyr	Asn	Asp	Asp
		100					105					110			
Thr	Leu	Tyr	Ile	Asn	Gly	Lys	Lys	Thr	Val	Glu	Pro	Tyr	Leu	Ala	Glu
	115					120						125			
Tyr	Leu	Lys	Gln	Phe	Lys	Asn	Asp	Lys	Leu	Gln	Lys	Thr	Tyr	Ala	Tyr
	130				135						140				
Asn	Thr	Leu	Phe	Gln	Gln	Leu	Ala	Glu	Thr	Ser	Asp	Ala	Phe	Thr	Thr
145					150					155					160
Asn	Ser	Glu	Gly	Gln	Thr	Arg	Phe	Glu	Met	Ser	Val	Pro	Lys	Gly	Glu
			165					170					175		
Tyr	Leu	Leu	Leu	Gly	Asp	Asp	Arg	Ile	Val	Ser	Arg	Asp	Ser	Arg	Glu
		180					185					190			
Val	Gly	Ser	Phe	Lys	Lys	Glu	Asn	Leu	Ile	Gly	Glu	Val	Lys	Ala	Arg
	195						200					205			
Phe	Trp	Pro	Leu	Asn	Lys	Met	Thr	Val	Phe	Asn					

210

215

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<210> SEQ ID NO 201
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 201
atgatggaat catatgaaca cttttatgcc aaactatctc aaccttttag aaaaacccca      60
cagttaataa ttcttttaaa tgttttacta aaaataatca caggagtgat gtacatactt      120
tatccatctt ttctgatatt tacgctttgg caagggatga catttcaatt atggttaagg      180
ttattaatta ttctgctgtg tggctttata gctttgtctt acattaggaa acgctttgat      240
tttccacgac cgtatgaaaa atggaatatt aaacctttaa ttgataagga tacaaaggga      300
aggccaatgc ctagcagaca tgttttttca gctacgatga ttagtatgtg tttgttacga      360
tattatgttt actttggaat agttttgtta atattatcgg ctttattggc aatttgccgt      420
gtgatagcag gtattcacta tcctaaggat gttattgtag gttaccttat tggcttgatg      480
ttagggcttt gtttattgat ttag                                         504

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<210> SEQ ID NO 202
<211> LENGTH: 167
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 202
Met Met Glu Ser Tyr Glu His Phe Tyr Ala Lys Leu Ser Gln Pro Phe
1          5          10          15
Arg Lys Thr Pro Gln Leu Ile Ile Leu Leu Asn Val Leu Leu Lys Ile
20          25          30
Ile Thr Gly Val Met Tyr Ile Leu Tyr Pro Ser Phe Leu Ile Phe Thr
35          40          45
Leu Trp Gln Gly Met Thr Phe Gln Leu Trp Leu Arg Leu Leu Ile Ile
50          55          60
Pro Ala Val Gly Phe Ile Ala Leu Ser Tyr Ile Arg Lys Arg Phe Asp
65          70          75          80
Phe Pro Arg Pro Tyr Glu Lys Trp Asn Ile Lys Pro Leu Ile Asp Lys
85          90          95
Asp Thr Lys Gly Arg Ser Met Pro Ser Arg His Val Phe Ser Ala Thr
100         105         110
Met Ile Ser Met Cys Leu Leu Arg Tyr Tyr Val Tyr Phe Gly Ile Val
115         120         125
Cys Leu Ile Leu Ser Ala Leu Leu Ala Ile Cys Arg Val Ile Ala Gly
130         135         140
Ile His Tyr Pro Lys Asp Val Ile Val Gly Tyr Leu Ile Gly Leu Met
145         150         155         160
Leu Gly Leu Cys Leu Leu Ile
165

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<210> SEQ ID NO 203
<211> LENGTH: 1884
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<220> FEATURE:
<221> NAME/KEY: Unsure
<222> LOCATION: (1700)..(1700)
<223> OTHER INFORMATION: unsure
<400> SEQUENCE: 203
atggataatc gtcagattgc agctgaagtg attgaggctt taggtggccg agaaaatgtg      60
agaagtgttg cccactgtgc aactcgcctt cgcgatgatg tttatgatga aggaaagatt      120
gataaggaaa aagcagaagc tattgacaag gttaaaggag ctttctttta ctctgggtcaa      180

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tatcagatga	tttttggaac	tggtagcggt	aataacattt	atgacgaagt	tgttgctctt	240
ggtttacc	cgatcatcaac	cagtgagcaa	aaggcagaag	caggcaaaca	tggaatattc	300
ttccaacggg	cgattcgtac	gtttggagat	gtctttgttc	ccattattcc	agctattgta	360
gcaacgggtc	tctttatggg	ggttcgtggg	ttggtagacc	agccagctat	tatggattta	420
tttgggggtc	atgagtacgg	ggaaaatttt	ctcatgtaca	ctcgtattct	aacggataca	480
gcctttgtct	acttgccagc	tttggtaggt	tggtagcgct	ttaggggtctt	tggtgggtaat	540
cctattatcg	gtattgtttt	aggattgatg	ctggttttcca	atgagttgcc	taatgcttgg	600
gtagttgcct	ctggtaggaga	tgtaagccg	ctaaccctct	ttggatttgt	tcctgttgtt	660
ggttatcaag	gtaccgtttt	acccgccttc	tttgttggtc	tggtaggagc	taagttggag	720
aaatggttgc	acaaaaaggt	tccagaagct	ttggacttat	tggtcacacc	gtttttaacg	780
tttgctatta	tgagtacctt	gggactattt	gtgattggac	cagttttcca	ttctcttgaa	840
aaccttggtc	tggctgggac	acaggccgtc	ttgcatttgc	cgtttggcat	tgagggttg	900
attgttgggg	gaatccaaca	attaatcgta	gtgactggta	ttcaccatat	ctttaacttc	960
ctagaagcgc	agctgattgc	caataccgga	aaagatcctt	tcaatgctta	cctaacagca	1020
gcaacagctg	ctcaagctgg	agctacctta	gctgttgctg	ttaaaaccaa	atcaacaaaa	1080
ctaaaagggtc	tggcctttcc	atcaaccttg	tcagctcttt	tagggattac	tgaaccagct	1140
atttttgggg	tcaacctccg	ttatccaaaa	gtctttgttt	caggctcttat	tggtggtagc	1200
ttaggtaggt	gggtcgctgg	gctctttggc	attgcaggaa	ctggttttgg	gattaccgtc	1260
ttaccaggaa	ctctccttta	cttgaatggc	caattattac	aataccttgt	gactatgctt	1320
gtcggctctg	gggtagcctt	tgcaattgct	tatacttggg	gttatcaaga	tagagaaacc	1380
cttccgttac	cagctgtcga	agttgatcaa	acggctgac	agccagcctt	agcagaggaa	1440
actttatata	gtcctttgaa	tggaacagtt	gtagacttat	ctgcgggtttc	agaccctgtt	1500
ttttcatcag	gtgctatggg	tcaaggctta	gcaattaagc	cagaagataa	taccctatac	1560
tcaccagttg	atggtaaagt	tgaaattgtc	tttgaaacag	gtcatgccta	tgctataacg	1620
tcaagtcaag	gagcagaagt	gttacttcat	attggtattg	ataccgagtc	gatggcagga	1680
gatggctttg	aatctcttgn	agcagtagga	caggcgggta	aaaacggtga	tcttctaggc	1740
tgctttgatc	ctagcaagat	tgcaagaagc	gcactagatg	acaccgcccgt	gatgattgtg	1800
accaatagca	ctgactatca	aagcgtggac	attcgtgctc	aaggacatgt	tttgagtggg	1860
gatcaagtgg	cacttatcaa	ataa				1884

<210> SEQ ID NO 204

<211> LENGTH: 627

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<220> FEATURE:

<221> NAME/KEY: UNSURE

<222> LOCATION: (567)..(567)

<223> OTHER INFORMATION: unsure

<400> SEQUENCE: 204

Met	Asp	Asn	Arg	Gln	Ile	Ala	Ala	Glu	Val	Ile	Glu	Ala	Leu	Gly	Gly
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Arg	Glu	Asn	Val	Arg	Ser	Val	Ala	His	Cys	Ala	Thr	Arg	Leu	Arg	Val
			20					25					30		
Met	Val	Tyr	Asp	Glu	Gly	Lys	Ile	Asp	Lys	Glu	Lys	Ala	Glu	Ala	Ile
		35				40						45			
Asp	Lys	Val	Lys	Gly	Ala	Phe	Phe	Asn	Ser	Gly	Gln	Tyr	Gln	Met	Ile
	50				55					60					
Phe	Gly	Thr	Gly	Thr	Val	Asn	Asn	Ile	Tyr	Asp	Glu	Val	Val	Ala	Leu
65				70					75					80	
Gly	Leu	Pro	Thr	Ser	Ser	Thr	Ser	Glu	Gln	Lys	Ala	Glu	Ala	Gly	Lys
			85					90						95	
His	Gly	Asn	Ile	Phe	Gln	Arg	Ala	Ile	Arg	Thr	Phe	Gly	Asp	Val	Phe
		100						105					110		
Val	Pro	Ile	Ile	Pro	Ala	Ile	Val	Ala	Thr	Gly	Leu	Phe	Met	Gly	Val
	115					120					125				
Arg	Gly	Leu	Val	Thr	Gln	Pro	Ala	Ile	Met	Asp	Leu	Phe	Gly	Val	His
	130					135					140				

Glu	Tyr	Gly	Glu	Asn	Phe	Leu	Met	Tyr	Thr	Arg	Ile	Leu	Thr	Asp	Thr	145	150	155	160
Ala	Phe	Val	Tyr	Leu	Pro	Ala	Leu	Val	Ala	Trp	Ser	Ala	Phe	Arg	Val	165	170		175
Phe	Gly	Gly	Asn	Pro	Ile	Ile	Gly	Ile	Val	Leu	Gly	Leu	Met	Leu	Val	180	185		190
Ser	Asn	Glu	Leu	Pro	Asn	Ala	Trp	Val	Val	Ala	Ser	Gly	Gly	Asp	Val	195	200	205	
Lys	Pro	Leu	Thr	Phe	Phe	Gly	Phe	Val	Pro	Val	Val	Gly	Tyr	Gln	Gly	210	215	220	
Thr	Val	Leu	Pro	Ala	Phe	Phe	Val	Gly	Leu	Val	Gly	Ala	Lys	Leu	Glu	225	230	235	240
Lys	Trp	Leu	His	Lys	Lys	Val	Pro	Glu	Ala	Leu	Asp	Leu	Leu	Val	Thr	245	250		255
Pro	Phe	Leu	Thr	Phe	Ala	Ile	Met	Ser	Thr	Leu	Gly	Leu	Phe	Val	Ile	260	265		270
Gly	Pro	Val	Phe	His	Ser	Leu	Glu	Asn	Leu	Val	Leu	Ala	Gly	Thr	Gln	275	280	285	
Ala	Val	Leu	His	Leu	Pro	Phe	Gly	Ile	Ala	Gly	Leu	Ile	Val	Gly	Gly	290	295	300	
Ile	Gln	Gln	Leu	Ile	Val	Val	Thr	Gly	Ile	His	His	Ile	Phe	Asn	Phe	305	310	315	320
Leu	Glu	Ala	Gln	Leu	Ile	Ala	Asn	Thr	Gly	Lys	Asp	Pro	Phe	Asn	Ala	325	330		335
Tyr	Leu	Thr	Ala	Ala	Thr	Ala	Ala	Gln	Ala	Gly	Ala	Thr	Leu	Ala	Val	340	345		350
Ala	Val	Lys	Thr	Lys	Ser	Thr	Lys	Leu	Lys	Gly	Leu	Ala	Phe	Pro	Ser	355	360	365	
Thr	Leu	Ser	Ala	Leu	Leu	Gly	Ile	Thr	Glu	Pro	Ala	Ile	Phe	Gly	Val	370	375	380	
Asn	Leu	Arg	Tyr	Pro	Lys	Val	Phe	Val	Ser	Gly	Leu	Ile	Gly	Gly	Ala	385	390	395	400
Leu	Gly	Gly	Trp	Val	Ala	Gly	Leu	Phe	Gly	Ile	Ala	Gly	Thr	Gly	Phe	405	410		415
Gly	Ile	Thr	Val	Leu	Pro	Gly	Thr	Leu	Leu	Tyr	Leu	Asn	Gly	Gln	Leu	420	425		430
Leu	Gln	Tyr	Leu	Val	Thr	Met	Leu	Val	Gly	Leu	Gly	Val	Ala	Phe	Ala	435	440	445	
Ile	Ala	Tyr	Thr	Trp	Gly	Tyr	Gln	Asp	Arg	Glu	Thr	Leu	Pro	Leu	Pro	450	455	460	
Ala	Val	Glu	Val	Asp	Gln	Thr	Ala	Asp	Gln	Pro	Ala	Leu	Ala	Glu	Glu	465	470	475	480
Thr	Leu	Tyr	Ser	Pro	Leu	Asn	Gly	Thr	Val	Val	Asp	Leu	Ser	Ala	Val	485	490		495
Ser	Asp	Pro	Val	Phe	Ser	Ser	Gly	Ala	Met	Gly	Gln	Gly	Leu	Ala	Ile	500	505		510
Lys	Pro	Glu	Asp	Asn	Thr	Leu	Tyr	Ser	Pro	Val	Asp	Gly	Lys	Val	Glu	515	520	525	
Ile	Val	Phe	Glu	Thr	Gly	His	Ala	Tyr	Ala	Ile	Thr	Ser	Ser	Gln	Gly	530	535	540	
Ala	Glu	Val	Leu	Leu	His	Ile	Gly	Ile	Asp	Thr	Glu	Ser	Met	Ala	Gly	545	550	555	560
Asp	Gly	Phe	Glu	Ser	Leu	Xaa	Ala	Val	Gly	Gln	Ala	Val	Lys	Asn	Gly	565	570		575
Asp	Leu	Leu	Gly	Cys	Phe	Asp	Pro	Ser	Lys	Ile	Ala	Glu	Ala	Ala	Leu	580	585		590
Asp	Asp	Thr	Ala	Val	Met	Ile	Val	Thr	Asn	Ser	Thr	Asp	Tyr	Gln	Ser				

			180					185				190					
Pro	Ser	Gly	Ser	Asp	Leu	Ser	Leu	Pro	Phe	Pro	Leu	Gln	Glu	Ala	Leu		
		195					200					205					
Ser	Leu	Glu	Ser	Ser	Leu	Val	His	Val	Lys	Met	Ile	Ser	Ala	Gly	Asp		
	210					215					220						
Thr	Val	Gly	Tyr	Gly	Ala	Thr	Tyr	Thr	Ala	Lys	Lys	Ser	Glu	Tyr	Val		
225					230					235					240		
Gly	Thr	Val	Pro	Ile	Gly	Tyr	Ala	Asp	Gly	Trp	Thr	Arg	Asn	Met	Gln		
			245						250					255			
Gly	Phe	Ser	Val	Leu	Val	Asp	Gly	Gln	Phe	Cys	Glu	Ile	Ile	Gly	Arg		
		260					265						270				
Val	Ser	Met	Asp	Gln	Leu	Thr	Ile	Arg	Leu	Pro	Lys	Ala	Tyr	Pro	Leu		
	275						280					285					
Gly	Thr	Lys	Val	Thr	Leu	Ile	Gly	Ser	Asn	Gln	Gln	Lys	Asn	Ile	Ser		
	290				295						300						
Thr	Thr	Asp	Ile	Ala	Asn	Tyr	Arg	Asn	Thr	Ile	Asn	Tyr	Glu	Val	Leu		
305					310					315					320		
Cys	Leu	Leu	Ser	Asp	Arg	Ile	Pro	Arg	Ile	Tyr							
				325					330								

<210> SEQ ID NO 207
 <211> LENGTH: 1512
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 207

atgaataaaa	acaaactatt	aagagttgcc	atgctactaa	gtctcttagc	cccgacagca	60
gaaagcatga	cagtgtctggc	tcaagatgta	atgcttgaga	cgcataaagc	aactacaaat	120
gaaaccagtg	attcttcttc	aaaagaggaa	aataataaaa	atgcagcacc	tacaacatca	180
gataaaactg	accaaggtcc	ccttgatgct	tctgcagaaa	caaactctaa	tagtcttggt	240
aacgcggatg	ataaaaaaag	aagcgattct	agtcagtctg	ctataggctc	ttcggacaac	300
aaggcagaag	cagaaaacca	ggtagatgat	aaatcaactg	atcattcgaa	atcaactgat	360
cattcgaaac	caactgacca	gcccaaacca	tcaccatcta	aagttgatac	ggcacctgct	420
tcttcattgt	cgaacaact	gccagaggca	agaactccta	ttcagtcgtt	gtccccttac	480
gtatcagatt	tagatttgag	tgagatagat	atcccttctg	tcaacacata	cgcggcatat	540
gtagagcatt	ggagtggtaa	aaatgcctat	accaccatc	ttttatctcg	ccgttatggg	600
attaaagctg	accagattga	tagttactta	aaatcaacag	gcattgccta	tgacagcaca	660
cgtattaatg	gtgagaagct	attgcaatgg	gaaaagaaaa	gtgggctgga	tgttcgagct	720
atcgtagcta	ttgcgatgtc	tgagagttct	ttaggaactc	aagggattgc	aactttgctt	780
ggagctaata	tgtttggtta	tgagagttct	gatctagatc	cgactcaagc	aagtaagttt	840
aatgatgata	gtgctattgt	caaaatgaca	caagacacca	ttattaaaaa	caaaaatagc	900
aattttgcac	ttcaagattt	aaaagcggct	aagttttcac	gaggtcaatt	aaactttgca	960
agtgcagggg	gtgtttatct	tactgatact	actggtagtg	gtaaacgtcg	cgcacaaatt	1020
atggaagacc	tggataagtg	gattgatgac	catggtggca	caccagccat	tccagccgaa	1080
ttgaaagtg	agtcatcagc	tagttttgca	tctgtgccag	caggttataa	gctctctaag	1140
agttatgatg	tcttgggtta	tcaagcttcg	agttatgctt	ggggacaatg	cacttggtat	1200
gtgtataatc	gcgccaaga	attgggttac	caatttgatc	cttttatggg	aaatggtgga	1260
gattggaagt	ataaagtagg	gtatgccctt	tcaaagactc	caaaagtagg	ttatgctatt	1320
tcatttgcac	cagggcaagc	gggcgctgat	ggcacttatg	gccacgtatc	aattgtagaa	1380
gatgttagaa	aagatgggtc	tattcttatt	tcagagtcta	actgtatcgg	cttaggtaag	1440
atttcttata	gtacctttac	agctcagcag	gctgaacagc	taacatatgt	tattggcaag	1500
agtaaaaaact	aa					1512

<210> SEQ ID NO 208
 <211> LENGTH: 503
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 208

Met	Asn	Lys	Asn	Lys	Leu	Leu	Arg	Val	Ala	Met	Leu	Leu	Ser	Leu	Leu		
1				5					10					15			
Ala	Pro	Thr	Ala	Glu	Ser	Met	Thr	Val	Leu	Ala	Gln	Asp	Val	Met	Leu		
			20					25					30				
Glu	Thr	His	Lys	Ala	Thr	Thr	Asn	Glu	Thr	Ser	Asp	Ser	Ser	Ser	Lys		
		35					40					45					
Glu	Glu	Asn	Asn	Lys	Asn	Ala	Ala	Pro	Thr	Thr	Ser	Asp	Lys	Thr	Asp		
	50					55					60						
Gln	Gly	Pro	Leu	Asp	Ala	Ser	Ala	Glu	Thr	Asn	Ser	Asn	Ser	Leu	Val		
65					70					75					80		
Asn	Ala	Asp	Asp	Lys	Lys	Arg	Ser	Asp	Ser	Ser	Gln	Ser	Ala	Ile	Gly		
				85					90					95			
Ser	Ser	Asp	Asn	Lys	Ala	Glu	Ala	Glu	Asn	Gln	Val	Asp	Asp	Lys	Ser		
			100					105					110				
Thr	Asp	His	Ser	Lys	Ser	Thr	Asp	His	Ser	Lys	Pro	Thr	Asp	Gln	Pro		
		115					120					125					
Lys	Pro	Ser	Pro	Ser	Lys	Val	Asp	Thr	Ala	Pro	Ala	Ser	Ser	Leu	Ser		
	130					135					140						
Lys	Gln	Leu	Pro	Glu	Ala	Arg	Thr	Pro	Ile	Gln	Ser	Leu	Ser	Pro	Tyr		
145					150					155					160		
Val	Ser	Asp	Leu	Asp	Leu	Ser	Glu	Ile	Asp	Ile	Pro	Ser	Val	Asn	Thr		
				165					170					175			
Tyr	Ala	Ala	Tyr	Val	Glu	His	Trp	Ser	Gly	Lys	Asn	Ala	Tyr	Thr	His		
			180					185					190				
His	Leu	Leu	Ser	Arg	Arg	Tyr	Gly	Ile	Lys	Ala	Asp	Gln	Ile	Asp	Ser		
	195						200					205					
Tyr	Leu	Lys	Ser	Thr	Gly	Ile	Ala	Tyr	Asp	Ser	Thr	Arg	Ile	Asn	Gly		
	210					215					220						
Glu	Lys	Leu	Leu	Gln	Trp	Glu	Lys	Lys	Ser	Gly	Leu	Asp	Val	Arg	Ala		
225					230					235					240		
Ile	Val	Ala	Ile	Ala	Met	Ser	Glu	Ser	Ser	Leu	Gly	Thr	Gln	Gly	Ile		
				245					250					255			
Ala	Thr	Leu	Leu	Gly	Ala	Asn	Met	Phe	Gly	Tyr	Ala	Ala	Phe	Asp	Leu		
			260					265					270				
Asp	Pro	Thr	Gln	Ala	Ser	Lys	Phe	Asn	Asp	Asp	Ser	Ala	Ile	Val	Lys		
		275					280					285					
Met	Thr	Gln	Asp	Thr	Ile	Ile	Lys	Asn	Lys	Asn	Ser	Asn	Phe	Ala	Leu		
	290					295					300						
Gln	Asp	Leu	Lys	Ala	Ala	Lys	Phe	Ser	Arg	Gly	Gln	Leu	Asn	Phe	Ala		
305					310					315					320		
Ser	Asp	Gly	Gly	Val	Tyr	Phe	Thr	Asp	Thr	Thr	Gly	Ser	Gly	Lys	Arg		
				325					330					335			
Arg	Ala	Gln	Ile	Met	Glu	Asp	Leu	Asp	Lys	Trp	Ile	Asp	Asp	His	Gly		
			340					345					350				
Gly	Thr	Pro	Ala	Ile	Pro	Ala	Glu	Leu	Lys	Val	Gln	Ser	Ser	Ala	Ser		
		355					360					365					
Phe	Ala	Ser	Val	Pro	Ala	Gly	Tyr	Lys	Leu	Ser	Lys	Ser	Tyr	Asp	Val		
	370					375					380						
Leu	Gly	Tyr	Gln	Ala	Ser	Ser	Tyr	Ala	Trp	Gly	Gln	Cys	Thr	Trp	Tyr		
385					390					395					400		
Val	Tyr	Asn	Arg	Ala	Lys	Glu	Leu	Gly	Tyr	Gln	Phe	Asp	Pro	Phe	Met		
				405					410					415			
Gly	Asn	Gly	Gly	Asp	Trp	Lys	Tyr	Lys	Val	Gly	Tyr	Ala	Leu	Ser	Lys		
			420					425					430				
Thr	Pro	Lys	Val	Gly	Tyr	Ala	Ile	Ser	Phe	Ala	Pro	Gly	Gln	Ala	Gly		
		435					440					445					
Ala	Asp	Gly	Thr	Tyr	Gly	His	Val	Ser	Ile	Val	Glu	Asp	Val	Arg	Lys		

			180					185					190				
Ser	Gln	Lys	Pro	Val	Asp	Thr	Lys	Leu	Gly	Glu	Ser	Gln	Asp	Glu	Ser		
		195					200					205					
His	Thr	Gly	Ala	Met	Ile	Thr	Gln	Asn	Lys	Pro	Lys	Ala	Asn	Ser	Ser		
	210					215					220						
Asn	Asn	Lys	Ser	Leu	Ser	Asp	Lys	Lys	Ile	Leu	Pro	Ser	Lys	Met	Gly		
225				230						235					240		
Leu	Thr	Thr	Ser	Leu	Glu	Leu	Lys	Lys	Glu	Asp	Lys	Phe	Arg	Ser	Lys		
			245						250					255			
Lys	Asp	Leu	Ser	Ile	Met	Ile	Tyr	Tyr	Phe	Pro	Thr	Phe	Phe	Leu	Met		
		260					265						270				
Leu	Gly	Gly	Phe	Ala	Val	Trp	Val	Trp	Lys	Lys	Arg	Lys	Lys	Asn	Asp		
	275						280					285					
Lys	Thr	Met															
	290																

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<210> SEQ ID NO 211
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 211
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ctactggcta aaaaacgttt cagaagtggc ctttatctag ttcttttaat tctcagcctc    120
ctatTTTTTg cggttattgc cttatccctt ggtggtttgg cggtttctta tggggcaatt    180
gtcaagggac tgtttgtggc ttatgacccc caagtggcct tgatttatga tttgcgtttt    240
ccaagaattg tcattgcttt attagcagga gcagggatag ctgtttcggg agttcttttt    300
caagcagtgt tgaaaaatcc tatttcagac cctgctatta tagggatttg tagtggtgct    360
agttttatgg ttttagtctc tagtttactt ctgccgcagt tgctgctgta tgggtccaatc    420
gtatcctttt taggaggcgg agtgtctttc ctgctgattt atggtttagc atggaagaaa    480
gggcttaatc ctattcggct tattctaaca gggattgcta ttaatgcttt atttatgggg    540
ttatcaactg ctttaaccag ctttttcacc tcagctagtc ccatgggtcaa tgctctttta    600
gcaggtcata ttagtcaaaa aacatgggct gatgtagggg ttttattccc ttatacatte    660
attggccttg tactagcttt gttattgtca aaaacttgta accttcttct tttagatgat    720
cagggtgattc gtcatttagg aatcgatgct acagcgttac ggttggaat ttccttggtt    780
gctgttttat tggcttcggg agccacttcg atcgttgagg tggtttcttt cctaggcttg    840
attgtccctc atatgagccg cttgctgggt ggaagtaagc accaaatctt aattcctttt    900
tcagctttgc ttggagcctt tgtctttttg ctagccgata ctttaggaag aagtcttgct    960
taccatttgg aaattagccc tgcgattata atgagtattg taggcgggcc ttactttatt   1020
tacctgctaa ggaggtctga tattatatga                               1050

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<210> SEQ ID NO 212
<211> LENGTH: 349
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 212
Met Thr Thr Trp Glu Ile Ile Arg Asn Met Thr Ala Ser Asp Leu Gln
1          5          10          15
Arg Asp Gln Ser Leu Leu Ala Lys Lys Arg Phe Arg Ser Gly Leu Tyr
20          25          30
Leu Val Leu Leu Ile Leu Ser Leu Leu Phe Leu Ala Val Ile Ala Leu
35          40          45
Ser Leu Gly Gly Leu Ala Val Ser Tyr Gly Ala Ile Val Lys Gly Leu
50          55          60
Phe Val Ala Tyr Asp Pro Gln Val Ala Leu Ile Tyr Asp Leu Arg Phe
65          70          75          80
Pro Arg Ile Val Ile Ala Leu Leu Ala Gly Ala Gly Ile Ala Val Ser
85          90          95

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caaggaaaaa	caagtctagc	tcaactcctc	ttgaaacgcc	agtctgcaac	gactggggcat	1200
attttatttg	acggtttaga	cagtgacaat	ttgtcgcaag	aaactatcaa	ccagcaggtt	1260
ctttatgtat	cggaccaatc	taccttattg	aaccgtagca	tttacgataa	tttaaggtta	1320
gcagcaaadc	tctctaaaaa	agaaatctta	gattggatag	atcaacatgg	tttgtaaagc	1380
ttcatcaact	ggctaccaga	tggctctgac	acaatagtgt	gtgaaaatgg	taacctgtta	1440
tcaccaggcc	aaaagcaaca	ggtgatttgc	gcaagagctc	tattaagtaa	gaggtctctt	1500
tatatctttg	atgaggcaac	atctagtcta	gatgcagaaa	atgaacgtat	tattgacaat	1560
ttaataacga	gattagctaa	gacagcaata	gttattgtga	ttactcataa	gatgtctcga	1620
ctgaaaggag	ctaaccaagt	actcttttta	aacacagggc	agcctgcttg	tttaggcaaa	1680
ccttgcgacc	tttatcggga	ccaaccaact	tatcgtcacc	tagttgatac	tcaagcaaga	1740
ctggaggcaa	gtatttatgg	ctaa				1764

<210> SEQ ID NO 214

<211> LENGTH: 587

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 214

Met	Met	Glu	Thr	Glu	Asp	Thr	Ile	Ser	Arg	Gly	Lys	Arg	Lys	Arg	Leu
1				5					10					15	
Leu	Lys	Arg	Leu	Arg	Glu	Arg	Ile	Ala	Pro	Lys	Arg	Tyr	Leu	Leu	Tyr
			20					25					30		
Val	Ser	Ala	Phe	Leu	Ser	Trp	Leu	Gln	Phe	Val	Met	Arg	Met	Ile	Ser
		35					40				45				
Phe	Tyr	Leu	Ile	Ala	Lys	Thr	Phe	Ser	Thr	Phe	Ile	Leu	Gly	His	Ala
	50					55					60				
Ile	Ala	Leu	Gly	Arg	Leu	Ala	Gly	Leu	Leu	Leu	Leu	Leu	Asn	Val	Val
65					70					75				80	
Gly	Phe	Val	Leu	Ala	Ile	Leu	Gly	Lys	Gln	Leu	Gln	Gly	Ile	Ala	Ser
			85					90					95		
Gln	Phe	Ala	Arg	Asp	Ser	Leu	Lys	Gln	Ser	Phe	Phe	Glu	Ala	Phe	Ile
			100					105					110		
Asp	Leu	Asp	Gly	Gln	Phe	Asp	Ala	His	Ala	Ser	Asp	Ala	Asp	Ile	Leu
		115					120					125			
Thr	Leu	Ala	Ser	Gln	Gly	Ile	Asp	Ser	Leu	Asp	Thr	Tyr	Tyr	Gly	Tyr
	130					135					140				
Tyr	Leu	Ser	Leu	Ser	Met	Arg	Thr	Lys	Trp	Asn	Cys	Thr	Thr	Ile	Met
145					150					155				160	
Ile	Leu	Val	Phe	Leu	Ile	Tyr	Pro	Leu	Ala	Gly	Leu	Val	Phe	Leu	Gly
			165					170						175	
Val	Leu	Pro	Leu	Ile	Pro	Leu	Ser	Ile	Val	Ala	Met	Gln	Lys	Arg	Ser
			180					185					190		
Gln	Pro	Asn	Met	Ser	His	Tyr	Trp	Ser	Ser	Tyr	Met	Asp	Val	Gly	Asn
		195					200					205			
Leu	Phe	Met	Asp	Asp	Leu	Lys	Gly	Leu	Asn	Thr	Leu	Tyr	Ser	Tyr	Gln
	210					215					220				
Ala	Thr	Glu	Arg	Tyr	Glu	Gln	Glu	Phe	Ser	Gly	Lys	Ala	Glu	Gln	Phe
225					230					235				240	
Arg	Lys	Ala	Thr	Met	Ser	Leu	Leu	Gly	Phe	Gln	Leu	Gln	Ala	Val	Gly
			245					250						255	
Tyr	Met	Asp	Ala	Val	Met	Tyr	Leu	Gly	Ile	Gly	Leu	Ser	Gly	Phe	Leu
		260						265					270		
Ala	Val	Gln	Ala	Leu	Ala	Thr	Gly	Gln	Leu	Ser	Phe	Phe	Asn	Phe	Leu
		275					280					285			
Phe	Phe	Leu	Leu	Ile	Ala	Thr	Glu	Phe	Phe	Thr	Pro	Ile	Arg	Glu	Gln
	290					295					300				
Gly	Tyr	Gly	Met	His	Leu	Val	Met	Met	Asn	Thr	Lys	Met	Ala	Asp	Arg
305					310					315				320	

acaaaacaaa	tagatcgttt	aaggagtgtt	tcttttgagg	acctcagttt	tgcttatcca	1080
aagcgccaag	agctggtttt	taaggattta	acagttacct	ttcaagaaaa	ggggattatt	1140
ggcattaaag	gcgaatcagg	atctggtaaa	tcaactttgg	tgaaattaat	tatgaaatgg	1200
tataattgga	agacaggaga	tatttttctt	aatgatagga	atagttgctt	actaaatgct	1260
gctaaattac	aagatactat	tgcttatgtg	ccacaaacag	cgcagctttt	ccaacagtct	1320
atccgtgaaa	atcttatctt	tggccgtcaa	gatatttcag	atgagtccat	ttggaattta	1380
gctgaggctt	gtggtatgaa	agacagactg	ttagcttgta	aggaagggtt	ggatacgatt	1440
atcaagagtc	cttctgactt	ttcagctgga	gaaggtaaac	gtttagagtt	gatgcgagct	1500
ttattgaaa	atgcgagttg	ctatatTTTT	gatgaaccca	cgtcaaattt	agattctcta	1560
aatgaagcta	tcttgcttga	tttaattaaa	acacattgtc	aaggattggg	cttcttaatt	1620
tctcacaggc	catcaaccct	agcttgtgtt	gatcatctat	tttgcgtaaa	aaatgggttc	1680
ctaaaagagg	tgaataaaaa	atga				1704

<210> SEQ ID NO 216

<211> LENGTH: 567

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 216

Met	Ile	Leu	Lys	Gln	Asp	Trp	Arg	Gln	Val	Phe	Met	Ala	Lys	Pro	Asn
1				5					10					15	
Arg	Ser	Thr	Leu	Ser	Leu	Val	Trp	Arg	Leu	Leu	Thr	Leu	Met	Lys	Thr
			20					25					30		
Leu	Leu	Pro	Trp	Ile	Ile	Leu	Ala	Val	Gly	Phe	Ala	Val	Met	Gly	Phe
		35					40					45			
Val	Ile	Thr	Val	Ser	Ile	Pro	Thr	Gly	Ile	Ala	Tyr	Leu	Gly	Leu	Leu
	50				55						60				
Ala	Ile	Arg	Gln	Glu	Val	Ile	Pro	Ile	Leu	Ala	Leu	Tyr	Leu	Leu	Ile
65				70					75					80	
Ala	Leu	Ala	Phe	Leu	Arg	Gly	Phe	Val	Arg	Tyr	Gly	Glu	His	Tyr	Phe
			85					90					95		
Gly	His	Phe	Val	Ala	Phe	His	Ser	Leu	Ala	Ala	Phe	Arg	Asn	Leu	Ile
			100					105					110		
Phe	Lys	Lys	Leu	Arg	Ala	Leu	Ser	Pro	Ala	Cys	Leu	Asp	Ser	Gln	Asp
		115					120					125			
Ser	Gly	Tyr	Leu	Leu	Lys	Met	Ile	Gly	Glu	Asp	Ile	Glu	Ala	Leu	Glu
	130					135					140				
Val	Phe	Phe	Ala	His	Thr	Ile	Ala	Pro	Ile	Cys	Thr	Ala	Ile	Leu	Ser
145					150					155				160	
Ala	Gly	Leu	Met	Phe	Trp	Tyr	Phe	Cys	Gln	Ser	Ser	Trp	Gln	Leu	Ala
			165					170						175	
Leu	Leu	Ala	Leu	Ala	Thr	Tyr	Ala	Cys	Leu	Ala	Ile	Val	Ile	Pro	Ile
			180					185					190		
Tyr	Phe	Ala	Asn	Ile	Leu	Gln	Val	Leu	Leu	Lys	Ser	Gln	Asn	Glu	Gly
			195				200					205			
Arg	Lys	Asp	Tyr	Leu	Ser	Tyr	Phe	Leu	Glu	Ser	Leu	Arg	Ser	Val	Lys
	210					215					220				
Asp	Leu	Leu	Gln	Phe	Gln	Val	Leu	Asp	Glu	Gln	Phe	Glu	Arg	Leu	Ile
225					230					235				240	
Lys	Lys	Ser	Asn	His	Val	Asn	Ala	Leu	Asp	Arg	Asn	Val	Ala	Gln	Ala
			245						250					255	
Gln	Phe	Leu	Gln	Met	Ala	Leu	Thr	Phe	Phe	Trp	Leu	Gly	Leu	Met	Ile
			260					265					270		
Leu	Ala	Phe	Ser	Tyr	Met	Val	Phe	Asp	Gly	Ile	Cys	His	Asp	Ser	Leu
		275					280					285			
Ser	Phe	Asp	Lys	Gly	Leu	Leu	Thr	Phe	Ile	Ala	Phe	Thr	Ala	Ser	Phe
	290					295					300				
Ser	Pro	Phe	Leu	Glu	Leu	Gly	Arg	Leu	Pro	Leu	Gly	Phe	Lys	Arg	Ala

305		310		315		320									
Met	Asn	Ala	Ala	Arg	Asn	Ile	Phe	Asp	Leu	Leu	Asp	Glu	Asn	Val	Ile
				325					330					335	
Val	Asp	Glu	Gly	Thr	Lys	Gln	Ile	Asp	Arg	Leu	Arg	Ser	Val	Ser	Phe
			340					345					350		
Glu	Asp	Leu	Ser	Phe	Ala	Tyr	Pro	Lys	Arg	Gln	Glu	Leu	Val	Phe	Lys
	355						360				365				
Asp	Leu	Thr	Val	Thr	Phe	Gln	Glu	Lys	Gly	Ile	Ile	Gly	Ile	Lys	Gly
	370					375					380				
Glu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Val	Lys	Leu	Ile	Met	Lys	Trp
385					390					395					400
Tyr	Asn	Trp	Lys	Thr	Gly	Asp	Ile	Phe	Leu	Asn	Asp	Arg	Asn	Ser	Cys
			405						410					415	
Leu	Leu	Asn	Ala	Ala	Lys	Leu	Gln	Asp	Thr	Ile	Ala	Tyr	Val	Pro	Gln
		420						425					430		
Thr	Ala	Gln	Leu	Phe	Gln	Gln	Ser	Ile	Arg	Glu	Asn	Leu	Ile	Phe	Gly
	435						440					445			
Arg	Gln	Asp	Ile	Ser	Asp	Glu	Ser	Ile	Trp	Asn	Leu	Ala	Glu	Ala	Cys
	450				455					460					
Gly	Met	Lys	Asp	Arg	Leu	Leu	Ala	Cys	Lys	Glu	Gly	Leu	Asp	Thr	Ile
465				470					475						480
Ile	Lys	Ser	Pro	Ser	Asp	Phe	Ser	Ala	Gly	Glu	Gly	Gln	Arg	Leu	Glu
			485					490					495		
Leu	Met	Arg	Ala	Leu	Leu	Lys	Asp	Ala	Ser	Cys	Tyr	Ile	Phe	Asp	Glu
		500					505					510			
Pro	Thr	Ser	Asn	Leu	Asp	Ser	Leu	Asn	Glu	Ala	Ile	Leu	Leu	Asp	Leu
	515					520						525			
Ile	Lys	Thr	His	Cys	Gln	Gly	Leu	Val	Phe	Leu	Ile	Ser	His	Arg	Pro
	530				535					540					
Ser	Thr	Leu	Ala	Cys	Val	Asp	His	Leu	Phe	Cys	Val	Lys	Asn	Gly	Ser
545				550					555						560
Leu	Lys	Glu	Val	Asn	Lys	Lys									
				565											

<210> SEQ ID NO 217

<211> LENGTH: 777

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 217

ttggtttgta	ggaattgttc	ttgcaggagc	cttattaggg	tcagtttttg	cacattat	60
actaaagaaa	cattttatca	aatcaggatt	gttatcatga	ggcttgatgt	tcgcaccaa	120
ctgcttttgt	tggtagctgc	caatgcctgc	ttcttttttc	gtggtgatgg	cttttttaga	180
tttataattg	ttatttttct	cttattactt	ttgtctgctt	taaataagaa	aaagctagcg	240
ttcaagttgg	cggttgttta	tctgttaatg	atcgggtctat	ctgtaatccc	gctatcgatt	300
ttcccttctt	atcttgacca	cttattgagt	tttgtctcaa	tagcaggaag	gttagttttc	360
ccttctttac	tagcagggtt	aattactatt	aagacaaacta	ccatctacga	attgggttcat	420
ggattacgca	aatggcggtt	cccagaagtc	tggctattga	ccttggccgt	tatgtgccgt	480
ttcataccaa	tgattagaca	agaatgttgt	gttattcatc	gctctttaaa	aatcaggggg	540
attatttttaa	caaaatggtc	tattttgatc	agacctaaac	aatacttgga	gtatttaaatg	600
gttccattgc	ttttatcttt	gataagaagt	agccaagaac	taactatcgc	tagtctaact	660
aaagggctag	cagtcaacaa	aggcaccagt	gaatgcttta	gctcacactt	aacatggaaa	720
gattggggggg	tgcagatttg	gattactgtt	atcataatca	tcacgatact	gcaatga	777

<210> SEQ ID NO 218

<211> LENGTH: 258

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 218

```
Met Val Cys Arg Asn Cys Ser Cys Arg Ser Leu Ile Arg Val Ser Phe
1      5      10      15
Cys Thr Leu Phe Thr Lys Glu Thr Phe Tyr Gln Ile Arg Ile Val Ile
      20      25      30
Met Arg Leu Asp Val Arg Thr Lys Leu Leu Leu Leu Val Leu Ala Asn
      35      40      45
Ala Cys Phe Phe Phe Arg Val Asp Gly Phe Leu Glu Phe Ile Ile Val
      50      55      60
Ile Phe Leu Leu Leu Leu Ser Ala Leu Asn Lys Lys Lys Leu Ala
      65      70      75      80
Phe Lys Leu Ala Val Val Tyr Leu Leu Met Ile Gly Leu Ser Val Ile
      85      90      95
Pro Leu Ser Ile Phe Pro Ser Tyr Leu Asp His Leu Leu Ser Phe Val
      100     105     110
Ser Ile Ala Gly Arg Leu Val Phe Pro Ser Leu Leu Ala Gly Leu Ile
      115     120     125
Thr Ile Lys Thr Thr Thr Ile Tyr Glu Leu Val His Gly Leu Arg Lys
      130     135     140
Trp Arg Phe Pro Glu Val Trp Leu Leu Thr Leu Ala Val Met Cys Arg
      145     150     155     160
Phe Ile Pro Met Ile Arg Gln Glu Cys Cys Val Ile His Arg Ser Leu
      165     170     175
Lys Ile Arg Gly Ile Ile Leu Thr Lys Trp Ser Ile Leu Ile Arg Pro
      180     185     190
Lys Gln Tyr Leu Glu Tyr Leu Met Val Pro Leu Leu Leu Ser Leu Ile
      195     200     205
Arg Ser Ser Gln Glu Leu Thr Ile Ala Ser Leu Thr Lys Gly Leu Ala
      210     215     220
Val Asn Lys Gly Thr Ser Glu Cys Phe Ser Ser His Leu Thr Trp Lys
      225     230     235     240
Asp Trp Gly Val Gln Ile Trp Ile Thr Val Ile Ile Ile Thr Ile
      245     250     255
Leu Gln
```

<210> SEQ ID NO 219

<211> LENGTH: 744

<212> TYPE: DNA

<213> ORGANISM: *Streptococcus pyogenes*

<400> SEQUENCE: 219

```
atgaaatata attcgttaaa ctatttagtg caattgctaa ttgttattgt ttttttagga      60
gggctttacc tctttataaa accagaagag tcagtaacac caactcagtt gaataaaaaa      120
gaaatccaac aaaaagatat caaaaaaacg gaccgtttac gagctttacc taaggatatct      180
gttgaagatt gggagttggt tttagtaaac cgcgatcaca ttacaaaaga aatgagtcct      240
gaattagctg acattaatgg tatttctgtg gataaacgca ttgagcaagc cactagtgac      300
tttttagcag cagcacaagc tatcgacttg caagaacatc ttatctctgg gtaccgttcc      360
gtagactacc aaacagagct ttaccaatct tatattaaaa aagagatggc taacgatcca      420
acattgacac aagaagctgc ggaggctttg gtgcaaacct attcacagcc gccaggggct      480
agtgaacatc aactgggtct tgctattgac atgagcactg tagatacttt aaatgccagt      540
gatccatcag tagctaaaagc agttcaaaaa attgcacctg attatgggtt tgtcttgccg      600
tttccagaag gaaaaaagac tagtacaggg gttgattatg aggattggca ttaccgctat      660
gtaggcaagg cgtctgctcg ttatatggct cagcacaacc taacgttgga agagtacatt      720
gctgctttaa aggagaaacg atga                                     744
```

<210> SEQ ID NO 220

<211> LENGTH: 247

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 220

```
Met Lys Tyr Asn Ser Leu Asn Tyr Leu Val Gln Leu Leu Ile Val Ile
 1           5           10          15
Val Phe Leu Gly Gly Leu Tyr Leu Phe Ile Lys Pro Glu Glu Ser Val
      20           25          30
Thr Pro Thr Gln Leu Asn Lys Lys Glu Ile Gln Gln Lys Asp Ile Lys
      35           40          45
Lys Thr Asp Arg Leu Arg Ala Leu Pro Lys Val Ser Val Glu Asp Trp
      50           55          60
Glu Leu Val Leu Val Asn Arg Asp His Ile Thr Lys Glu Met Ser Pro
      65           70          75          80
Glu Leu Ala Asp Ile Asn Gly Ile Ser Val Asp Lys Arg Ile Glu Gln
      85           90          95
Ala Thr Ser Asp Phe Leu Ala Ala Ala Gln Ala Ile Asp Leu Gln Glu
      100          105          110
His Leu Ile Ser Gly Tyr Arg Ser Val Asp Tyr Gln Thr Glu Leu Tyr
      115          120          125
Gln Ser Tyr Ile Lys Lys Glu Met Ala Asn Asp Pro Thr Leu Thr Gln
      130          135          140
Glu Ala Ala Glu Ala Leu Val Gln Thr Tyr Ser Gln Pro Pro Gly Ala
      145          150          155          160
Ser Glu His His Thr Gly Leu Ala Ile Asp Met Ser Thr Val Asp Thr
      165          170          175
Leu Asn Ala Ser Asp Pro Ser Val Ala Lys Ala Val Gln Lys Ile Ala
      180          185          190
Pro Asp Tyr Gly Phe Val Leu Arg Phe Pro Glu Gly Lys Lys Thr Ser
      195          200          205
Thr Gly Val Asp Tyr Glu Asp Trp His Tyr Arg Tyr Val Gly Lys Ala
      210          215          220
Ser Ala Arg Tyr Met Ala Gln His Asn Leu Thr Leu Glu Glu Tyr Ile
      225          230          235          240
Ala Ala Leu Lys Glu Lys Arg
      245
```

<210> SEQ ID NO 221

<211> LENGTH: 570

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 221

```
atgagaaaac gactaaagtt tccgtatttt ttaacgcttc tagcttgctt tttattgctg      60
attgtttgtc ctttactgag tagccaaagg atagctagtg cagataaaga agtaagggtg      120
aactacagcc aaaaacaatt tattacaaaa atgggtaaaag aagttaaacc attggcaaaa      180
tattatggca ttagaccatc tattttgatt gctcaaattc ttttggaac ccatgatgga      240
aaaacattac tagcgtctaa gtatcataat ctttttagca agaaagcaac tccaggacaa      300
gtggccatta ccctaaagtc ccctaaacaa accaaccaaa acgtgagata tgctatttat      360
aaagatgacg ctagtgcaat tagagattat ttacgaatgc ttcggcaggg aaaagaagtc      420
gataagcggt tgtatcgtaa tcttgctaca gaaaaagggt ataaagcacc agctaaaagt      480
ttacaaaagt atttgcatta tactgataaa acctatgcta ggcgactaat tcaggtcatt      540
gaaagtaacg atttaacaaa ctatgactga
                                         570
```

<210> SEQ ID NO 222

<211> LENGTH: 189

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 222

```
Met Arg Lys Arg Leu Lys Phe Pro Tyr Phe Leu Thr Leu Leu Ala Cys
```

1				5					10					15			
Phe	Leu	Leu	Leu	Ile	Val	Cys	Pro	Leu	Leu	Ser	Ser	Gln	Arg	Ile	Ala		
			20						25					30			
Ser	Ala	Asp	Lys	Glu	Val	Arg	Val	Asn	Tyr	Ser	Gln	Lys	Gln	Phe	Ile		
		35					40					45					
Thr	Lys	Met	Gly	Lys	Glu	Val	Lys	Pro	Leu	Ala	Lys	Tyr	Tyr	Gly	Ile		
	50					55					60						
Arg	Pro	Ser	Ile	Leu	Ile	Ala	Gln	Ile	Leu	Leu	Glu	Thr	His	Asp	Gly		
65					70					75					80		
Lys	Thr	Leu	Leu	Ala	Ser	Lys	Tyr	His	Asn	Leu	Phe	Ser	Lys	Lys	Ala		
			85						90					95			
Thr	Pro	Gly	Gln	Val	Ala	Ile	Thr	Leu	Lys	Ser	Pro	Lys	Gln	Thr	Asn		
		100						105					110				
Gln	Asn	Val	Arg	Tyr	Ala	Ile	Tyr	Lys	Asp	Asp	Ala	Ser	Ala	Ile	Arg		
		115					120				125						
Asp	Tyr	Leu	Arg	Met	Leu	Arg	Gln	Gly	Lys	Glu	Val	Asp	Lys	Arg	Leu		
	130				135					140							
Tyr	Arg	Asn	Leu	Ala	Thr	Glu	Lys	Gly	Tyr	Lys	Ala	Pro	Ala	Lys	Ser		
145					150					155					160		
Leu	Gln	Lys	Tyr	Leu	His	Tyr	Thr	Asp	Lys	Thr	Tyr	Ala	Arg	Arg	Leu		
			165					170						175			
Ile	Gln	Val	Ile	Glu	Ser	Asn	Asp	Leu	Thr	Asn	Tyr	Asp					
		180						185									

<210> SEQ ID NO 223

<211> LENGTH: 912

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 223

atgactgaac	aaattaaatt	aactaaatca	gaccgtcaac	gtgtttggtg	gcgttcacaa	60
ttcttacaag	gttcttgga	ctacgaacgt	atgcaaaaaca	tgggctgggc	ttatgcactt	120
atccctgctc	ttaaaaaatt	gtatacgtct	cctgaagacc	gtgcagctgc	tcttgagcgc	180
cacatggaat	tctttaacac	tcacccatac	gttgagctc	caatcattgg	tgtaacactt	240
gcccttgaag	aagaacgcgc	aaatggtacg	ccaattgatg	acaaggctat	ccaaggggtt	300
aaaatcggtg	tgatgggacc	tcttgctggt	atcggtgacc	cagtattctg	gtttacgatt	360
cgctctatcc	ttggggcact	tggtgcttct	ttggcttcaa	caggtaacat	cgttggtcca	420
cttctgttct	tctttggatg	gaaccttatc	cgtatggcct	tcttatggta	tactcaagaa	480
tttggttaca	aagctgggtc	tgaaattact	aaagacatgt	caggcggtat	cctccaagac	540
attactaaag	gtgcttcaat	ccttggaatg	tttatccttg	cagtgccttg	tcaacgttgg	600
gtatctatca	actttactat	cgaccttcct	ggaaaaacaat	tgtcagatgg	tgcttatgtg	660
gtcttcccag	atggcgctgt	taaagggtgct	gaattgaaaa	ctatccttgc	caacgctatt	720
ggtggtatga	gccttgataa	agtccaagct	caaacccttc	aaggacaatt	ggactctctt	780
atcccagggt	tagctggatt	actccttaca	ttcctttgca	tgtggttatt	gaagaaaaaa	840
gtttctccaa	tcgcaatcat	catcggtctg	tttgcatctg	gtatccttgc	tcaccttgca	900
ggtattatgt	aa					912

<210> SEQ ID NO 224

<211> LENGTH: 303

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 224

Met	Thr	Glu	Gln	Ile	Lys	Leu	Thr	Lys	Ser	Asp	Arg	Gln	Arg	Val	Trp
1				5					10					15	
Trp	Arg	Ser	Gln	Phe	Leu	Gln	Gly	Ser	Trp	Asn	Tyr	Glu	Arg	Met	Gln
		20						25				30			
Asn	Met	Gly	Trp	Ala	Tyr	Ala	Leu	Ile	Pro	Ala	Leu	Lys	Lys	Leu	Tyr
		35					40					45			

<400> SEQUENCE: 226

```

Met Ser Asp Ile Ser Ile Ile Ser Ala Ile Leu Val Val Ile Ile Ala
1           5           10          15
Phe Phe Ala Gly Leu Glu Gly Ile Leu Asp Gln Phe Gln Met His Gln
20          25          30
Pro Leu Val Ala Cys Thr Leu Ile Gly Leu Val Thr Gly His Leu Glu
35          40          45
Ala Gly Val Ile Leu Gly Gly Thr Leu Gln Met Leu Ala Leu Gly Trp
50          55          60
Ala Asn Ile Gly Ala Ala Val Ala Pro Asp Ala Ala Leu Ala Ser Val
65          70          75          80
Ala Ala Ala Ile Ile Met Val Lys Ser Gly Asp Phe Thr Gln Lys Gly
85          90          95
Ile Thr Phe Ala Tyr Ser Thr Ala Ile Pro Leu Ala Val Ala Gly Leu
100         105         110
Phe Leu Thr Met Ile Val Arg Thr Leu Ser Thr Ala Leu Val His Ala
115         120         125
Gly Asp Lys Ala Ala Ala Glu Gly Asn Phe Ala Gly Ile Glu Arg Phe
130         135         140
His Phe Ile Ala Leu Leu Leu Gln Gly Leu Arg Ile Ala Val Pro Ala
145         150         155         160
Ala Leu Leu Val Ala Val Pro Thr Ser Ala Val Gln Ser Val Leu Asn
165         170         175
Ala Met Pro Asn Trp Leu Asn Glu Gly Met Gln Ile Gly Gly Ala Met
180         185         190
Val Val Ala Val Gly Tyr Ala Met Val Ile Asn Met Met Ala Thr Arg
195         200         205
Glu Val Trp Pro Phe Phe Ala Leu Gly Phe Ala Leu Ala Ala Ile Ser
210         215         220
Gln Leu Thr Leu Ile Ala Met Gly Val Ile Gly Val Ala Ile Ala Phe
225         230         235         240
Ile Tyr Leu Asn Leu Ser Lys Lys Gly Gly Asn Gly Gly Asn Ala Ala
245         250         255
Gly Ser Ala Asp Pro Ile Gly Asp Ile Leu Glu Asp Tyr
260         265

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<210> SEQ ID NO 227

<211> LENGTH: 1461

<212> TYPE: DNA

<213> ORGANISM: *Streptococcus pyogenes*

<400> SEQUENCE: 227

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atggaaaagt tttttaagtt aagcgaaaat gggacaactg tctcaactga gattatggct      60
ggtttaacga ctttttttgc catgtcctat attttgtttg ttaacccaag tatttttaggt      120
gcagcgggga tgccctctaa tgctgtcttt ttggctacga ttatcgcagc agccatatca      180
accttaatta tgggactatt tgccaatgtg ccttatgcgt tggcaccagg aatgggactt      240
aacgcttttt tcactttatac agttgttttt gctttaaggt tttcatggca agaagccttg      300
gcaatgggtt tcattttgtgg attattcaat atttttatta ccgtaaccaa gtttcgtaaa      360
agtatcatca aggcgattcc agttagttta cagcatgcta ttggtggggg aattggtgtc      420
ttttagtctt atttaggatt taaaaacgca aatatcatta ctttttctat ctctgctgaa      480
aatatagtaa tggtaaattg tgttgaaccg gctaaagcat cggctaaaac atttgcagat      540
ggtctattat ttgtagacgc caatggtgga gttgtacctt cgatttctag ttttacggat      600
tccggtgtat tacttgctat ttttggttta cttttgacga cagctcttgt gattcgaaat      660
tttagagggt ctattttaat tggattgtgc gcaacaactc ttgtaggtgt tccttttagga      720
atagtggatg tgtccaacct caattttggg atcagccata ttggtgaagc ttggactgaa      780
ttaggtacaa ctttccttgc agctttcgat ggtttgagtt ctctttttag cgattcaagt      840
cgtttaccgc tagttttcat gactattttt gcttttagtc tatcagatac ttttgacaca      900
attggtacct ttatcggaac tggtcgtcga acaggatatt tctctcaaga cgatgagaat      960

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gctttggaaa	atagtatagg	ctttagttca	aaaatggacc	gtgcgctttt	tgcagatgct	1020
atcggtagctt	ctattggggc	tttggttgga	acttcaaata	cgactaccta	tgttgaatca	1080
gcagcaggaa	ttgctgaagg	tggacgtact	ggactaacag	cagtctccac	cgcagtatgc	1140
ttcttattat	caatattgct	attaccgctt	gtaggtattg	tcccagctgc	tgctacggct	1200
ccagctttaa	ttattgtggg	tgtcatgatg	gtgtcttctt	ttcttgatgt	taattggagt	1260
aaatttgcag	atgctcttcc	agcttttttt	gcagctttct	ttatggcgct	gtgttactct	1320
atttcctatg	gtattgccgc	tgcctttatt	ttctattgtc	tagtaaaagt	tgttgaggga	1380
aaaacaaaag	atattcaccc	tattatttgg	ggagcaacct	tcttgttcat	tgtaaatttc	1440
atcatattaa	ctatcttata	a				1461

<210> SEQ ID NO 228
 <211> LENGTH: 486
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 228

Met	Glu	Lys	Phe	Phe	Lys	Leu	Ser	Glu	Asn	Gly	Thr	Thr	Val	Ser	Thr
1				5					10					15	
Glu	Ile	Met	Ala	Gly	Leu	Thr	Thr	Phe	Phe	Ala	Met	Ser	Tyr	Ile	Leu
			20					25					30		
Phe	Val	Asn	Pro	Ser	Ile	Leu	Gly	Ala	Ala	Gly	Met	Pro	Ser	Asn	Ala
		35				40					45				
Val	Phe	Leu	Ala	Thr	Ile	Ile	Ala	Ala	Ala	Ile	Ser	Thr	Leu	Ile	Met
	50				55					60					
Gly	Leu	Phe	Ala	Asn	Val	Pro	Tyr	Ala	Leu	Ala	Pro	Gly	Met	Gly	Leu
65				70				75						80	
Asn	Ala	Phe	Phe	Thr	Tyr	Thr	Val	Val	Phe	Ala	Leu	Arg	Phe	Ser	Trp
			85					90					95		
Gln	Glu	Ala	Leu	Ala	Met	Val	Phe	Ile	Cys	Gly	Leu	Phe	Asn	Ile	Phe
		100						105					110		
Ile	Thr	Val	Thr	Lys	Phe	Arg	Lys	Ser	Ile	Ile	Lys	Ala	Ile	Pro	Val
	115					120					125				
Ser	Leu	Gln	His	Ala	Ile	Gly	Gly	Gly	Ile	Gly	Val	Phe	Val	Ala	Tyr
	130				135						140				
Leu	Gly	Phe	Lys	Asn	Ala	Asn	Ile	Ile	Thr	Phe	Ser	Ile	Ser	Ala	Glu
145				150					155					160	
Asn	Ile	Val	Met	Val	Asn	Gly	Val	Glu	Pro	Ala	Lys	Ala	Ser	Ala	Lys
			165					170					175		
Thr	Phe	Ala	Asp	Gly	Leu	Leu	Phe	Val	Asp	Ala	Asn	Gly	Gly	Val	Val
		180						185				190			
Pro	Thr	Ile	Ser	Ser	Phe	Thr	Asp	Ser	Gly	Val	Leu	Leu	Ala	Ile	Phe
	195					200						205			
Gly	Leu	Leu	Leu	Thr	Thr	Ala	Leu	Val	Ile	Arg	Asn	Phe	Arg	Gly	Ala
	210				215					220					
Ile	Leu	Ile	Gly	Ile	Val	Ala	Thr	Thr	Leu	Val	Gly	Val	Pro	Leu	Gly
225				230					235					240	
Ile	Val	Asp	Val	Ser	Asn	Leu	Asn	Phe	Gly	Ile	Ser	His	Ile	Gly	Glu
		245						250				255			
Ala	Trp	Thr	Glu	Leu	Gly	Thr	Thr	Phe	Leu	Ala	Ala	Phe	Asp	Gly	Leu
		260						265				270			
Ser	Ser	Leu	Phe	Ser	Asp	Ser	Ser	Arg	Leu	Pro	Leu	Val	Phe	Met	Thr
	275					280						285			
Ile	Phe	Ala	Phe	Ser	Leu	Ser	Asp	Thr	Phe	Asp	Thr	Ile	Gly	Thr	Phe
	290					295					300				
Ile	Gly	Thr	Gly	Arg	Arg	Thr	Gly	Ile	Phe	Ser	Gln	Asp	Asp	Glu	Asn
305				310						315				320	
Ala	Leu	Glu	Asn	Ser	Ile	Gly	Phe	Ser	Ser	Lys	Met	Asp	Arg	Ala	Leu
			325					330						335	

50		55		60
Ile	Pro	Leu	Leu	Leu
65		70		75
Ala	Asp	Gln	His	Phe
		85		90
Ile	Lys	Gln	Ala	Glu
		100		105
Thr	Ala	Val	Leu	Leu
		115		120
Ser	Leu	Phe	Ile	Phe
		130		135
Arg	Val	Val	Leu	Ser
145		150		155
Leu	Asp	Trp	Ala	Lys
		165		170
Ile	Leu	Lys	Phe	Tyr
		180		185
Lys	Val	Lys	Glu	Arg
		195		200
Gln	Thr	Pro	Ser	Asn
		210		215
Arg	Ser	Ser	Asp	Tyr
225		230		235
Ser	Leu	Ser	Val	Phe
		245		250
Ala	Leu	Ile	Phe	Asn
		260		265
Tyr	His	Tyr	Asp	Tyr
		275		280
Arg	Ser	Lys	Lys	Lys
		290		295
Leu	Met	Leu	Ile	Val
305		310		315
Leu	Ile	Leu	Ile	Val
		325		330
Tyr	Lys	Leu	Lys	Lys
		340		

<210> SEQ ID NO 231

<211> LENGTH: 987

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 231

ttgaaacatc	ctattcgaaa	aacacttgct	accttaggtc	tattactgac	cttatgcctg	60
ccgactccag	ttgcagctag	ttctcgttct	tggaagagct	ggtttatcga	gcaatatttc	120
tggttaaaac	gtgacaagag	ttactattct	aaacaagatg	acccaagctt	ccaaagatac	180
cttgatgcct	gtcgtgaaca	atctgataaa	ccttatcaac	tagatactaa	tttagtcaat	240
gggtcccttg	ttcaagaaaa	tctttatggc	atgcagggtt	actcttggaa	tgataatgga	300
aaacctgac	aaaaaacaat	tatttatctt	gccgggtggt	cttatcttaa	caatccaacg	360
acataccata	ttaatatggt	aaagacatta	tccacaagtc	ttgacgctaa	aattgtttta	420
cccattttat	ctaaagcccc	acgttatacc	tataactata	ctatgccaaa	attgggtcaat	480
ctttaccaac	actattacca	taaaaatcag	aatgttttcc	ttatgggaga	ttcagcaggt	540
ggagggttag	ccttaggtct	agctcatgcc	ctacacaatg	aatcagtccc	tcaaccaaag	600
cagctcgttc	ttttatcacc	ttggtttagat	gttactatgt	cacaccaga	gattccagaa	660
tacgaagatg	ctgatcctat	tctatcttct	tggggattaa	aacgagtggg	agaattgtgg	720
gcctactctg	ctgataatac	caaccatatt	tatgtcagtc	ctaaaaatgg	tccgatcact	780
tatctaccac	caattacttt	atttactggg	acacgagaga	tcttttatcc	tgatattcgc	840

gattatgccg caaaactgaa agccgctaac cacaatatta cctttattac ccaagaaggc	900
atgaaccacg tttaaccaat ttatcctatc gaagaggcaa aaacagctca ataccaaadc	960
attgatgccca tcaacaaaac tccttaa	987

<210> SEQ ID NO 232
 <211> LENGTH: 328
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 232

Met	Lys	His	Pro	Ile	Arg	Lys	Thr	Leu	Val	Thr	Leu	Gly	Leu	Leu	Leu
1				5					10					15	
Thr	Leu	Cys	Leu	Pro	Thr	Pro	Val	Ala	Ala	Ser	Ser	Arg	Ser	Trp	Lys
			20					25					30		
Ser	Trp	Phe	Ile	Glu	Gln	Tyr	Phe	Trp	Leu	Lys	Arg	Asp	Lys	Ser	Tyr
		35					40					45			
Tyr	Ser	Lys	Gln	Asp	Asp	Pro	Ser	Phe	Gln	Arg	Tyr	Leu	Asp	Ala	Cys
	50					55					60				
Arg	Glu	Gln	Ser	Asp	Lys	Pro	Tyr	Gln	Leu	Asp	Thr	Asn	Leu	Val	Asn
65					70					75					80
Gly	Pro	Leu	Val	Gln	Glu	Asn	Leu	Tyr	Gly	Met	Gln	Val	Tyr	Ser	Trp
				85					90					95	
Asn	Asp	Asn	Gly	Lys	Pro	Asp	Gln	Lys	Thr	Ile	Ile	Tyr	Leu	Ala	Gly
			100					105					110		
Gly	Ser	Tyr	Leu	Asn	Asn	Pro	Thr	Thr	Tyr	His	Ile	Asn	Met	Leu	Lys
		115					120					125			
Thr	Leu	Ser	Thr	Ser	Leu	Asp	Ala	Lys	Ile	Val	Leu	Pro	Ile	Tyr	Pro
	130					135						140			
Lys	Ala	Pro	Arg	Tyr	Thr	Tyr	Asn	Tyr	Thr	Met	Pro	Lys	Leu	Val	Asn
145					150					155					160
Leu	Tyr	Gln	His	Tyr	Tyr	His	Lys	Asn	Gln	Asn	Val	Phe	Leu	Met	Gly
				165					170					175	
Asp	Ser	Ala	Gly	Gly	Gly	Leu	Ala	Leu	Gly	Leu	Ala	His	Ala	Leu	His
			180					185					190		
Asn	Glu	Ser	Val	Pro	Gln	Pro	Lys	Gln	Leu	Val	Leu	Leu	Ser	Pro	Trp
		195					200					205			
Leu	Asp	Val	Thr	Met	Ser	His	Pro	Glu	Ile	Pro	Glu	Tyr	Glu	Asp	Ala
	210					215					220				
Asp	Pro	Ile	Leu	Ser	Ser	Trp	Gly	Leu	Lys	Arg	Val	Gly	Glu	Leu	Trp
225					230					235					240
Ala	Tyr	Ser	Ala	Asp	Asn	Thr	Asn	His	Ile	Tyr	Val	Ser	Pro	Lys	Asn
				245					250					255	
Gly	Pro	Ile	Thr	Tyr	Leu	Pro	Pro	Ile	Thr	Leu	Phe	Thr	Gly	Thr	Arg
			260					265					270		
Glu	Ile	Phe	Tyr	Pro	Asp	Ile	Arg	Asp	Tyr	Ala	Ala	Lys	Leu	Lys	Ala
		275				280						285			
Ala	Asn	His	Asn	Ile	Thr	Phe	Ile	Thr	Gln	Glu	Gly	Met	Asn	His	Val
	290					295					300				
Tyr	Pro	Ile	Tyr	Pro	Ile	Glu	Glu	Ala	Lys	Thr	Ala	Gln	Tyr	Gln	Ile
305					310					315					320
Ile	Asp	Ala	Ile	Asn	Lys	Thr	Pro								
				325											

<210> SEQ ID NO 233
 <211> LENGTH: 1452
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 233

```

atgatgcaac cttttttaga cattattaac aagattctgg gatttcctat tcagttggga      60
tcaggtgtgg tcatgctgat tgtcatgaca ggtttagcca tgattttcgg ggtaaattc      120
acaaaggcac tggaagggtgg gattaagtta gccatcgctt tgacagggat tggagccatt      180
attggaattt tgacggggggc tttttcagag tctttacagg cctttgttaa aaatacaggg      240
atcagtttaa acattattga tgtcggttgg gcaccgcttg caacaattac ctgggggttcc      300
ccttacaccc tttatttctt gctggtgatg ctggtgggta atattgtcat gattgtcatg      360
aaaaaacgg acacccttga cgtcgatatt tttgatattt ggcatttgtc cattacgggt      420
ctattgatta tgtggtatgc ggctcgtaac catttaccag tctttgtgtc tcttttgatt      480
gctactgtgg cagttattct tgttggggta ctgaaaatca ttaactctga tttgatgaaa      540
ccgaccttgg atgaccttct tgggacaggg cctcaatcac caatgacttc aactcacatg      600
aactacatga tgaatccaat cattatgggtc ttagataaga tttttgacaa ggtctttccg      660
gggctggata aatatgactt tgatgctgct aaattgaaca aaaaaattgg cttctggggc      720
tctaagttct ttatcggaat ggctctagggt tttgtgattg ggattatggg agatcctcat      780
ttcactgttg aatctatcaa aaattgggtt ggcttaggct ttaccgcggtg tgcctgcttg      840
gaacttttct ctttgattgg ctcttggttt atcgcgctgt ttgagccttt gtcacaaggg      900
attaccaatt ttgccaatgc tagaatgcat gggcgctcgtt tcaatatcgg tttggactgg      960
cccttcattg ctggtcgtgc tgaaatctgg gcctgtgccca atattcttgc cccaatcatg     1020
ttgattgaag ccgttctcct atcaaaagtt ggcaatggga ttttaccact ggcaggaatt     1080
attgctatgg ggatgacacc agctcttctt gtggtcacac gtggtcgttt gattcgcatg     1140
attatttttg gttccctctt attgccatta ttcctcttgt caggaactat gattgctcca     1200
tttgcgacag agttggctaa aaaagtaggg gcttttccag caggtacaag cgctggttcc     1260
ttgattacgc attcaacact tgaaggacca atggaaaaaa tttttgggta tgtgattggg     1320
caagcgacaa caggtcagat tgcctcaatc atcacgctaa tcattcttgt ggccatttac     1380
ctaagtctct ttgcttggtg tgctaaccac atgaaggcac gtaacgctga atatgcgaaa     1440
acaatgaaat aa                                     1452

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<210> SEQ ID NO 234

<211> LENGTH: 483

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 234

```

Met Met Gln Pro Phe Leu Asp Ile Ile Asn Lys Ile Leu Gly Phe Pro
1          5          10          15
Ile Gln Leu Gly Ser Gly Val Val Met Leu Ile Val Met Thr Gly Leu
          20          25          30
Ala Met Ile Phe Gly Val Lys Phe Thr Lys Ala Leu Glu Gly Gly Ile
          35          40          45
Lys Leu Ala Ile Ala Leu Thr Gly Ile Gly Ala Ile Ile Gly Ile Leu
          50          55          60
Thr Gly Ala Phe Ser Glu Ser Leu Gln Ala Phe Val Lys Asn Thr Gly
65          70          75          80
Ile Ser Leu Asn Ile Ile Asp Val Gly Trp Ala Pro Leu Ala Thr Ile
          85          90          95
Thr Trp Gly Ser Pro Tyr Thr Leu Tyr Phe Leu Leu Val Met Leu Val
          100         105         110
Val Asn Ile Val Met Ile Val Met Lys Lys Thr Asp Thr Leu Asp Val
          115         120         125
Asp Ile Phe Asp Ile Trp His Leu Ser Ile Thr Gly Leu Leu Ile Met
          130         135         140
Trp Tyr Ala Ala Arg Asn His Leu Pro Val Phe Val Ser Leu Leu Ile
145         150         155         160
Ala Thr Val Ala Val Ile Leu Val Gly Val Leu Lys Ile Ile Asn Ser
          165         170         175
Asp Leu Met Lys Pro Thr Phe Asp Asp Leu Leu Gly Thr Gly Pro Gln
          180         185         190
Ser Pro Met Thr Ser Thr His Met Asn Tyr Met Met Asn Pro Ile Ile
          195         200         205

```

Met	Val	Leu	Asp	Lys	Ile	Phe	Asp	Lys	Val	Phe	Pro	Gly	Leu	Asp	Lys
210						215					220				
Tyr	Asp	Phe	Asp	Ala	Ala	Lys	Leu	Asn	Lys	Lys	Ile	Gly	Phe	Trp	Gly
225				230						235					240
Ser	Lys	Phe	Phe	Ile	Gly	Met	Ala	Leu	Gly	Phe	Val	Ile	Gly	Ile	Met
				245					250					255	
Gly	Asp	Pro	His	Phe	Thr	Val	Glu	Ser	Ile	Lys	Asn	Trp	Phe	Gly	Leu
			260					265					270		
Gly	Phe	Thr	Ala	Gly	Ala	Cys	Leu	Glu	Leu	Phe	Ser	Leu	Ile	Gly	Ser
		275					280					285			
Trp	Phe	Ile	Ala	Ala	Val	Glu	Pro	Leu	Ser	Gln	Gly	Ile	Thr	Asn	Phe
290						295					300				
Ala	Asn	Ala	Arg	Met	His	Gly	Arg	Arg	Phe	Asn	Ile	Gly	Leu	Asp	Trp
305				310						315					320
Pro	Phe	Ile	Ala	Gly	Arg	Ala	Glu	Ile	Trp	Ala	Cys	Ala	Asn	Ile	Leu
				325					330					335	
Ala	Pro	Ile	Met	Leu	Ile	Glu	Ala	Val	Leu	Leu	Ser	Lys	Val	Gly	Asn
			340					345					350		
Gly	Ile	Leu	Pro	Leu	Ala	Gly	Ile	Ile	Ala	Met	Gly	Met	Thr	Pro	Ala
		355				360					365				
Leu	Leu	Val	Val	Thr	Arg	Gly	Arg	Leu	Ile	Arg	Met	Ile	Ile	Phe	Gly
370						375					380				
Ser	Leu	Leu	Leu	Pro	Leu	Phe	Leu	Leu	Ser	Gly	Thr	Met	Ile	Ala	Pro
385				390						395					400
Phe	Ala	Thr	Glu	Leu	Ala	Lys	Lys	Val	Gly	Ala	Phe	Pro	Ala	Gly	Thr
				405					410					415	
Ser	Ala	Gly	Ser	Leu	Ile	Thr	His	Ser	Thr	Leu	Glu	Gly	Pro	Met	Glu
			420					425					430		
Lys	Ile	Phe	Gly	Tyr	Val	Ile	Gly	Gln	Ala	Thr	Thr	Gly	Gln	Ile	Ala
		435					440					445			
Ser	Ile	Ile	Thr	Leu	Ile	Ile	Phe	Val	Ala	Ile	Tyr	Leu	Ser	Leu	Phe
450						455					460				
Ala	Trp	Tyr	Ala	Asn	Gln	Met	Lys	Ala	Arg	Asn	Ala	Glu	Tyr	Ala	Lys
465				470						475					480
Thr	Met	Lys													

<210> SEQ ID NO 235

<211> LENGTH: 723

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 235

atggctacga	tgaacaata	tcataaagga	gattccatga	ctaaatcaca	aaaagaggcg	60
ctttattgga	tgttgagtgt	tctaactatc	actctaatag	gtggctcctg	ccttattttt	120
ggatccccacc	ctcaaacgca	agataaggta	gctaaacatt	ctaaaagtgc	tgctagttta	180
ctaaaaaaag	cagttaaagc	agttaatgac	gctgatcggt	tagccactgc	agctgctatc	240
caagaagccc	agaaagctgt	tgataaatta	gcagaatctt	ctaagaaaaa	aacgctacaa	300
gaacagctaa	acgttgccaa	agcaaagcaa	gagcaagaag	atgcagctac	tcaagcagtt	360
aaagctgctg	aggagactct	caatcaaaat	cttaaagata	tcgccccaaa	agcagttaac	420
gacttaagta	acaaaggtaa	aaaagccgct	ttacaatctc	ggttagacgc	tattttacca	480
gcgaaaccca	ttattgatga	atttccaaga	caaagtggag	aaataacaga	taactcttac	540
tggacacctt	tcccaggaga	cgtctcagat	acttatgata	attcccagtc	acctacttta	600
gacccaagct	cagaatcttc	agcttcagat	gttacaccac	aacctagtca	tcctgatcca	660
attccacctc	agacctcttc	agaaccttcc	gactcaggag	acaagcaatc	atcaaaagag	720
taa						723

<210> SEQ ID NO 236

<211> LENGTH: 240

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 236

```
Met Ala Thr Met Lys Gln Tyr His Lys Gly Asp Ser Met Thr Lys Ser
1      5      10      15
Gln Lys Glu Ala Leu Tyr Trp Met Leu Ser Val Leu Thr Ile Thr Leu
20      25      30
Ile Gly Gly Ser Cys Leu Ile Phe Gly Ser His Pro Gln Thr Gln Asp
35      40      45
Lys Val Ala Lys His Ser Lys Ser Ala Ala Ser Leu Leu Lys Lys Ala
50      55      60
Val Lys Ala Val Asn Asp Ala Asp Arg Leu Ala Thr Ala Ala Ile
65      70      75      80
Gln Glu Ala Gln Lys Ala Val Asp Lys Leu Ala Glu Ser Ser Lys Lys
85      90      95
Lys Thr Leu Gln Glu Gln Leu Asn Val Ala Lys Ala Lys Gln Glu Gln
100     105     110
Glu Asp Ala Ala Thr Gln Ala Val Lys Ala Ala Glu Glu Thr Leu Asn
115     120     125
Gln Asn Leu Lys Asp Ile Ala Gln Lys Ala Val Asn Asp Leu Ser Asn
130     135     140
Lys Gly Lys Lys Ala Ala Leu Gln Ser Arg Leu Asp Ala Ile Leu Pro
145     150     155     160
Ala Lys Pro Ile Ile Asp Glu Phe Pro Arg Gln Ser Gly Glu Ile Thr
165     170     175
Asp Asn Ser Tyr Trp Thr Pro Phe Pro Gly Asp Val Ser Asp Thr Tyr
180     185     190
Asp Asn Ser Gln Ser Pro Thr Leu Asp Pro Ser Ser Glu Ser Ser Ala
195     200     205
Ser Asp Val Thr Pro Gln Pro Ser His Pro Asp Pro Ile Pro Pro Gln
210     215     220
Thr Ser Ser Glu Pro Ser Asp Ser Gly Asp Lys Gln Ser Ser Lys Glu
225     230     235     240
```

<210> SEQ ID NO 237

<211> LENGTH: 555

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 237

```
ttgaaaataa ggagccgtat tgtgaccatc tttttagtga tgtagctat gtttactatt      60
cgtttagtat ttttgaagaa atcgataaca aatgaaaaag ccatattagc ccaaggagga      120
caggaatttg gtgctcagaa cacgaaattt ttgacgttac ttcacattat gatttatgtg      180
tttgcggtga ttgaagcgct gcttaaacaa attaagtttg atggcattag ttttttaggt      240
cttttgttga tgttattatc agtagctgtt ttatatgaag tgacacgtat cttaggtgac      300
atttggaactg taaaattgat gttagcaaaa gaccacaaat atgtggatca ctggttggtc      360
aaaacgatta aacatcctaa ctacttttta aatatcgccc ctgagctggt gggcatagcc      420
ttactttgcc atgctaaaat tacggctatg cttcttttcc catgctacat tgtagtaata      480
tatttacgta ttcgagaaga aaacaagcta ttagcggaag tgattattcc aaacggtact      540
cgaacaaaac cttaa                                     555
```

<210> SEQ ID NO 238

<211> LENGTH: 184

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 238

```
Met Lys Ile Arg Ser Arg Ile Val Thr Ile Phe Leu Val Met Leu Ala
1      5      10      15
```



```

Met Phe Thr Ile Arg Leu Val Phe Leu Lys Lys Ser Ile Thr Asn Glu
    20                25                30
Lys Ala Ile Leu Ala Gln Gly Gly Gln Glu Phe Gly Ala Gln Asn Thr
    35                40                45
Lys Phe Leu Thr Leu Leu His Ile Met Ile Tyr Val Phe Ala Val Ile
    50                55                60
Glu Ala Leu Leu Lys Gln Ile Lys Phe Asp Gly Ile Ser Phe Leu Gly
    65                70                75                80
Leu Leu Leu Met Leu Leu Ser Val Ala Val Leu Tyr Glu Val Thr Arg
    85                90                95
Ile Leu Gly Asp Ile Trp Thr Val Lys Leu Met Leu Ala Lys Asp His
   100                105                110
Lys Tyr Val Asp His Trp Leu Phe Lys Thr Ile Lys His Pro Asn Tyr
   115                120                125
Phe Leu Asn Ile Ala Pro Glu Leu Val Gly Ile Ala Leu Leu Cys His
   130                135                140
Ala Lys Ile Thr Ala Met Leu Leu Phe Pro Cys Tyr Ile Val Val Ile
   145                150                155                160
Tyr Leu Arg Ile Arg Glu Glu Asn Lys Leu Leu Ala Glu Val Ile Ile
   165                170                175
Pro Asn Gly Thr Arg Thr Lys Pro
   180

```

<210> SEQ ID NO 239

<211> LENGTH: 702

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 239

```

atggatatct ttggcgaaatt tttgggtaca gccttattgg ttttactagg aaatgggtgtg      60
gtagcagggg ttgtcttgcc caaaacgaaa acccatgctt ctggctggat cgtgattgcg      120
actggctggg gaattgcagt tgctgtggca gtctttatca gtggcaaagt tgcccctgcc      180
cacctcaatc cagctgttag ccttgctttt gccatgagtg gaaccattgc ctggtcaaca      240
gccattgcct atagccttgc ccaactattg ggagctatgg ttggttcaac tctggtattc      300
cttcagttca ggccacatta tctggctgct gagagtcagg ctgatatttt agggacattt      360
gcgacaggtc ctgctattcg agatactagc tcaaacctat tgagtgaat ctttgggacc      420
tttgtcttga tgcttggtat tttggcattt ggcttatatg atatgccagc aggactagga      480
accctctgtg taggtacctt ggttattggg attgggttat ccttaggagg aacgacaggt      540
tacgccatta acccagcacg tgatttagga cctcgtctag ttcattgctat tctaccactc      600
aacaacaagg gagattctga ttggtcttat gcttggatac ctgtttagg accaattatt      660
ggagcggctc tagcagtttt gcttttccaa gtcattgcct aa              702

```

<210> SEQ ID NO 240

<211> LENGTH: 233

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 240

```

Met Asp Ile Phe Gly Glu Phe Leu Gly Thr Ala Leu Leu Val Leu Leu
 1          5          10          15
Gly Asn Gly Val Val Ala Gly Val Val Leu Pro Lys Thr Lys Thr His
 20          25          30
Ala Ser Gly Trp Ile Val Ile Ala Thr Gly Trp Gly Ile Ala Val Ala
 35          40          45
Val Ala Val Phe Ile Ser Gly Lys Val Ala Pro Ala His Leu Asn Pro
 50          55          60
Ala Val Ser Leu Ala Phe Ala Met Ser Gly Thr Ile Ala Trp Ser Thr
 65          70          75          80
Ala Ile Ala Tyr Ser Leu Ala Gln Leu Leu Gly Ala Met Val Gly Ser

```

				85						90					95				
Thr	Leu	Val	Phe	Leu	Gln	Phe	Arg	Pro	His	Tyr	Leu	Ala	Ala	Glu	Ser				
			100					105					110						
Gln	Ala	Asp	Ile	Leu	Gly	Thr	Phe	Ala	Thr	Gly	Pro	Ala	Ile	Arg	Asp				
		115					120				125								
Thr	Ser	Ser	Asn	Leu	Leu	Ser	Glu	Ile	Phe	Gly	Thr	Phe	Val	Leu	Met				
		130				135					140								
Leu	Gly	Ile	Leu	Ala	Phe	Gly	Leu	Tyr	Asp	Met	Pro	Ala	Gly	Leu	Gly				
145					150				155					160					
Thr	Leu	Cys	Val	Gly	Thr	Leu	Val	Ile	Gly	Ile	Gly	Leu	Ser	Leu	Gly				
			165						170					175					
Gly	Thr	Thr	Gly	Tyr	Ala	Ile	Asn	Pro	Ala	Arg	Asp	Leu	Gly	Pro	Arg				
			180					185					190						
Leu	Val	His	Ala	Ile	Leu	Pro	Leu	Asn	Asn	Lys	Gly	Asp	Ser	Asp	Trp				
		195				200					205								
Ser	Tyr	Ala	Trp	Ile	Pro	Val	Val	Gly	Pro	Ile	Ile	Gly	Ala	Val	Leu				
	210				215						220								
Ala	Val	Leu	Leu	Phe	Gln	Val	Met	Ser											
225					230														

<210> SEQ ID NO 241

<211> LENGTH: 1671

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 241

ttgaactcgc	tgggcgtaag	gcgcaagaag	aggggtgatg	gcatgaattg	gtctactatt	60
tgggaactta	tcaagataaa	cattctttat	tccaatccac	aaagttagc	taacctcaaa	120
aagcgtcagg	aaaaacaccc	gaaagaaaac	ttcaaaagcct	ataaaagcat	gatgaggcaa	180
caggccttaa	tgattgccat	gtttttggtg	atttaccttt	ttatgtttat	tgggtgcgat	240
ttcagtcatt	atccaggact	tttctccttt	gacgttgcta	tgttttttat	catgtcaacc	300
ttgacagcct	ttagctctct	ttacaccatt	ttttatgaaa	gtaatgacct	aaaactttat	360
attcacttac	cagtaacgtc	agaagaactc	tattattgcaa	aaattgtctc	gtcgcctagg	420
atgggtgctg	tctttttgat	gcctcttata	tctcttctct	taattgccta	ttggcaactc	480
ttgggaaatc	ctttgtctat	tttagtagct	atcgtgctct	tttagtggt	actagttagt	540
tctatggtat	tagctattta	tatcaatgct	tgggtaggca	aaatcattgt	aagaagtcgc	600
aaacgaaaac	tcatttcaac	tatcatgatg	tttgtctcaa	cttttggcgc	tttcgtctta	660
atttttgcga	ttaatattag	taacaacaag	cgtacgatga	cggatggcgt	atttactgat	720
tacccaacta	ttccctat	caaaggattc	tatgatgttg	ttcaggcacc	gttttctact	780
gcggccctcc	ttaacttttg	gttgccattg	ttacttatcc	tagctatggt	atatggtatt	840
gtcacaaaag	tgatgccaac	ttattatcgt	gaggcttttt	atattagtaa	cgagaacaaa	900
gtcaagcaaa	ctaaaaaacc	agttaatcgt	cctcatcaga	atcaatcact	ggcgcagttg	960
ttgcgaaaac	atcacctatt	aacgttacaa	aatgcaactt	tactgacaca	aacctatctc	1020
atgcccctga	tgtatgtgat	gctttttatc	ggtccaagtt	tgtcacgtgg	cacagggttc	1080
tttaagcata	tttccccaga	ttactttggg	gtagccttat	tatttggggt	tagtttgggt	1140
gtcatgtgtg	caacaccaac	cagctttatt	ggagtaggta	tttcacttga	aaaggataac	1200
tttaccttta	ttaaaagctt	accaataacg	ttaaaaaaat	tcttgatgga	taaattttgc	1260
ttgcttgtag	gtctgcagct	gattgtgcct	atggtgattt	atcttgtgtt	tgggtctctt	1320
gtgttgccac	tgcatcctct	tctaacgatt	gctttttgtc	ttggctacgc	cctatcactg	1380
attgtgcaag	gggaattgat	gtatcgctcg	gactaccggc	ttctggattt	aaaatggcaa	1440
gacatgacgc	aactctttac	cagaggagat	gggcaatggg	taacaatggg	acttatcttt	1500
ggtaatttaa	tagttgcagg	tgtgctagg	tttggagctg	ttatcattgc	caatattatc	1560
caacaacctc	tgttgattag	tattctattg	agttgtctaa	tactaatggt	tttaggtcct	1620
gcgcaattat	ggattcaaaa	aaccttctgg	aaaagccttag	agaggcttta	a	1671

<210> SEQ ID NO 242

<211> LENGTH: 556

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 242

Met	Asn	Ser	Leu	Gly	Val	Arg	Arg	Lys	Lys	Arg	Gly	Asp	Gly	Met	Asn
1				5					10					15	
Trp	Ser	Thr	Ile	Trp	Glu	Leu	Ile	Lys	Ile	Asn	Ile	Leu	Tyr	Ser	Asn
			20					25				30			
Pro	Gln	Ser	Leu	Ala	Asn	Leu	Lys	Lys	Arg	Gln	Glu	Lys	His	Pro	Lys
		35					40					45			
Glu	Asn	Phe	Lys	Ala	Tyr	Lys	Ser	Met	Met	Arg	Gln	Gln	Ala	Leu	Met
	50					55					60				
Ile	Ala	Met	Phe	Leu	Val	Ile	Tyr	Leu	Phe	Met	Phe	Ile	Gly	Val	Asp
65				70						75					80
Phe	Ser	His	Tyr	Pro	Gly	Leu	Phe	Ser	Phe	Asp	Val	Ala	Met	Phe	Phe
				85					90					95	
Ile	Met	Ser	Thr	Leu	Thr	Ala	Phe	Ser	Ser	Leu	Tyr	Thr	Ile	Phe	Tyr
			100					105					110		
Glu	Ser	Asn	Asp	Leu	Lys	Leu	Tyr	Ile	His	Leu	Pro	Val	Thr	Ser	Glu
		115					120					125			
Glu	Leu	Tyr	Ile	Ala	Lys	Ile	Val	Ser	Ser	Leu	Gly	Met	Gly	Ala	Val
	130					135					140				
Phe	Leu	Met	Pro	Leu	Ile	Ser	Leu	Leu	Leu	Ile	Ala	Tyr	Trp	Gln	Leu
145					150					155					160
Leu	Gly	Asn	Pro	Leu	Ser	Ile	Leu	Val	Ala	Ile	Val	Leu	Phe	Leu	Val
				165					170					175	
Leu	Leu	Val	Ser	Ser	Met	Val	Leu	Ala	Ile	Tyr	Ile	Asn	Ala	Trp	Val
			180					185					190		
Gly	Lys	Ile	Ile	Val	Arg	Ser	Arg	Lys	Arg	Lys	Leu	Ile	Ser	Thr	Ile
	195						200					205			
Met	Met	Phe	Val	Ser	Thr	Phe	Gly	Ala	Phe	Val	Leu	Ile	Phe	Ala	Ile
	210					215					220				
Asn	Ile	Ser	Asn	Asn	Lys	Arg	Thr	Met	Thr	Asp	Gly	Val	Phe	Thr	Asp
225				230						235					240
Tyr	Pro	Thr	Ile	Pro	Tyr	Phe	Lys	Gly	Phe	Tyr	Asp	Val	Val	Gln	Ala
				245					250					255	
Pro	Phe	Ser	Thr	Ala	Ala	Leu	Leu	Asn	Phe	Trp	Leu	Pro	Leu	Leu	Leu
			260					265					270		
Ile	Leu	Ala	Met	Val	Tyr	Gly	Ile	Val	Thr	Lys	Val	Met	Pro	Thr	Tyr
	275						280					285			
Tyr	Arg	Glu	Ala	Phe	Tyr	Ile	Ser	Asn	Glu	Asn	Lys	Val	Lys	Gln	Thr
	290					295					300				
Lys	Lys	Pro	Val	Asn	Arg	Pro	His	Gln	Asn	Gln	Ser	Leu	Ala	Gln	Leu
305				310						315					320
Leu	Arg	Lys	His	His	Leu	Leu	Thr	Leu	Gln	Asn	Ala	Thr	Leu	Leu	Thr
				325					330					335	
Gln	Thr	Tyr	Leu	Met	Pro	Leu	Met	Tyr	Val	Met	Leu	Phe	Ile	Gly	Pro
			340					345					350		
Ser	Leu	Ser	Arg	Gly	Thr	Gly	Phe	Phe	Lys	His	Ile	Ser	Pro	Asp	Tyr
		355					360					365			
Phe	Gly	Val	Ala	Leu	Leu	Phe	Gly	Val	Ser	Leu	Gly	Val	Met	Cys	Ala
	370					375					380				
Thr	Pro	Thr	Ser	Phe	Ile	Gly	Val	Gly	Ile	Ser	Leu	Glu	Lys	Asp	Asn
385				390						395					400
Phe	Thr	Phe	Ile	Lys	Ser	Leu	Pro	Ile	Thr	Leu	Lys	Lys	Phe	Leu	Met
				405					410					415	
Asp	Lys	Phe	Cys	Leu	Leu	Val	Gly	Leu	Gln	Leu	Ile	Val	Pro	Met	Val
			420					425					430		
Ile	Tyr	Leu	Val	Phe	Gly	Leu	Phe	Val	Leu	His	Leu	His	Pro	Leu	Leu

aaaggaacag attctggtcg tgttatgaaa caaagtgttg atgttggttaa gtccttgaaa 2220
 aaaataaaaa aaatgaccat tacttttagga gattaa 2256

<210> SEQ ID NO 244
 <211> LENGTH: 751
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 244

Met	Lys	Lys	Trp	Gln	Lys	Tyr	Val	Leu	Asp	Tyr	Val	Val	Arg	Asp	Arg
1				5					10					15	
Arg	Thr	Pro	Val	Glu	Asn	Arg	Val	Arg	Val	Gly	Gln	Asn	Met	Met	Leu
			20					25					30		
Leu	Thr	Ile	Phe	Ile	Phe	Phe	Ile	Phe	Ile	Ile	Asn	Phe	Met	Ile	Ile
			35				40					45			
Ile	Gly	Thr	Asp	Gln	Lys	Phe	Gly	Val	Ser	Leu	Ser	Glu	Gly	Ala	Lys
	50					55					60				
Lys	Val	Tyr	Gln	Glu	Thr	Val	Thr	Ile	Gln	Ala	Lys	Arg	Gly	Thr	Ile
65					70					75					80
Tyr	Asp	Arg	Asn	Gly	Thr	Ala	Ile	Ala	Val	Asp	Ser	Thr	Thr	Tyr	Ser
			85						90					95	
Ile	Tyr	Ala	Ile	Leu	Asp	Lys	Ser	Phe	Val	Ser	Ala	Ser	Asp	Glu	Lys
			100					105					110		
Leu	Tyr	Val	Gln	Pro	Ser	Gln	Tyr	Glu	Thr	Val	Ala	Asp	Ile	Leu	Lys
			115				120					125			
Lys	His	Leu	Gly	Met	Lys	Lys	Thr	Asp	Val	Ile	Lys	Gln	Leu	Lys	Arg
	130					135					140				
Lys	Gly	Leu	Phe	Gln	Val	Ser	Phe	Gly	Pro	Ser	Gly	Ser	Gly	Ile	Ser
145					150					155					160
Tyr	Ser	Thr	Met	Ser	Thr	Ile	Gln	Lys	Ala	Met	Glu	Asp	Ala	Lys	Ile
			165						170					175	
Lys	Gly	Ile	Ala	Phe	Thr	Thr	Ser	Pro	Gly	Arg	Met	Tyr	Pro	Asn	Gly
			180					185						190	
Thr	Phe	Ala	Ser	Glu	Phe	Ile	Gly	Leu	Ala	Ser	Leu	Thr	Glu	Asp	Lys
			195				200						205		
Lys	Thr	Gly	Val	Lys	Ser	Leu	Val	Gly	Lys	Thr	Gly	Leu	Glu	Ala	Ser
	210					215					220				
Phe	Asp	Lys	Ile	Leu	Ser	Gly	Gln	Asp	Gly	Val	Ile	Thr	Tyr	Gln	Lys
225					230					235					240
Asp	Arg	Asn	Gly	Thr	Thr	Leu	Leu	Gly	Thr	Gly	Lys	Thr	Val	Lys	Lys
			245						250					255	
Ala	Ile	Asp	Gly	Lys	Asp	Ile	Tyr	Thr	Thr	Leu	Ser	Glu	Pro	Ile	Gln
			260					265					270		
Thr	Phe	Leu	Glu	Thr	Gln	Met	Asp	Val	Phe	Gln	Ala	Lys	Ser	Asn	Gly
			275				280					285			
Gln	Leu	Ala	Ser	Ala	Thr	Leu	Val	Asn	Ala	Lys	Thr	Gly	Glu	Ile	Leu
	290					295					300				
Ala	Thr	Thr	Gln	Arg	Pro	Thr	Tyr	Asn	Ala	Asp	Thr	Leu	Lys	Gly	Leu
305					310					315					320
Glu	Asn	Thr	Asn	Tyr	Lys	Trp	Tyr	Ser	Ala	Leu	His	Gln	Gly	Asn	Phe
			325						330					335	
Glu	Pro	Gly	Ser	Thr	Met	Lys	Val	Met	Thr	Leu	Ala	Ala	Ala	Ile	Asp
			340					345					350		
Asp	Lys	Val	Phe	Asn	Pro	Asn	Glu	Thr	Phe	Ser	Asn	Ala	Asn	Gly	Leu
			355				360					365			
Thr	Ile	Ala	Asp	Ala	Thr	Ile	Gln	Asp	Trp	Ser	Ile	Asn	Glu	Gly	Ile
	370					375					380				
Ser	Thr	Gly	Gln	Tyr	Met	Asn	Tyr	Ala	Gln	Gly	Phe	Ala	Phe	Ser	Ser

385					390					395				400	
Asn	Val	Gly	Met	Thr	Lys	Leu	Glu	Gln	Lys	Met	Gly	Asn	Ala	Lys	Trp
				405					410					415	
Met	Asn	Tyr	Leu	Thr	Lys	Phe	Arg	Phe	Gly	Phe	Pro	Thr	Arg	Phe	Gly
			420					425					430		
Leu	Lys	Asp	Glu	Asp	Ala	Gly	Ile	Phe	Pro	Ser	Asp	Asn	Ile	Val	Thr
		435				440						445			
Gln	Ala	Met	Ser	Ala	Phe	Gly	Gln	Gly	Ile	Ser	Val	Thr	Gln	Ile	Gln
	450					455					460				
Met	Leu	Arg	Ala	Phe	Thr	Ala	Ile	Ser	Asn	Asn	Gly	Glu	Met	Leu	Glu
465					470				475					480	
Pro	Gln	Phe	Ile	Ser	Gln	Ile	Tyr	Asp	Pro	Asn	Thr	Ala	Ser	Phe	Arg
				485					490					495	
Thr	Ala	Asn	Lys	Glu	Ile	Val	Gly	Lys	Pro	Val	Ser	Lys	Lys	Ala	Ala
		500					505						510		
Ser	Glu	Thr	Arg	Gln	Tyr	Met	Ile	Gly	Val	Gly	Thr	Asp	Pro	Glu	Phe
	515					520						525			
Gly	Thr	Leu	Tyr	Ser	Lys	Thr	Phe	Gly	Pro	Ile	Ile	Lys	Val	Gly	Asp
	530					535					540				
Leu	Pro	Val	Ala	Val	Lys	Ser	Gly	Thr	Ala	Gln	Ile	Gly	Ser	Glu	Asp
545					550				555					560	
Gly	Ser	Gly	Tyr	Gln	Asp	Gly	Gly	Leu	Thr	Asn	Tyr	Val	Tyr	Ser	Val
			565					570					575		
Val	Ala	Met	Val	Pro	Ala	Asp	Lys	Pro	Asp	Phe	Leu	Met	Tyr	Val	Thr
		580					585						590		
Met	Thr	Lys	Pro	Gln	His	Phe	Gly	Pro	Leu	Phe	Trp	Gln	Asp	Val	Val
	595					600						605			
Asn	Pro	Val	Leu	Glu	Glu	Ala	Tyr	Leu	Met	Gln	Asp	Thr	Leu	Thr	Lys
	610					615					620				
Pro	Val	Val	Ser	Asp	Ala	Asn	Arg	Gln	Thr	Thr	Tyr	Lys	Leu	Pro	Asn
625					630				635					640	
Phe	Val	Gly	Lys	Asn	Pro	Gly	Glu	Thr	Ser	Ser	Glu	Leu	Arg	Arg	Asn
			645					650					655		
Leu	Val	Gln	Pro	Val	Val	Leu	Gly	Thr	Gly	Ser	Lys	Ile	Lys	Lys	Val
		660					665						670		
Ser	His	Gln	Pro	Gly	Gln	Thr	Leu	Thr	Glu	Asn	Gln	Gln	Val	Leu	Ile
	675					680						685			
Leu	Ser	Asp	Arg	Phe	Val	Glu	Val	Pro	Asp	Met	Tyr	Gly	Trp	Thr	Lys
	690					695					700				
Ser	Asn	Val	Lys	Thr	Phe	Ala	Lys	Trp	Thr	Gly	Ile	Asp	Ile	Ser	Phe
705					710				715					720	
Lys	Gly	Thr	Asp	Ser	Gly	Arg	Val	Met	Lys	Gln	Ser	Val	Asp	Val	Gly
			725					730					735		
Lys	Ser	Leu	Lys	Lys	Ile	Lys	Lys	Met	Thr	Ile	Thr	Leu	Gly	Asp	
		740					745						750		

<210> SEQ ID NO 245

<211> LENGTH: 855

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 245

ttgcagcaat	catatccttt	atggatatctg	ctttcacaat	gcccttatttt	tatcaaattc	60
tatcaattga	aaaaaattgg	tgggcaacaa	atgcatgaag	atgtcaagca	acatttagct	120
aaagctggaa	caccgactat	ggggggaact	gtttttcttt	tagtagctac	ggcagtatcg	180
ttattgggta	gtctattttc	gatcaaaaac	actcaaagtt	tagctttgat	ttcaggcatt	240
ttatcaattg	ttgtcattta	cgggattatc	ggatttttgg	atgatttttt	aaaaattttt	300
aagcaaatca	atgaaggatt	gacagccaaa	caaaagttag	ccttgcagtt	ggttggagga	360

ttgatgttct	atTTTTtaca	tgtagtcca	agtggcattt	cctctattaa	tggtgttggg	420
tatcagctgc	cgctgggaat	tttctaccta	ttctttgttt	tgttttgggt	ggttggtttt	480
tcaaagccg	ttaatttgac	agatgggtatc	gatggccttag	cttctatctc	agtgggtgatt	540
agtctagtga	cttacggcgt	tattgcctac	gttcagagtc	aatttgatgt	tttgttactg	600
attggagcaa	tgattggagc	cttgcttggc	ttcttctgct	ttaatcacia	acctgctaaa	660
gtatttatgg	gagatgtagg	tagtttagcc	cttggagcta	tgttggctgc	catttctatt	720
gcgcttcgtc	aagaatggac	tctcctgatt	attgggatcg	tttatgttct	tgaacaagt	780
tctgtgatgt	tgcaagtgtc	ctatttcaag	tacaccaaga	aaaaatatgg	agaagtcgtc	840
gtatttttag	aatga					855

<210> SEQ ID NO 246
 <211> LENGTH: 284
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 246

Met	Gln	Gln	Ser	Tyr	Pro	Leu	Trp	Tyr	Leu	Leu	Ser	Gln	Cys	Pro	Tyr
1				5					10					15	
Phe	Ile	Lys	Phe	Tyr	Gln	Leu	Lys	Lys	Ile	Gly	Gly	Gln	Gln	Met	His
			20					25					30		
Glu	Asp	Val	Lys	Gln	His	Leu	Ala	Lys	Ala	Gly	Thr	Pro	Thr	Met	Gly
		35					40					45			
Gly	Thr	Val	Phe	Leu	Leu	Val	Ala	Thr	Ala	Val	Ser	Leu	Leu	Val	Ser
	50					55					60				
Leu	Phe	Ser	Ile	Lys	Asn	Thr	Gln	Ser	Leu	Ala	Leu	Ile	Ser	Gly	Ile
65				70						75				80	
Leu	Ser	Ile	Val	Val	Ile	Tyr	Gly	Ile	Ile	Gly	Phe	Leu	Asp	Asp	Phe
			85						90				95		
Leu	Lys	Ile	Phe	Lys	Gln	Ile	Asn	Glu	Gly	Leu	Thr	Ala	Lys	Gln	Lys
			100					105					110		
Leu	Ala	Leu	Gln	Leu	Val	Gly	Gly	Leu	Met	Phe	Tyr	Phe	Leu	His	Val
		115				120					125				
Ser	Pro	Ser	Gly	Ile	Ser	Ser	Ile	Asn	Val	Phe	Gly	Tyr	Gln	Leu	Pro
	130					135					140				
Leu	Gly	Ile	Phe	Tyr	Leu	Phe	Phe	Val	Leu	Phe	Trp	Val	Val	Gly	Phe
145				150						155				160	
Ser	Asn	Ala	Val	Asn	Leu	Thr	Asp	Gly	Ile	Asp	Gly	Leu	Ala	Ser	Ile
			165					170					175		
Ser	Val	Val	Ile	Ser	Leu	Val	Thr	Tyr	Gly	Val	Ile	Ala	Tyr	Val	Gln
			180					185					190		
Ser	Gln	Phe	Asp	Val	Leu	Leu	Leu	Ile	Gly	Ala	Met	Ile	Gly	Ala	Leu
	195					200					205				
Leu	Gly	Phe	Phe	Cys	Phe	Asn	His	Lys	Pro	Ala	Lys	Val	Phe	Met	Gly
	210				215						220				
Asp	Val	Gly	Ser	Leu	Ala	Leu	Gly	Ala	Met	Leu	Ala	Ala	Ile	Ser	Ile
225				230						235				240	
Ala	Leu	Arg	Gln	Glu	Trp	Thr	Leu	Leu	Ile	Ile	Gly	Ile	Val	Tyr	Val
			245						250				255		
Leu	Glu	Thr	Ser	Ser	Val	Met	Leu	Gln	Val	Ser	Tyr	Phe	Lys	Tyr	Thr
		260					265					270			
Lys	Lys	Lys	Tyr	Gly	Glu	Val	Val	Phe	Leu	Glu					
	275					280									

<210> SEQ ID NO 247
 <211> LENGTH: 894
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 247

ttgcttattg	ctataatacg	aatttactat	tttacatgtg	ggctctaagag	tgttagaata	60
ttaagacaaa	caaatacaaa	ggggaaatac	atgacatcag	tgtttttaac	cagtgggttg	120
gctttttatg	attacctcat	ctcaccgatt	ccacatggga	aacttttttag	ttggcatgct	180
gtttttgatg	ccattccaaa	tattatccaa	cggcttccaa	ttacgcttgg	tttgacacta	240
tcaggagcaa	cctttggctt	ggttttggct	ttgatttttg	cccttggtcaa	aattaataaa	300
gtgaagctac	tataccctat	tcaagctatt	tttgtgagtt	tcttgcgagg	aactcctatt	360
ttggtacagt	tgatgttgac	ctactacggg	attcccctct	ttctaaaatt	tctcaatcag	420
aagtatggct	ttgattggaa	tgtaaatgca	attccggcct	ctattttttgc	cattacagcc	480
tttgctttta	atgaagcagc	ctacgctagt	gaaactattc	gggcagccat	tttatcagta	540
gatacagggtg	aaattgaagc	agcaaaaagt	ctaggcatga	cttctgtgca	ggtttaccgt	600
cgtgtcatta	ttcctaatac	aactgttggtg	gctattccaa	ccttgattaa	tgggttaatt	660
ggcttaacta	aaggaacatc	gcttgccctt	aatgcaggga	ttgtcgaaat	gtttgccag	720
gctcaaattc	taggcggatc	agattaccgt	tattttgaac	gttatatctc	tgttgctctt	780
gtctattggg	ctatcagtat	tttgatggag	caagtaggtc	gcttgattga	aaacaagatg	840
gccatcaaag	caccagaaca	agctagaaat	gaaaagttag	gagaattgcy	ttga	894

<210> SEQ ID NO 248

<211> LENGTH: 297

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 248

Met	Leu	Ile	Ala	Ile	Ile	Arg	Ile	Tyr	Tyr	Phe	Thr	Cys	Gly	Ser	Lys
1				5					10					15	
Ser	Val	Arg	Ile	Leu	Arg	Gln	Thr	Asn	Thr	Lys	Gly	Lys	Tyr	Met	Thr
			20					25					30		
Ser	Val	Phe	Leu	Thr	Ser	Gly	Trp	Ala	Phe	Tyr	Asp	Tyr	Leu	Ile	Ser
		35					40					45			
Pro	Ile	Pro	His	Gly	Lys	Leu	Phe	Ser	Trp	His	Ala	Val	Phe	Asp	Ala
	50					55					60				
Ile	Pro	Asn	Ile	Ile	Gln	Arg	Leu	Pro	Ile	Thr	Leu	Gly	Leu	Thr	Leu
65					70					75				80	
Ser	Gly	Ala	Thr	Phe	Gly	Leu	Val	Leu	Ala	Leu	Ile	Phe	Ala	Leu	Val
				85					90					95	
Lys	Ile	Asn	Lys	Val	Lys	Leu	Leu	Tyr	Pro	Ile	Gln	Ala	Ile	Phe	Val
			100					105						110	
Ser	Phe	Leu	Arg	Gly	Thr	Pro	Ile	Leu	Val	Gln	Leu	Met	Leu	Thr	Tyr
			115				120					125			
Tyr	Gly	Ile	Pro	Leu	Phe	Leu	Lys	Phe	Leu	Asn	Gln	Lys	Tyr	Gly	Phe
	130					135					140				
Asp	Trp	Asn	Val	Asn	Ala	Ile	Pro	Ala	Ser	Ile	Phe	Ala	Ile	Thr	Ala
145					150					155				160	
Phe	Ala	Phe	Asn	Glu	Ala	Ala	Tyr	Ala	Ser	Glu	Thr	Ile	Arg	Ala	Ala
				165					170					175	
Ile	Leu	Ser	Val	Asp	Thr	Gly	Glu	Ile	Glu	Ala	Ala	Lys	Ser	Leu	Gly
			180				185						190		
Met	Thr	Ser	Val	Gln	Val	Tyr	Arg	Arg	Val	Ile	Ile	Pro	Asn	Ala	Thr
		195					200						205		
Val	Val	Ala	Ile	Pro	Thr	Leu	Ile	Asn	Gly	Leu	Ile	Gly	Leu	Thr	Lys
	210					215						220			
Gly	Thr	Ser	Leu	Ala	Phe	Asn	Ala	Gly	Ile	Val	Glu	Met	Phe	Ala	Gln
225					230					235				240	
Ala	Gln	Ile	Leu	Gly	Gly	Ser	Asp	Tyr	Arg	Tyr	Phe	Glu	Arg	Tyr	Ile
				245					250					255	
Ser	Val	Ala	Leu	Val	Tyr	Trp	Ser	Ile	Ser	Ile	Leu	Met	Glu	Gln	Val
			260					265					270		
Gly	Arg	Leu	Ile	Glu	Asn	Lys	Met	Ala	Ile	Lys	Ala	Pro	Glu	Gln	Ala
	275						280						285		

Arg Asn Glu Lys Leu Gly Glu Leu Arg
290 295

<210> SEQ ID NO 249

<211> LENGTH: 1392

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 249

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atggagttta gaatgtctat aaaagaacaa acagacaata acgaactaga aaatggaatg      60
gtaaggggct tagaaaatcg tcatgtgcag ttaattgcga tcgcaggaac gattggaaca      120
ggctctcttt taggggcagg acgctctatt gccctaacag gaccatctat tatttttgtg      180
tatatgatta caggtgcctt catgtttatg atgatgcgtg ccatcggtgga aatgctctat      240
tatgatccag atcaacacac ctttatcaat tttatttcca aatacattgg tccaggctgg      300
ggttattttt cggttctatc ctattggatt tcccttattt ttattggaat ggcagaaatc      360
acagcagtag gtgcttatgt gcaattttgg ttcccaagct ggccagcctg gttgattcag      420
ttggttttct tagtcttact tagttcgatc aacttaattg ctgtgcgcgt ttttggggaa      480
acagagtttt ggtttgccat gattaagatt ttagctattt tagctttgat tgcaacagct      540
attttcatgg tattgacagg ttttgaaact cacacaggcc atgctagcct ttccaatatt      600
tttgaccatt tttccatgtt cccaaatggg aaactaaagt tctttatggc cttccaaatg      660
gttttctttg cttatcaagc tatcgaattt gtgggaatta ccacttctga gacggctaac      720
ccaagaaaag ttctaccaa ggctattcaa gaaattccaa cccgtattgt gatcttttat      780
gtgggagcct tggctctctat tatggcaatt gtgccatggc atcagttacc agttgatgaa      840
tctccttttg tgatgggtgtt caaattgatt ggtattaaat gggcagcagc cttgattaac      900
tttgtgggtc tgacatcagc agcgtcagcg ctttaactcaa ccctttattc aaccggtcgt      960
catctctatc agattgctaa tgagactcca aacgctttga ccaatcgctt aaagattaat     1020
actttatctc gacaaggggt gccaaagtcgt gccattattg cttcagcggg tgtggttggg     1080
atctcagctt tgattaatat cctaccagga gttgcagatg cgttctcact cattacggcc     1140
tcctcatcag gtgtatatat tgctatctac gccttaacca tgattgctca ctggaagtac     1200
cgtcaatcta aggactttat ggcagatggg tatttgatgc caaaatataa agtgacaacg     1260
cctttgacct ttgctttctt tgcttttgtc tttatctctc ttttcttaca agaatccacc     1320
tatatcggcg ccattggagc aacgatttgg attattattt ttgggattta tagcaatgtc     1380
aaatttaaataa aa                                     1392

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<210> SEQ ID NO 250

<211> LENGTH: 463

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 250

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Met Glu Phe Arg Met Ser Ile Lys Glu Gln Thr Asp Asn Asn Glu Leu
1      5      10      15
Glu Asn Gly Met Val Arg Gly Leu Glu Asn Arg His Val Gln Leu Ile
20      25      30
Ala Ile Ala Gly Thr Ile Gly Thr Gly Leu Phe Leu Gly Ala Gly Arg
35      40      45
Ser Ile Ala Leu Thr Gly Pro Ser Ile Ile Phe Val Tyr Met Ile Thr
50      55      60
Gly Ala Phe Met Phe Met Met Met Arg Ala Ile Gly Glu Met Leu Tyr
65      70      75      80
Tyr Asp Pro Asp Gln His Thr Phe Ile Asn Phe Ile Ser Lys Tyr Ile
85      90      95
Gly Pro Gly Trp Gly Tyr Phe Ser Gly Leu Ser Tyr Trp Ile Ser Leu
100     105     110
Ile Phe Ile Gly Met Ala Glu Ile Thr Ala Val Gly Ala Tyr Val Gln
115     120     125
Phe Trp Phe Pro Ser Trp Pro Ala Trp Leu Ile Gln Leu Val Phe Leu
130     135     140
Val Leu Leu Ser Ser Ile Asn Leu Ile Ala Val Arg Val Phe Gly Glu

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145					150					155				160
Thr	Glu	Phe	Trp	Phe	Ala	Met	Ile	Lys	Ile	Leu	Ala	Ile	Leu	Ala
				165					170					175
Ile	Ala	Thr	Ala	Ile	Phe	Met	Val	Leu	Thr	Gly	Phe	Glu	Thr	His
			180					185					190	
Gly	His	Ala	Ser	Leu	Ser	Asn	Ile	Phe	Asp	His	Phe	Ser	Met	Phe
		195					200					205		
Asn	Gly	Lys	Leu	Lys	Phe	Phe	Met	Ala	Phe	Gln	Met	Val	Phe	Phe
	210					215					220			
Tyr	Gln	Ala	Ile	Glu	Phe	Val	Gly	Ile	Thr	Thr	Ser	Glu	Thr	Ala
225					230					235				240
Pro	Arg	Lys	Val	Leu	Pro	Lys	Ala	Ile	Gln	Glu	Ile	Pro	Thr	Arg
			245						250					255
Val	Ile	Phe	Tyr	Val	Gly	Ala	Leu	Val	Ser	Ile	Met	Ala	Ile	Val
		260						265					270	
Trp	His	Gln	Leu	Pro	Val	Asp	Glu	Ser	Pro	Phe	Val	Met	Val	Phe
	275					280						285		
Leu	Ile	Gly	Ile	Lys	Trp	Ala	Ala	Ala	Leu	Ile	Asn	Phe	Val	Val
	290				295						300			
Thr	Ser	Ala	Ala	Ser	Ala	Leu	Asn	Ser	Thr	Leu	Tyr	Ser	Thr	Gly
305					310					315				320
His	Leu	Tyr	Gln	Ile	Ala	Asn	Glu	Thr	Pro	Asn	Ala	Leu	Thr	Asn
			325					330					335	
Leu	Lys	Ile	Asn	Thr	Leu	Ser	Arg	Gln	Gly	Val	Pro	Ser	Arg	Ala
		340						345					350	
Ile	Ala	Ser	Ala	Val	Val	Val	Gly	Ile	Ser	Ala	Leu	Ile	Asn	Ile
	355						360					365		
Pro	Gly	Val	Ala	Asp	Ala	Phe	Ser	Leu	Ile	Thr	Ala	Ser	Ser	Ser
	370				375						380			
Val	Tyr	Ile	Ala	Ile	Tyr	Ala	Leu	Thr	Met	Ile	Ala	His	Trp	Lys
385					390					395				400
Arg	Gln	Ser	Lys	Asp	Phe	Met	Ala	Asp	Gly	Tyr	Leu	Met	Pro	Lys
			405						410					415
Lys	Val	Thr	Thr	Pro	Leu	Thr	Leu	Ala	Phe	Phe	Ala	Phe	Val	Phe
		420						425					430	
Ser	Leu	Phe	Leu	Gln	Glu	Ser	Thr	Tyr	Ile	Gly	Ala	Ile	Gly	Ala
	435						440					445		
Ile	Trp	Ile	Ile	Ile	Phe	Gly	Ile	Tyr	Ser	Asn	Val	Lys	Phe	Lys
	450					455					460			

<210> SEQ ID NO 251

<211> LENGTH: 573

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 251

ttgatctggt	ttcttagcct	tttctcctcc	acaagtagcc	actttctcac	tatttgtggt	60
atgataaagt	gtaaaacaaa	ggagattgaa	atgacaaaag	aagttatcgt	cgaaagtgtt	120
gagctagatc	atactattgt	aaaggccctt	tatgttcgtc	ttatttctga	agaatttgga	180
cccaagggcg	atcgtattac	aaattttgat	gttcgcctag	tgcagcctaa	ccaaaattct	240
attgaaacag	ccggtttgca	taccattgaa	cacttacttg	ccaagctcat	ccgccaacgc	300
attgatggga	tgattgattg	ctctcctttt	ggctgtcgaa	caggttttca	ccttatcatg	360
tggggaaaac	acagttctac	tgatattgcc	aaggtgatta	aatccagcct	agaagaaatt	420
gcaactggga	ttacttggga	agatgttcct	ggaacaactc	ttgaatcctg	tgggaactat	480
aaggatcata	gcctctttgc	cgccaaagaa	tgggctcaat	tgattattga	tcaagggtat	540
tcagacgatc	cttttagtcg	ccatgtcatc	tga			573

<210> SEQ ID NO 252

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<211> LENGTH: 190
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 252
Met Ile Cys Phe Leu Ser Leu Phe Ser Ser Thr Ser Ser His Phe Leu
1           5           10           15
Thr Ile Cys Val Met Ile Lys Cys Lys Thr Lys Glu Ile Glu Met Thr
20           25           30
Lys Glu Val Ile Val Glu Ser Phe Glu Leu Asp His Thr Ile Val Lys
35           40           45
Ala Pro Tyr Val Arg Leu Ile Ser Glu Glu Phe Gly Pro Lys Gly Asp
50           55           60
Arg Ile Thr Asn Phe Asp Val Arg Leu Val Gln Pro Asn Gln Asn Ser
65           70           75           80
Ile Glu Thr Ala Gly Leu His Thr Ile Glu His Leu Leu Ala Lys Leu
85           90           95
Ile Arg Gln Arg Ile Asp Gly Met Ile Asp Cys Ser Pro Phe Gly Cys
100          105          110
Arg Thr Gly Phe His Leu Ile Met Trp Gly Lys His Ser Ser Thr Asp
115          120          125
Ile Ala Lys Val Ile Lys Ser Ser Leu Glu Glu Ile Ala Thr Gly Ile
130          135          140
Thr Trp Glu Asp Val Pro Gly Thr Thr Leu Glu Ser Cys Gly Asn Tyr
145          150          155          160
Lys Asp His Ser Leu Phe Ala Ala Lys Glu Trp Ala Gln Leu Ile Ile
165          170          175
Asp Gln Gly Ile Ser Asp Asp Pro Phe Ser Arg His Val Ile
180          185          190

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<210> SEQ ID NO 253
<211> LENGTH: 1608
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 253
atgggtaata ttattttatt aattgtttct gccctcattg gtttaatat aggttatgca      60
cttatttcga ttagactcaa gtctgcgaag gaagctgcag agttgactct tttaaacgct      120
gaacaagaag ctggtgatat tcgtggcaaa gcagaagtag atgctgaaca catcaaaaaa      180
acagctaaac gtgaaagtaa agcaaatcgt aaagaattac ttttagaagc aaaagaagag      240
gcaagaaaat atcgtgaaga gattgaacaa gaatttaagt ctgaaagaca agagcttaaa      300
caactcgaga cacgcttagc ggagcgctcc ttaactcttg accgtaaaga tgaaaaccta      360
tcaagtaaag aaaagg tact agatagtaaa gaacaaagtc tgaccgataa atctaaacac      420
attgatgagc ggcaacttca agtggaaaaa cttgaagagg agaaaaaagc agaactggaa      480
aaagttgctg cgatgacgat tgcagaagcg cgtgaagtga ttttaatgga gacggaaaac      540
aaactgaccc atgaaattgc gacgcgcatt cgagatgccg aacgtgacat caaggaccga      600
acagttaaaa cagccaagga cttgttagcg caagccatgc aacgccttgc tggtagtat      660
gtgactgaac aaactattac cagtgtccat ctcccagacg acaacatgaa gggccgaatt      720
attggacgtg aaggccgtaa tattcg tact ttagagagct tgactggcat tgacgttatt      780
attgacgata ctctgaagt tgttatctta tcaggatttg atcctattcg acgtgaaatt      840
gctcgatatg ccttggaatc tctgattgct gatggtcgca tccatccagc tcgtatcgag      900
gaattggttg agaaaaatcg tcttgaaatg gataatcgta ttcgtgagta cgggtgaagct      960
gcagcctatg agattggtgc accaaacctt catcctgatt tgattaaaaat catgggacgc      1020
ctgcaattcc gtacctcgtt tgggtcaaaat gtcctacgtc actctgttga ggttggttaag      1080
ttagctggta ttttagctgg tgagttagggt gaaaatgttg ctcttgcccc cgtgctggt      1140
ttcttgcatg atatgggtaa agctattgac cgtgaggttg aaggcagtc caagtgagatt      1200
ggaaatggaat ttgcacgtaa atacaaagaa catccagttg ttgtcaacac tattgctagc      1260
caccacggag atgtggagcc agattctgtg atcgctgtgc tagtagctgc agcagacgct      1320
ctcagttcgg ctcgtccagg cgctcgtaat gaggcaatgg agaattacat caagcgctct      1380

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cgtgatttag	aagaaatcgc	gacaagtttt	gatgggggtac	aaaatagttt	tgctctacaa	1440
gctggacgtg	agattcgtat	tatggttcaa	cctgaaaaaa	tttcagatga	tcaggttgtc	1500
atattgtcgc	ataaagtaag	agaaaaaatt	gaaaacaatc	tagattaccc	aggaaatatt	1560
aaagtaactg	ttattcgtga	gatgagagcg	gttgattatg	ccaagtag		1608

<210> SEQ ID NO 254

<211> LENGTH: 535

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 254

Met	Val	Asn	Ile	Ile	Leu	Leu	Ile	Val	Ser	Ala	Leu	Ile	Gly	Leu	Ile
1			5						10				15		
Leu	Gly	Tyr	Ala	Leu	Ile	Ser	Ile	Arg	Leu	Lys	Ser	Ala	Lys	Glu	Ala
		20						25					30		
Ala	Glu	Leu	Thr	Leu	Leu	Asn	Ala	Glu	Gln	Glu	Ala	Val	Asp	Ile	Arg
		35					40					45			
Gly	Lys	Ala	Glu	Val	Asp	Ala	Glu	His	Ile	Lys	Lys	Thr	Ala	Lys	Arg
	50					55					60				
Glu	Ser	Lys	Ala	Asn	Arg	Lys	Glu	Leu	Leu	Leu	Glu	Ala	Lys	Glu	Glu
65				70						75				80	
Ala	Arg	Lys	Tyr	Arg	Glu	Glu	Ile	Glu	Gln	Glu	Phe	Lys	Ser	Glu	Arg
			85						90					95	
Gln	Glu	Leu	Lys	Gln	Leu	Glu	Thr	Arg	Leu	Ala	Glu	Arg	Ser	Leu	Thr
		100						105					110		
Leu	Asp	Arg	Lys	Asp	Glu	Asn	Leu	Ser	Ser	Lys	Glu	Lys	Val	Leu	Asp
	115						120					125			
Ser	Lys	Glu	Gln	Ser	Leu	Thr	Asp	Lys	Ser	Lys	His	Ile	Asp	Glu	Arg
	130					135					140				
Gln	Leu	Gln	Val	Glu	Lys	Leu	Glu	Glu	Glu	Lys	Lys	Ala	Glu	Leu	Glu
145					150					155				160	
Lys	Val	Ala	Ala	Met	Thr	Ile	Ala	Glu	Ala	Arg	Glu	Val	Ile	Leu	Met
			165						170					175	
Glu	Thr	Glu	Asn	Lys	Leu	Thr	His	Glu	Ile	Ala	Thr	Arg	Ile	Arg	Asp
		180						185					190		
Ala	Glu	Arg	Asp	Ile	Lys	Asp	Arg	Thr	Val	Lys	Thr	Ala	Lys	Asp	Leu
	195						200					205			
Leu	Ala	Gln	Ala	Met	Gln	Arg	Leu	Ala	Gly	Glu	Tyr	Val	Thr	Glu	Gln
	210					215					220				
Thr	Ile	Thr	Ser	Val	His	Leu	Pro	Asp	Asp	Asn	Met	Lys	Gly	Arg	Ile
225				230						235				240	
Ile	Gly	Arg	Glu	Gly	Arg	Asn	Ile	Arg	Thr	Leu	Glu	Ser	Leu	Thr	Gly
			245						250					255	
Ile	Asp	Val	Ile	Ile	Asp	Asp	Thr	Pro	Glu	Val	Val	Ile	Leu	Ser	Gly
		260						265					270		
Phe	Asp	Pro	Ile	Arg	Arg	Glu	Ile	Ala	Arg	Met	Thr	Leu	Glu	Ser	Leu
	275						280					285			
Ile	Ala	Asp	Gly	Arg	Ile	His	Pro	Ala	Arg	Ile	Glu	Glu	Leu	Val	Glu
	290					295					300				
Lys	Asn	Arg	Leu	Glu	Met	Asp	Asn	Arg	Ile	Arg	Glu	Tyr	Gly	Glu	Ala
305					310					315				320	
Ala	Ala	Tyr	Glu	Ile	Gly	Ala	Pro	Asn	Leu	His	Pro	Asp	Leu	Ile	Lys
			325						330					335	
Ile	Met	Gly	Arg	Leu	Gln	Phe	Arg	Thr	Ser	Phe	Gly	Gln	Asn	Val	Leu
		340						345					350		
Arg	His	Ser	Val	Glu	Val	Gly	Lys	Leu	Ala	Gly	Ile	Leu	Ala	Gly	Glu
	355						360					365			
Leu	Gly	Glu	Asn	Val	Ala	Leu	Ala	Arg	Arg	Ala	Gly	Phe	Leu	His	Asp

370		375		380
Met Gly Lys Ala Ile Asp Arg Glu Val Glu Gly Ser His Val Glu Ile				
385		390		400
Gly Met Glu Phe Ala Arg Lys Tyr Lys Glu His Pro Val Val Val Asn				
	405		410	415
Thr Ile Ala Ser His His Gly Asp Val Glu Pro Asp Ser Val Ile Ala				
	420		425	430
Val Leu Val Ala Ala Ala Asp Ala Leu Ser Ser Ala Arg Pro Gly Ala				
	435		440	445
Arg Asn Glu Ser Met Glu Asn Tyr Ile Lys Arg Leu Arg Asp Leu Glu				
	450		455	460
Glu Ile Ala Thr Ser Phe Asp Gly Val Gln Asn Ser Phe Ala Leu Gln				
465		470		480
Ala Gly Arg Glu Ile Arg Ile Met Val Gln Pro Glu Lys Ile Ser Asp				
	485		490	495
Asp Gln Val Val Ile Leu Ser His Lys Val Arg Glu Lys Ile Glu Asn				
	500		505	510
Asn Leu Asp Tyr Pro Gly Asn Ile Lys Val Thr Val Ile Arg Glu Met				
	515		520	525
Arg Ala Val Asp Tyr Ala Lys				
530		535		

<210> SEQ ID NO 255

<211> LENGTH: 687

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 255

atgcaatttt	ccaggaattc	tgataaaata	caaagaaata	aggggaaact	aatgaaaaaa	60
tttcaattct	ttttacttat	cgagtgtata	ctgctagcta	tgggtatcat	gacaatcttg	120
gataatgatt	tatcaagttt	tatcctaatt	ctagtctcta	tcttattagc	attacgcttt	180
tataaccaag	atagccgcaa	taatttttta	ctaactgtca	gtttattggt	tcttttttta	240
attttcatgc	ttaatcccta	cattatcatg	gctgttcttt	tggggatagt	ttacattttc	300
attaaccatt	tttcacaagt	caaaaagaag	aatcgctttg	ccttgattcg	tttcaaggaa	360
gaaaagattg	aagtgaacaa	taccaagcat	caatggattg	gtactgctaa	ttatgaaagt	420
gattattatt	gttttgatga	cattaacatc	attcgaatct	caggaaatga	cacggttgac	480
ttaaccaatg	ttattgtgac	aggaatggat	aatatcattg	tgatacgtaa	aatttttggg	540
aatacgacta	tattggtacc	tattgatgtc	actgttactt	tagatgtag	ttccatatac	600
ggaagcgttg	attttttttag	atgtcagcaa	tatgatttgc	gcaacgaatc	tattaagttg	660
aaagaaacgg	ataaccaatc	ccttttaa				687

<210> SEQ ID NO 256

<211> LENGTH: 228

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 256

Met Gln Phe Ser Arg Asn Ser Asp Lys Ile Gln Arg Asn Lys Gly Lys					
1	5		10		15
Leu Met Lys Lys Phe Gln Phe Phe Leu Leu Ile Glu Cys Ile Leu Leu					
	20		25		30
Ala Met Gly Ile Met Thr Ile Leu Asp Asn Asp Leu Ser Ser Phe Ile					
	35		40		45
Leu Ile Leu Val Leu Ile Leu Leu Ala Leu Arg Phe Tyr Asn Gln Asp					
	50		55		60
Ser Arg Asn Asn Phe Leu Leu Thr Val Ser Leu Leu Phe Leu Phe Leu					
65		70		75	80
Ile Phe Met Leu Asn Pro Tyr Ile Ile Met Ala Val Leu Leu Gly Ile					
	85		90		95

Val	Tyr	Ile	Phe	Ile	Asn	His	Phe	Ser	Gln	Val	Lys	Lys	Lys	Asn	Arg
			100					105					110		
Phe	Ala	Leu	Ile	Arg	Phe	Lys	Glu	Glu	Lys	Ile	Glu	Val	Asn	Asn	Thr
		115					120					125			
Lys	His	Gln	Trp	Ile	Gly	Thr	Ala	Asn	Tyr	Glu	Ser	Asp	Tyr	Tyr	Cys
		130				135					140				
Phe	Asp	Asp	Ile	Asn	Ile	Ile	Arg	Ile	Ser	Gly	Asn	Asp	Thr	Val	Asp
145					150					155				160	
Leu	Thr	Asn	Val	Ile	Val	Thr	Gly	Met	Asp	Asn	Ile	Ile	Val	Ile	Arg
			165					170						175	
Lys	Ile	Phe	Gly	Asn	Thr	Thr	Ile	Leu	Val	Pro	Ile	Asp	Val	Thr	Val
		180						185					190		
Thr	Leu	Asp	Val	Ser	Ser	Ile	Tyr	Gly	Ser	Val	Asp	Phe	Phe	Arg	Cys
		195					200					205			
Gln	Gln	Tyr	Asp	Leu	Arg	Asn	Glu	Ser	Ile	Lys	Leu	Lys	Glu	Thr	Asp
		210				215					220				
Asn	Gln	Ser	Leu												
225															

<210> SEQ ID NO 257
 <211> LENGTH: 1005
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 257

atgaaaaaac	gttactatgc	tcttgtttgg	ctctactcaa	ccattacccat	tttatctatt	60
gtttttgtgg	tcattggataa	tttaggaatc	acttttaact	accttcgcaa	tcatttatgg	120
caggctcgac	gtctagggtt	ttcgatttta	ttggttgattg	tttctgtgac	tttattattg	180
ttgttattgt	ggattattat	ggatgataac	agtaagcgta	acatcaacca	aaatctaaaa	240
tatattctca	ataatcgacg	actctatcta	gatgagacat	cagaaatcaa	tactaattta	300
agtcgacttt	ctaaaaaaat	gtctcacctg	actgctaaca	tgcaaaaagaa	agaaagtgtc	360
tatattcttg	atagccaaga	agttgtaaaa	caagagcgca	aacgaattgc	aagagattta	420
catgacacag	tcagtcaaga	gctattcgct	tcgtcattga	ttttatcagg	aatttcgatg	480
agtttggaac	aactggacaa	aacacaatta	caaacacagt	taacaacggt	tgaagcaatg	540
ttgcaaaatg	ctcaaaaatga	tctacgcatt	ctccttttgc	atcttagacc	taccgagcta	600
gctaatacga	ctttatctga	gggccttcat	atgattctta	aggaattaac	agataaaagt	660
gatattgaag	tcattttataa	ggaaaccatt	gctcagcttc	ctaaaaacaat	ggaagataat	720
cttttttagaa	ttgccaaga	attcattagc	aacacgttaa	aacatgctaa	agctagtcga	780
attgaagttt	atctcaatca	aacctcaaca	gaattacaat	tgaagatgat	tgatgatggt	840
gtaggatttg	atatggatca	ggtaagggat	ttgagttatg	gtctgaagaa	tattgaagac	900
cgtgtcaatg	athtagcagg	aaacctacat	ttaattagtc	aaaaaggcaa	aggagtttcc	960
atggatatta	gactgccgat	agtgaaggga	gatgacgatg	agtaa		1005

<210> SEQ ID NO 258
 <211> LENGTH: 334
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 258

Met	Lys	Lys	Arg	Tyr	Tyr	Ala	Leu	Val	Trp	Leu	Tyr	Ser	Thr	Ile	Thr
1			5						10					15	
Ile	Leu	Ser	Ile	Val	Phe	Val	Val	Met	Asp	Asn	Leu	Gly	Ile	Thr	Phe
		20						25				30			
Asn	Tyr	Leu	Arg	Asn	His	Leu	Trp	Gln	Val	Glu	Arg	Leu	Gly	Phe	Ser
		35				40					45				
Ile	Leu	Leu	Leu	Ile	Val	Ser	Val	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Trp
	50					55				60					
Ile	Ile	Met	Asp	Asp	Asn	Ser	Lys	Arg	Asn	Ile	Asn	Gln	Asn	Leu	Lys
65					70				75					80	

Met	Ile	Phe	Ala	Pro	Tyr	Ile	Gln	Gly	Leu	His	His	Leu	Thr	Ile	Gln
65					70					75					80
Asn	Phe	Cys	Leu	Leu	Trp	Ile	Lys	Leu	Val	Lys	Ser	Ser	Arg		
				85					90						

<210> SEQ ID NO 261

<211> LENGTH: 1356

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 261

```

atggttagaag attttcttca atttttagga tttatatttt tagatattat tgaaattatg      60
ttaacggttaa agcttttttag ctttgtaagt gcaattccgc ttcgcctgaa aaatattttt      120
tatttatcac ttagtatggt tttgtttcaa gtagtttttt gggctttctt tccagaccat      180
ttcattcttg atgttgatgat gttggctcag tttcttttct ttgcgcttat agccctatac      240
tatggtaaat caataaaaagc taagttttta atgttttatg ccttttttcc actagtgtct      300
attagtttgg ttaagcgatt tattgtattt tttgttatgc cattgtttgg tatgccttat      360
tcagttgtta aacataatac actactgatt tacagcatta cttgttttag tatttttttg      420
atztatcgct gcattcaagt ttttcatttc gattttttcaa cctggcgcca atattttcaa      480
tcacatagag ctagtaaaact attagtgttt actaactctt cgatggctct atattacttg      540
tgtgtccaag ggatagatgt gatgtcgcct tctttatcag gacttgctac aacgactgct      600
cgttcaatca tagtgctctt ttatttcatt ttgtttctta ctttattaat tcatttagag      660
cgttatgtaa aacaaaactc tattgaggca attgtgcaac aaaaagaata tcgtgagctg      720
attaattata gtcagcacct tggattgctg tatcaagata ttcaagagct taggcggcta      780
ttaactaccg tgtctagtcg tcttaagatt ggaatcgaac aaaatgatat ctctattgtg      840
agacttactt atgaagggtat cttgaatgct gaaaagaata atgctaaaga tgacagactt      900
gatttaactt gtttagataa attacaagtt gaagcaatca gacatattgt tttagctaaa      960
ttaattgagg caaaaaataa gaagcttaag gttgaggtat cgatccctaa ttgtattgca     1020
acgttttttc tagaagtagt agatttcact aagctattgt cattttttgt agataatgct     1080
atagaaatga gtttgagac aaagcaacct tgcttatcaa tagcatttct ggatcaaaac     1140
cataaacttg tcatagtcac tcaaagcagt actaaacaag gacaagatga tagtcaaagc     1200
gtgtttgcta taccggcttt gaaaaaaaga gatgactggc aatttgactt aaggaatgtc     1260
acgaccattt taaatcgtta tgactatctc acaattagct cgcagattca tgatggcatt     1320
ttaaccacgt taatagaaat agctaagcct gactga                                1356

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<210> SEQ ID NO 262

<211> LENGTH: 451

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 262

Met	Leu	Glu	Asp	Phe	Leu	Gln	Phe	Leu	Gly	Phe	Ile	Phe	Leu	Asp	Ile
1				5					10					15	
Ile	Glu	Ile	Met	Leu	Thr	Leu	Lys	Leu	Phe	Ser	Phe	Val	Ser	Ala	Ile
			20					25					30		
Pro	Leu	Arg	Leu	Lys	Asn	Ile	Phe	Tyr	Leu	Ser	Leu	Ser	Met	Val	Leu
		35				40						45			
Phe	Gln	Val	Val	Phe	Trp	Ala	Phe	Phe	Pro	Asp	His	Phe	Ile	Leu	Asp
	50				55				60						
Val	Val	Met	Leu	Ala	Gln	Phe	Leu	Phe	Phe	Ala	Leu	Ile	Ala	Leu	Tyr
65				70					75					80	
Tyr	Gly	Lys	Ser	Ile	Lys	Ala	Lys	Phe	Leu	Met	Phe	Tyr	Ala	Phe	Phe
			85					90					95		
Pro	Leu	Val	Ser	Ile	Ser	Leu	Val	Lys	Arg	Phe	Ile	Val	Phe	Phe	Val
			100					105					110		
Met	Pro	Leu	Phe	Gly	Met	Pro	Tyr	Ser	Val	Val	Lys	His	Asn	Thr	Leu
		115				120						125			
Leu	Ile	Tyr	Ser	Ile	Thr	Cys	Phe	Ser	Ile	Phe	Leu	Ile	Tyr	Arg	Cys
	130					135					140				

Ile	Gln	Val	Phe	His	Phe	Asp	Phe	Ser	Thr	Trp	Arg	Gln	Tyr	Phe	Gln	145	150	155	160
Ser	His	Arg	Ala	Ser	Lys	Leu	Leu	Val	Phe	Thr	Asn	Ser	Ser	Met	Ala	165	170	175	
Leu	Tyr	Tyr	Leu	Cys	Val	Gln	Gly	Ile	Asp	Val	Met	Ser	Pro	Ser	Leu	180	185	190	
Ser	Gly	Leu	Ala	Thr	Thr	Thr	Ala	Arg	Ser	Ile	Ile	Val	Leu	Phe	Tyr	195	200	205	
Phe	Ile	Leu	Phe	Leu	Thr	Leu	Leu	Ile	His	Leu	Glu	Arg	Tyr	Val	Lys	210	215	220	
Gln	Asn	Ser	Ile	Glu	Ala	Ile	Val	Gln	Gln	Lys	Glu	Tyr	Arg	Glu	Leu	225	230	235	240
Ile	Asn	Tyr	Ser	Gln	His	Leu	Gly	Leu	Leu	Tyr	Gln	Asp	Ile	Gln	Glu	245	250	255	
Leu	Arg	Arg	Leu	Leu	Thr	Thr	Val	Ser	Ser	Arg	Leu	Lys	Ile	Gly	Ile	260	265	270	
Glu	Gln	Asn	Asp	Ile	Ser	Ile	Val	Arg	Leu	Thr	Tyr	Glu	Gly	Ile	Leu	275	280	285	
Asn	Ala	Glu	Lys	Asn	Asn	Ala	Lys	Asp	Asp	Arg	Leu	Asp	Leu	Thr	Cys	290	295	300	
Leu	Asp	Lys	Leu	Gln	Val	Glu	Ala	Ile	Arg	His	Ile	Val	Leu	Ala	Lys	305	310	315	320
Leu	Ile	Glu	Ala	Lys	Asn	Lys	Lys	Leu	Lys	Val	Glu	Val	Ser	Ile	Pro	325	330	335	
Asn	Cys	Ile	Ala	Thr	Phe	Phe	Leu	Glu	Val	Val	Asp	Phe	Thr	Lys	Leu	340	345	350	
Leu	Ser	Phe	Leu	Leu	Asp	Asn	Ala	Ile	Glu	Met	Ser	Leu	Glu	Thr	Lys	355	360	365	
Gln	Pro	Cys	Leu	Ser	Ile	Ala	Phe	Leu	Asp	Gln	Asn	His	Lys	Leu	Val	370	375	380	
Ile	Val	Ile	Gln	Ser	Ser	Thr	Lys	Gln	Gly	Gln	Asp	Asp	Ser	Gln	Ser	385	390	395	400
Val	Phe	Ala	Ile	Pro	Ala	Leu	Lys	Lys	Arg	Asp	Asp	Trp	Gln	Phe	Asp	405	410	415	
Leu	Arg	Asn	Val	Thr	Thr	Ile	Leu	Asn	Arg	Tyr	Asp	Tyr	Leu	Thr	Ile	420	425	430	
Ser	Ser	Gln	Ile	His	Asp	Gly	Ile	Leu	Thr	Gln	Leu	Ile	Glu	Ile	Ala	435	440	445	
Lys	Pro	Asp														450			

<210> SEQ ID NO 263

<211> LENGTH: 999

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 263

ttgatatact	gtaactataa	cgtagattaac	acaaagggag	gttgggaaat	gataagacaa	60
accaacaaaa	agacatcctt	ttggaaaaat	gtgattaaat	accgggcctt	attattaatg	120
gtattaccag	gtttcatctg	gttcatcttt	ttcttttata	ttccagtttt	agccaatgtg	180
gttgctttta	aagattttca	ttattcagca	gggggcttta	tggaaagttt	gaaggagagc	240
ccttggggtg	gtttggctaa	cttcaaatac	ctcttttgctt	ccaaagatgc	ttgggttgatt	300
accagaaata	ccattgctta	caatgtgatt	ttcttactct	ttaatgtttt	ctttgcgatt	360
gcttttgcca	tatcatgag	tgagttacga	aataagagaa	cggttaaggt	ctatcacacc	420
atgtccttat	tgcccttattt	cttatcatgg	gtgggttattg	aatactttgt	ttctgccttt	480
ttaaatacgg	ataaagggttt	cattaatcag	ctcttgaccg	gaagtggagc	agatccaatc	540
aagtgggtatt	ccaatcccac	ttgggtggccc	ttgatttttac	ttttcatgag	tgtctggaag	600
gggctaggct	acaatagcat	tatctactat	gcttcagtc	aagggatttc	tgatacttat	660

tatgaagctg	ctatggtgga	tggtgcaagc	aaatggcaac	aaattaggaa	catcaccatt	720
ccacaattat	tgccaatgat	gtctatctta	ttgatcatta	atattggtaa	tattttttaa	780
tctgatttcg	gacttttcta	cgttattcct	aagaattcag	gcccacttta	tgacgtgacc	840
agtgtgtcag	atacctatgt	ctacaatgcc	ttgactgcta	caggagatat	tgggatggca	900
tcggcagcta	gccttttatca	gtcagtagtt	gggaccagca	tcttgttagt	caccaatgcg	960
attgttcgctc	gcatggaccc	tgatgcagcc	ttgttttag			999

<210> SEQ ID NO 264
 <211> LENGTH: 332
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 264

Met	Ile	Tyr	Cys	Asn	Tyr	Asn	Val	Ile	Asn	Thr	Lys	Gly	Gly	Trp	Glu	1	5	10	15
Met	Ile	Arg	Gln	Thr	Asn	Lys	Lys	Thr	Ser	Phe	Trp	Lys	Asn	Val	Ile	20	25	30	
Lys	Tyr	Arg	Ala	Leu	Leu	Leu	Met	Val	Leu	Pro	Gly	Phe	Ile	Trp	Phe	35	40	45	
Ile	Phe	Phe	Phe	Tyr	Ile	Pro	Val	Leu	Ala	Asn	Val	Val	Ala	Phe	Lys	50	55	60	
Asp	Phe	His	Tyr	Ser	Ala	Gly	Gly	Phe	Met	Glu	Ser	Leu	Lys	Glu	Ser	65	70	75	80
Pro	Trp	Val	Gly	Leu	Ala	Asn	Phe	Lys	Tyr	Leu	Phe	Ala	Ser	Lys	Asp	85	90	95	
Ala	Trp	Leu	Ile	Thr	Arg	Asn	Thr	Ile	Ala	Tyr	Asn	Val	Ile	Phe	Leu	100	105	110	
Leu	Phe	Asn	Val	Phe	Phe	Ala	Ile	Ala	Phe	Ala	Ile	Ile	Met	Ser	Glu	115	120	125	
Leu	Arg	Asn	Lys	Arg	Thr	Val	Lys	Val	Tyr	His	Thr	Met	Ser	Leu	Leu	130	135	140	
Pro	Tyr	Phe	Leu	Ser	Trp	Val	Val	Ile	Glu	Tyr	Phe	Val	Ser	Ala	Phe	145	150	155	160
Leu	Asn	Thr	Asp	Lys	Gly	Phe	Ile	Asn	Gln	Leu	Leu	Thr	Gly	Ser	Gly	165	170	175	
Ala	Asp	Pro	Ile	Lys	Trp	Tyr	Ser	Asn	Pro	Thr	Trp	Trp	Pro	Leu	Ile	180	185	190	
Leu	Leu	Phe	Met	Ser	Val	Trp	Lys	Gly	Leu	Gly	Tyr	Asn	Ser	Ile	Ile	195	200	205	
Tyr	Tyr	Ala	Ser	Val	Lys	Gly	Ile	Ser	Asp	Thr	Tyr	Tyr	Glu	Ala	Ala	210	215	220	
Met	Val	Asp	Gly	Ala	Ser	Lys	Trp	Gln	Gln	Ile	Arg	Asn	Ile	Thr	Ile	225	230	235	240
Pro	Gln	Leu	Leu	Pro	Met	Met	Ser	Ile	Leu	Leu	Ile	Ile	Asn	Ile	Gly	245	250	255	
Asn	Ile	Phe	Lys	Ser	Asp	Phe	Gly	Leu	Phe	Tyr	Val	Ile	Pro	Lys	Asn	260	265	270	
Ser	Gly	Pro	Leu	Tyr	Asp	Val	Thr	Ser	Val	Ser	Asp	Thr	Tyr	Val	Tyr	275	280	285	
Asn	Ala	Leu	Thr	Ala	Thr	Gly	Asp	Ile	Gly	Met	Ala	Ser	Ala	Ala	Ser	290	295	300	
Leu	Tyr	Gln	Ser	Val	Val	Gly	Thr	Ser	Ile	Leu	Leu	Val	Thr	Asn	Ala	305	310	315	320
Ile	Val	Arg	Arg	Met	Asp	Pro	Asp	Ala	Ala	Leu	Phe					325	330		

<210> SEQ ID NO 265
 <211> LENGTH: 927

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 265

```
atggagaaaa agaaaaaagt cgaaaagggt aatgttagaa cctttgatcg aaaaaccaat    60
gctatcttta atattctgat tggctctgtt gccatctctt gtatcattcc ttttatcttc    120
gtgattatta tttccttcac tgatgaaagt tacttgatta atcatgggta tagttttttt    180
ccagatgtct ggtcaactaa ggcttaccag tatatttttc aaggagccat gtcccataga    240
atcatgaggt catttgggat atccgtgttt attacagtgg tgggaacctt tattaacacg    300
accatgacat caacctatgc ttatgcgatt tcaagacctt atttcccata cagacgtttt    360
tttactgttt atgcacttat caccatgctc tttgcaccag ggatgggttg taattacttg    420
gtggtcagca atctccttca tttgaaggat acggtttggg ccttgatttt accaatggct    480
ctgggcccat ttggcatctt ggcatgaga acgttcttta aaaagacagt tccagatagc    540
attattgagt cggctcgtat ggatggggct agtgaatgga tgatttttat gaaaattgtc    600
ttaccattag ctgttccagg gattgccacc atcagtttat tttctgcctt aacttattgg    660
aatgattggt ttaacgcctt gctttatgtg caaagtgaga atctttaccc atgcagtagc    720
ttactgatga aaattcagag caacctacag gccttggcac aaaatgctgg catgagtgc    780
caaatggcag atagcttagc atcgctgcca aaagaatcag ttcgtatggc tatcgtgggt    840
attgcaacct tgccgattgc cttgacttac ccattcttcc aaaagtactt tgtcggtggt    900
ttgaaccatt gtggggtgaa ggaatag                                927
```

<210> SEQ ID NO 266

<211> LENGTH: 308

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 266

```
Met Glu Lys Lys Lys Lys Val Glu Lys Val Asn Val Arg Thr Phe Asp
1          5          10          15
Arg Lys Thr Asn Ala Ile Phe Asn Ile Leu Ile Gly Leu Phe Ala Ile
20          25          30
Ser Cys Ile Ile Pro Phe Ile Phe Val Ile Ile Ile Ser Phe Thr Asp
35          40          45
Glu Ser Tyr Leu Ile Asn His Gly Tyr Ser Phe Phe Pro Asp Val Trp
50          55          60
Ser Thr Lys Ala Tyr Gln Tyr Ile Phe Gln Gly Ala Met Ser His Arg
65          70          75          80
Ile Met Arg Ser Phe Gly Ile Ser Val Phe Ile Thr Val Val Gly Thr
85          90          95
Phe Ile Asn Thr Thr Met Thr Ser Thr Tyr Ala Tyr Ala Ile Ser Arg
100         105         110
Pro Tyr Phe Pro Tyr Arg Arg Phe Phe Thr Val Tyr Ala Leu Ile Thr
115         120         125
Met Leu Phe Ala Pro Gly Met Val Ala Asn Tyr Leu Val Val Ser Asn
130         135         140
Leu Leu His Leu Lys Asp Thr Val Trp Ala Leu Ile Leu Pro Met Ala
145         150         155         160
Leu Gly Pro Phe Gly Ile Leu Val Met Arg Thr Phe Phe Lys Lys Thr
165         170         175
Val Pro Asp Ser Ile Ile Glu Ser Ala Arg Met Asp Gly Ala Ser Glu
180         185         190
Trp Met Ile Phe Met Lys Ile Val Leu Pro Leu Ala Val Pro Gly Ile
195         200         205
Ala Thr Ile Ser Leu Phe Ser Ala Leu Thr Tyr Trp Asn Asp Trp Phe
210         215         220
Asn Ala Leu Leu Tyr Val Gln Ser Glu Asn Leu Tyr Pro Met Gln Tyr
225         230         235         240
Leu Leu Met Lys Ile Gln Ser Asn Leu Gln Ala Leu Ala Gln Asn Ala
245         250         255
```

Gly	Met	Ser	Ala	Gln	Met	Ala	Asp	Ser	Leu	Ala	Ser	Leu	Pro	Lys	Glu
			260					265					270		
Ser	Val	Arg	Met	Ala	Ile	Val	Val	Ile	Ala	Thr	Leu	Pro	Ile	Ala	Leu
		275					280					285			
Thr	Tyr	Pro	Phe	Phe	Gln	Lys	Tyr	Phe	Val	Gly	Gly	Leu	Thr	Ile	Gly
	290					295					300				
Gly	Val	Lys	Glu												
305															

<210> SEQ ID NO 267
 <211> LENGTH: 1728
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 267

ttgatgagtg	ttaaaacatt	gggaaggat	gtgactaacc	actttaagca	gggttttttg	60
attaatcgac	tgatgaaatt	atatagcctg	ctaattgtaa	gtttttttcac	tttagcagct	120
attggccttg	gcagttattc	tattagtagt	acttataaaa	gggtggatgc	tgaggcgcag	180
atgcgattgg	aggagactct	aggtagattg	cagtcacaaa	acgatattac	cctacgggtt	240
ttagaccagt	tggttgccg	ttcagaagat	taccataatc	tctatcaata	catgacgtta	300
accccaaacc	aataattttc	aaacgttttt	gaagactggg	aaaaaggaaa	agacacggtc	360
ctattttctg	aagagggtgag	gcgtcttttt	gacttgtacc	ctgatgtgac	ttctatgacc	420
ctactgctag	aggacagtag	tgcttatctg	tacgccgata	aggtcattaa	gacgggtcgt	480
ttgctttata	gcaagcctga	aaaagtaacc	ggaaatgttt	tagttcgctc	tattcgaaat	540
ccagaatcag	gagatgtgac	aggtcgtctt	tacctgacct	ttgacaaacc	accgactttg	600
gtagagacac	agcaggatca	ctatttagct	acttttgctt	ttgattacta	tggccgcaaa	660
ctcttccatc	aaggaggctg	gagatttcct	catttagagg	ctgagggttaa	aaaggctatc	720
aaggcagatc	gggcagctga	tcttagtaat	cttagcaagg	cttatcggat	gcagtacaat	780
cgctcgggag	acctcttggc	ttatgtggct	gtcagaaaaat	cctattttatt	agcggaagct	840
gtcaggacag	tttttgtgta	tggccttggt	tctctacttt	tagcttggct	gttattgcag	900
ttgctcttta	gggttttccg	aaattatatc	cagcagggtt	ctgaaattac	ggatactgtt	960
gaaatggttg	cagcaggcga	tttgtcttta	accatcgaca	acagccacat	ggaattggaa	1020
ctgtatcata	tctcagaagc	cattaatcag	atgttggcca	gcattaaagc	ttatattgac	1080
gaagtttatg	tgtttagagg	agagcaacga	gatgcccaaa	tgagagctct	gcagtctcaa	1140
atcaaccctc	attttttata	caacacgtta	gagtatatct	ggatgtacgc	ccttagttgt	1200
caacaagaag	aattagcaga	tgtcatttat	gcctttgcga	gtctgcttcg	caacaatatt	1260
agccaagata	agatgaccac	cttaaaagaa	gaactgggctt	tttgtaaaaa	gtacattttac	1320
ctttatcaaa	tgcggtatcc	agatagcttc	gcttatcatg	taaaaattga	tgagagtgtt	1380
gctgacttag	ccattcctaa	atttgtcatt	caacctctcg	ttgaaaaatta	ttttgtgcat	1440
gggattgatt	atagtcgcca	tgacaatgca	ctaagcatca	aggctttaga	tgagacggat	1500
catctcttga	ttcaggtgct	tgataatgga	cgtgggtatta	gtcaagagcg	cttagcagat	1560
atggaaaaaa	ggcttcaaga	gcaccaaaca	acaggcaata	gctctattgg	tttgcaaaat	1620
gtttacctcc	gtctctttca	tcattttcga	gacagggttt	cttgggtccat	ggctaaggag	1680
ccaaatggtg	gctttatcat	tcaaattagg	attagaaagg	atgcttga		1728

<210> SEQ ID NO 268
 <211> LENGTH: 575
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 268

Met	Met	Ser	Val	Lys	Thr	Leu	Gly	Arg	Tyr	Val	Thr	Asn	His	Phe	Lys
1			5						10					15	
Gln	Gly	Phe	Leu	Ile	Asn	Arg	Leu	Met	Lys	Leu	Tyr	Ser	Leu	Leu	Ile
		20					25					30			
Val	Ser	Phe	Phe	Thr	Leu	Ala	Ala	Ile	Gly	Leu	Ser	Ser	Tyr	Ser	Ile
		35				40					45				
Ser	Ser	Thr	Tyr	Lys	Arg	Val	Asp	Ala	Glu	Ala	Gln	Met	Arg	Leu	Glu
50						55					60				

Glu	Thr	Leu	Gly	Arg	Leu	Gln	Ser	Gln	Asn	Asp	Ile	Thr	Leu	Arg	Val	65	70	75	80
Leu	Asp	Gln	Leu	Val	Gly	Arg	Ser	Glu	Asp	Tyr	His	Asn	Leu	Tyr	Gln	85	90	95	
Tyr	Met	Thr	Leu	Thr	Pro	Asn	Gln	Tyr	Phe	Ser	Asn	Val	Phe	Glu	Asp	100	105	110	
Trp	Glu	Lys	Gly	Lys	Asp	Thr	Val	Leu	Phe	Ser	Glu	Glu	Val	Arg	Arg	115	120	125	
Leu	Phe	Asp	Leu	Tyr	Pro	Asp	Val	Thr	Ser	Met	Thr	Leu	Leu	Leu	Glu	130	135	140	
Asp	Ser	Ser	Ala	Tyr	Leu	Tyr	Ala	Asp	Lys	Val	Ile	Lys	Thr	Gly	Arg	145	150	155	160
Leu	Leu	Tyr	Ser	Lys	Pro	Glu	Lys	Val	Thr	Gly	Asn	Val	Leu	Val	Arg	165	170	175	
Ser	Ile	Arg	Asn	Pro	Glu	Ser	Gly	Asp	Val	Thr	Gly	Arg	Leu	Tyr	Leu	180	185	190	
Thr	Phe	Asp	Lys	Pro	Pro	Thr	Leu	Val	Glu	Thr	Gln	Gln	Asp	His	Tyr	195	200	205	
Leu	Ala	Thr	Phe	Ala	Phe	Asp	Tyr	Tyr	Gly	Arg	Lys	Leu	Phe	His	Gln	210	215	220	
Gly	Gly	Arg	Arg	Phe	Pro	His	Leu	Glu	Ala	Glu	Val	Lys	Lys	Ala	Ile	225	230	235	240
Lys	Ala	Asp	Arg	Ala	Ala	Asp	Leu	Ser	Asn	Leu	Ser	Lys	Ala	Tyr	Arg	245	250	255	
Met	Gln	Tyr	Asn	Arg	Ser	Gly	Asp	Leu	Leu	Ala	Tyr	Val	Ala	Val	Arg	260	265	270	
Lys	Ser	Tyr	Leu	Leu	Ala	Glu	Ala	Val	Arg	Thr	Val	Phe	Val	Tyr	Gly	275	280	285	
Leu	Val	Ser	Leu	Leu	Leu	Ala	Trp	Leu	Leu	Leu	Gln	Leu	Leu	Phe	Arg	290	295	300	
Val	Phe	Arg	Asn	Tyr	Ile	Gln	Gln	Val	Ser	Glu	Ile	Thr	Asp	Thr	Val	305	310	315	320
Glu	Met	Val	Ala	Ala	Gly	Asp	Leu	Ser	Leu	Thr	Ile	Asp	Asn	Ser	His	325	330	335	
Met	Glu	Leu	Glu	Leu	Tyr	His	Ile	Ser	Glu	Ala	Ile	Asn	Gln	Met	Leu	340	345	350	
Ala	Ser	Ile	Lys	Ala	Tyr	Ile	Asp	Glu	Val	Tyr	Val	Leu	Glu	Val	Glu	355	360	365	
Gln	Arg	Asp	Ala	Gln	Met	Arg	Ala	Leu	Gln	Ser	Gln	Ile	Asn	Pro	His	370	375	380	
Phe	Leu	Tyr	Asn	Thr	Leu	Glu	Tyr	Ile	Arg	Met	Tyr	Ala	Leu	Ser	Cys	385	390	395	400
Gln	Gln	Glu	Glu	Leu	Ala	Asp	Val	Ile	Tyr	Ala	Phe	Ala	Ser	Leu	Leu	405	410	415	
Arg	Asn	Asn	Ile	Ser	Gln	Asp	Lys	Met	Thr	Thr	Leu	Lys	Glu	Glu	Leu	420	425	430	
Ala	Phe	Cys	Glu	Lys	Tyr	Ile	Tyr	Leu	Tyr	Gln	Met	Arg	Tyr	Pro	Asp	435	440	445	
Ser	Phe	Ala	Tyr	His	Val	Lys	Ile	Asp	Glu	Ser	Val	Ala	Asp	Leu	Ala	450	455	460	
Ile	Pro	Lys	Phe	Val	Ile	Gln	Pro	Leu	Val	Glu	Asn	Tyr	Phe	Val	His	465	470	475	480
Gly	Ile	Asp	Tyr	Ser	Arg	His	Asp	Asn	Ala	Leu	Ser	Ile	Lys	Ala	Leu	485	490	495	
Asp	Glu	Thr	Asp	His	Leu	Leu	Ile	Gln	Val	Leu	Asp	Asn	Gly	Arg	Gly	500	505	510	
Ile	Ser	Gln	Glu	Arg	Leu	Ala	Asp	Met	Glu	Lys	Arg	Leu	Gln	Glu	His				

	515						520						525						
Gln	Thr	Thr	Gly	Asn	Ser	Ser	Ile	Gly	Leu	Gln	Asn	Val	Tyr	Leu	Arg				
	530						535					540							
Leu	Phe	His	His	Phe	Arg	Asp	Arg	Val	Ser	Trp	Ser	Met	Ala	Lys	Glu				
545					550					555					560				
Pro	Asn	Gly	Gly	Phe	Ile	Ile	Gln	Ile	Arg	Ile	Arg	Lys	Asp	Ala					
				565					570					575					

<210> SEQ ID NO 269

<211> LENGTH: 1107

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 269

atggaacata	aatggaaatt	atggctat	ttt	atcg	ttggag	tggtctt	gtt	aatagg	cgga	60	
gcttctgttc	tcattcagaa	agg	tcaagcc	aagg	ctttta	gtcaagg	caa	gcctca	acta	120	
ccagctaaaa	aagtcaa	atc	cactaa	agta	gatcc	caatg	ccc	ctgtt	ga	180	
at	tac	ctgg	ctg	ttt	ctgg	ggc	gtt	gaaga	aat	240	
gtt	ctag	atg	cgg	tgt	cagg	ctat	gcc	aat	ggtag	agg	300
at	cat	caga	ctg	gtc	atg	caacc	gtt	gaag	tgg	cct	360
tt	gaa	aga	aat	tatt	act	gca	tttt	ttcc	ga	attatt	420
gg	aat	gat	c	gcg	gtag	tca	atacc	gaact	ggg	attt	480
g	ct	att	tatt	g	ctt	caa	agaaaa	g	cta	agg	540
g	aaa	aag	cac	catt	gaa	aca	cttt	atta	ag	gcaga	600
a	aaa	at	ccaa	atgg	ctact	g	ccat	att	gac	atca	660
g	aa	gca	agt	ac	ccaaa	aacc	aag	tgcc	act	gagat	720
t	acc	gag	tga	cg	aaaa	aaaa	cg	aaa	act	gaa	780
ttt	gat	gcag	ga	att	ttac	gt	ag	ac	gtt	gtg	840
aa	att	tga	aat	cag	gtt	gtg	ttg	gcca	agc	tttag	900
cg	ct	aca	agg	aag	ata	agag	ttt	caat	atg	acg	960
a	att	ct	cat	c	tg	ggg	cat	gt	cttt	act	1020
t	gc	at	ca	ata	g	ctt	gt	ctat	tac	cttt	1080
g	gt	tatt	t	t	at	ccaaa	ag	ctg	atat	gga	1107

<210> SEQ ID NO 270

<211> LENGTH: 368

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 270

Met	Glu	His	Lys	Trp	Lys	Leu	Trp	Leu	Phe	Ile	Val	Gly	Val	Val	Leu
1			5						10					15	
Leu	Ile	Gly	Gly	Ala	Ser	Val	Leu	Ile	Gln	Lys	Gly	Gln	Ala	Lys	Ala
			20						25				30		
Phe	Ser	Gln	Gly	Lys	Pro	Gln	Leu	Pro	Ala	Lys	Lys	Val	Lys	Ser	Thr
			35						40				45		
Lys	Val	Asp	Pro	Asn	Ala	Pro	Val	Asp	Gln	Lys	Val	Ile	Tyr	Leu	Ala
			50						55				60		
Gly	Gly	Cys	Phe	Trp	Gly	Val	Glu	Glu	Tyr	Phe	Ser	Gln	Val	Asp	Gly
65									70				75		80
Val	Leu	Asp	Ala	Val	Ser	Gly	Tyr	Ala	Asn	Gly	Arg	Gly	Asp	Thr	Thr
									85				90		95
Asn	Tyr	Gln	Leu	Ile	His	Gln	Thr	Gly	His	Ala	Glu	Thr	Val	Glu	Val
			100						105				110		
Ala	Tyr	Asp	Ala	Asn	Arg	Ile	Ser	Leu	Lys	Glu	Leu	Leu	Leu	His	Phe
			115						120				125		
Phe	Arg	Ile	Ile	Asp	Pro	Thr	Ser	Leu	Asn	Lys	Gln	Gly	Asn	Asp	Arg
			130						135				140		
Gly	Ser	Gln	Tyr	Arg	Thr	Gly	Ile	Tyr	Tyr	Thr	Asp	Lys	Ala	Asp	Leu

145		150		155		160									
Ala	Ile	Ile	Asp	Glu	Val	Phe	Lys	Glu	Lys	Ala	Lys	Asp	Tyr	Lys	Lys
		165		170		175									
Lys	Ile	Val	Val	Glu	Lys	Ala	Pro	Leu	Lys	His	Phe	Ile	Lys	Ala	Glu
		180		185		190									
Asp	Tyr	His	Gln	Asp	Tyr	Leu	Lys	Lys	Asn	Pro	Asn	Gly	Tyr	Cys	His
	195			200		205									
Ile	Asp	Ile	Asn	Gln	Ala	Thr	Tyr	Pro	Val	Ile	Asp	Glu	Ser	Lys	Tyr
	210			215		220									
Pro	Lys	Pro	Ser	Ala	Thr	Glu	Ile	Lys	Glu	Lys	Leu	Ser	Ala	Asp	Glu
	225			230		235									
Tyr	Arg	Val	Thr	Gln	Lys	Asn	Glu	Thr	Glu	Lys	Ala	Phe	Ser	Asn	Arg
		245		250		255									
Tyr	Trp	Asp	Ser	Phe	Asp	Ala	Gly	Ile	Tyr	Val	Asp	Val	Val	Thr	Gly
	260			265		270									
Glu	Pro	Leu	Phe	Ser	Ser	Lys	Asp	Lys	Phe	Glu	Ser	Gly	Cys	Gly	Trp
	275			280		285									
Pro	Ser	Phe	Ser	Arg	Pro	Ile	Ser	Pro	Asp	Val	Val	Arg	Tyr	Lys	Glu
	290			295		300									
Asp	Lys	Ser	Phe	Asn	Met	Thr	Arg	Thr	Glu	Val	Arg	Ser	Arg	Ser	Gly
	305			310		315									
Asn	Ser	His	Leu	Gly	His	Val	Phe	Thr	Asp	Gly	Pro	Lys	Asp	Gln	Gly
		325		330		335									
Gly	Leu	Arg	Tyr	Cys	Ile	Asn	Ser	Leu	Ser	Ile	Thr	Phe	Ile	Pro	Lys
	340			345		350									
Ala	Asp	Met	Glu	Ala	Lys	Gly	Tyr	Gly	Tyr	Leu	Leu	Ser	Ser	Val	Glu
	355			360		365									

<210> SEQ ID NO 271

<211> LENGTH: 1035

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 271

atgaagcggtt	atccccctact	ggtccagttg	atttcgtatg	tttttgtgat	cgtaattgcc	60
ctcattacca	cgcttggttt	gctttattac	cagacgagtt	ctcgtaatat	caggcaacta	120
attgaacgtg	ataccgggca	gagcattcgg	caaagttccc	aatttattga	cgcttacatc	180
aagcctctta	aagaaacaac	ttcggtgctg	gcgaaaaata	cggaaattca	agcctttgct	240
agtcaaattc	atcaagaaaa	tgacaaacag	gttcttcagc	tcatgaagat	ggttcttgcg	300
accaattccg	atttacaagc	agctgttctg	gtgactaagg	atggtcgaac	ggtgtctacc	360
aattctcagt	tgaccatgaa	aacctccagt	gacatgatgg	cagaaccctg	gtataaagca	420
gccatagacc	gtcaagccat	gccaatctta	accccagctc	ggcaattatc	cctttcttct	480
aaaaaagaat	gggtagtttc	tgtgacccaa	gaggtagtag	atagggctgg	gcataattta	540
ggtgtgctaa	gacttgatat	tgcatacccg	accattaaag	cgtctttaga	tcagcttcag	600
ctaggccgcc	aaggctttgc	ctttattgtg	aatgataagc	atgaatttgt	ttaccatccc	660
aaaaagagtg	tttacagttc	ttctaaggag	atggctgcga	tgaaacctta	tttagcgatt	720
cagaatgggtt	acactaagga	caagacatct	tttgtttacc	aaaaactcat	tcctaacagt	780
caatggactt	tagtgggagt	ggcgtcactg	gatcagttgc	accgggtgca	gcgccaaatt	840
ttttggctct	tttcttgga	cagggcttct	accctgtctg	atttgtggct	ttgcaactgt	900
cttagtctta	cgcagatgga	ttcgtcccat	tcaacaattg	cagcaagtta	ttcttgctat	960
tcaaaaagga	gatcgtcagt	tacgtgccca	agaaacgggt	tctccagaat	tgacagacct	1020
tgcccaacag	tttaa					1035

<210> SEQ ID NO 272

<211> LENGTH: 344

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 272

Met	Lys	Arg	Tyr	Pro	Leu	Leu	Val	Gln	Leu	Ile	Ser	Tyr	Val	Phe	Val
1				5					10					15	
Ile	Val	Ile	Ala	Leu	Ile	Thr	Thr	Leu	Gly	Leu	Leu	Tyr	Tyr	Gln	Thr
			20					25					30		
Ser	Ser	Arg	Asn	Ile	Arg	Gln	Leu	Ile	Glu	Arg	Asp	Thr	Arg	Gln	Ser
		35				40					45				
Ile	Arg	Gln	Ser	Ser	Gln	Phe	Ile	Asp	Ala	Tyr	Ile	Lys	Pro	Leu	Lys
	50				55				60						
Glu	Thr	Thr	Ser	Val	Leu	Ala	Lys	Asn	Thr	Glu	Ile	Gln	Ala	Phe	Ala
65				70					75					80	
Ser	Gln	Ile	His	Gln	Glu	Asn	Asp	Lys	Gln	Val	Leu	Gln	Leu	Met	Lys
			85					90					95		
Met	Val	Leu	Ala	Thr	Asn	Ser	Asp	Leu	Gln	Ala	Ala	Val	Leu	Val	Thr
		100						105					110		
Lys	Asp	Gly	Arg	Thr	Val	Ser	Thr	Asn	Ser	Gln	Leu	Thr	Met	Lys	Thr
	115						120					125			
Ser	Ser	Asp	Met	Met	Ala	Glu	Pro	Trp	Tyr	Lys	Ala	Ala	Ile	Asp	Arg
	130				135						140				
Gln	Ala	Met	Pro	Ile	Leu	Thr	Pro	Ala	Arg	Gln	Leu	Ser	Leu	Ser	Ser
145				150					155					160	
Lys	Lys	Glu	Trp	Val	Val	Ser	Val	Thr	Gln	Glu	Val	Val	Asp	Arg	Ala
			165					170					175		
Gly	His	Asn	Leu	Gly	Val	Leu	Arg	Leu	Asp	Ile	Ala	Tyr	Pro	Thr	Ile
		180					185					190			
Lys	Ala	Ser	Leu	Asp	Gln	Leu	Gln	Leu	Gly	Arg	Gln	Gly	Phe	Ala	Phe
	195				200						205				
Ile	Val	Asn	Asp	Lys	His	Glu	Phe	Val	Tyr	His	Pro	Lys	Lys	Ser	Val
	210				215					220					
Tyr	Ser	Ser	Ser	Lys	Glu	Met	Ala	Ala	Met	Lys	Pro	Tyr	Leu	Ala	Ile
225				230					235					240	
Gln	Asn	Gly	Tyr	Thr	Lys	Asp	Lys	Thr	Ser	Phe	Val	Tyr	Gln	Lys	Leu
			245					250					255		
Ile	Pro	Asn	Ser	Gln	Trp	Thr	Leu	Val	Gly	Val	Ala	Ser	Leu	Asp	Gln
		260					265						270		
Leu	His	Arg	Val	Gln	Arg	Gln	Ile	Phe	Trp	Ser	Phe	Ser	Trp	Asn	Arg
	275					280					285				
Ala	Ser	Thr	Leu	Ser	Asp	Leu	Trp	Leu	Cys	Asn	Cys	Leu	Ser	Leu	Thr
	290				295				300						
Gln	Met	Asp	Ser	Ser	His	Ser	Thr	Ile	Ala	Ala	Ser	Tyr	Ser	Cys	Tyr
305				310				315						320	
Ser	Lys	Arg	Arg	Ser	Ser	Val	Thr	Cys	Pro	Arg	Asn	Gly	Phe	Ser	Arg
			325					330					335		
Ile	Asp	Arg	Pro	Cys	Pro	Thr	Val								
			340												

<210> SEQ ID NO 273

<211> LENGTH: 798

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 273

ttgcagcaag	ttattcttgc	tattcaaaaa	ggagatcgtc	agttacgtgc	ccaagaaacg	60
ggttctccag	aattgacaga	ccttgcccaa	cagtttaatg	cgctcttaga	tcaaattgat	120
agcttgatgg	tgccggttgc	ggataaggaa	aaggcgattg	ggcagtatag	gttacaagcc	180
ttggctagtc	agattaaccc	gcattttctc	tataacacct	tggacactat	tatttggtatg	240
gcagaattta	atgacagcaa	gcgcgtggta	gaagtgaacca	agtctctagc	taagtatttt	300
cgtttggccc	ttaatcaggg	gaacgaatac	attcgtttgg	cagatgaact	ggatcacgtt	360
agccaatacc	tctttattca	aaaacagcgc	tatggagaca	agctaagtta	tgaagtgcaa	420

ggcttagatg	tctacgcaga	ctttgttatt	cctaagctta	tcttacagcc	cttagtagaa	480
aatgctatct	accatggcat	caaagaagtc	gatcgcaagg	gcatgatcaa	ggttacggta	540
tctgatacag	ctcagcatct	gatgttgact	gtttgggata	atggtaaagg	cattgaagac	600
tcttcactga	ccaatagtca	gagcttggtg	gctaggggag	gtgtgggcct	taaaaaatgtt	660
gaccagcggg	taaaacttca	ctatggtgaa	ggctaccaca	tgaccattca	tagccagtca	720
gaccagttca	ctgaaataca	attaagcctt	cctaaaatgc	atgaattaat	ggcagacgac	780
acacaggaaa	acgagtaa					798

<210> SEQ ID NO 274
 <211> LENGTH: 265
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 274

Met	Gln	Gln	Val	Ile	Leu	Ala	Ile	Gln	Lys	Gly	Asp	Arg	Gln	Leu	Arg
1			5						10				15		
Ala	Gln	Glu	Thr	Gly	Ser	Pro	Glu	Leu	Thr	Asp	Leu	Ala	Gln	Gln	Phe
			20					25					30		
Asn	Ala	Leu	Leu	Asp	Gln	Ile	Asp	Ser	Leu	Met	Val	Ala	Val	Ala	Asp
		35					40					45			
Lys	Glu	Lys	Ala	Ile	Gly	Gln	Tyr	Arg	Leu	Gln	Ala	Leu	Ala	Ser	Gln
	50					55					60				
Ile	Asn	Pro	His	Phe	Leu	Tyr	Asn	Thr	Leu	Asp	Thr	Ile	Ile	Trp	Met
65				70						75					80
Ala	Glu	Phe	Asn	Asp	Ser	Lys	Arg	Val	Val	Glu	Val	Thr	Lys	Ser	Leu
			85						90					95	
Ala	Lys	Tyr	Phe	Arg	Leu	Ala	Leu	Asn	Gln	Gly	Asn	Glu	Tyr	Ile	Arg
			100					105					110		
Leu	Ala	Asp	Glu	Leu	Asp	His	Val	Ser	Gln	Tyr	Leu	Phe	Ile	Gln	Lys
		115					120					125			
Gln	Arg	Tyr	Gly	Asp	Lys	Leu	Ser	Tyr	Glu	Val	Gln	Gly	Leu	Asp	Val
	130					135					140				
Tyr	Ala	Asp	Phe	Val	Ile	Pro	Lys	Leu	Ile	Leu	Gln	Pro	Leu	Val	Glu
145				150						155					160
Asn	Ala	Ile	Tyr	His	Gly	Ile	Lys	Glu	Val	Asp	Arg	Lys	Gly	Met	Ile
			165					170						175	
Lys	Val	Thr	Val	Ser	Asp	Thr	Ala	Gln	His	Leu	Met	Leu	Thr	Val	Trp
			180					185						190	
Asp	Asn	Gly	Lys	Gly	Ile	Glu	Asp	Ser	Ser	Leu	Thr	Asn	Ser	Gln	Ser
		195					200						205		
Leu	Leu	Ala	Arg	Gly	Gly	Val	Gly	Leu	Lys	Asn	Val	Asp	Gln	Arg	Leu
	210					215						220			
Lys	Leu	His	Tyr	Gly	Glu	Gly	Tyr	His	Met	Thr	Ile	His	Ser	Gln	Ser
225				230						235				240	
Asp	Gln	Phe	Thr	Glu	Ile	Gln	Leu	Ser	Leu	Pro	Lys	Met	His	Glu	Leu
			245						250					255	
Met	Ala	Asp	Asp	Thr	Gln	Glu	Asn	Glu							
			260					265							

<210> SEQ ID NO 275
 <211> LENGTH: 1494
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 275

atgacagaag	aaaaaaaaacg	gggttttaga	attccttctt	cttacaccgt	tctttttatc	60
attatagcca	tcatggcagt	gttaacttgg	tttattccag	ctggcgccta	cgaaccgct	120
aagggcggtg	gtgttatctt	aggaacctac	aaaacagtag	catccaatcc	tcaaggattt	180
tttgacatct	tgatggctcc	cgttcgaggc	atgttaggtg	ttgaaggcac	tgatggtgct	240

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attcaagtgt ctttctttat cttaatgggtt gggggcctttt taggagttgt caacaaaaca 300
ggtgctcttg acacagggat tgcgtcagtg gttcgtaaaa acaaaggtag agaaaaaatg 360
ctgattgcta ttttaatccc tttgtttgct ctagggtggaa cgacctatgg tatgggggaa 420
gaaacccatgg cctttttaccc actttttaatt cctgttatga ttgctggttg ttttgacagt 480
attgtttgctg tagccattat tttgattggg tctcaaattg ggtgtctagc ctccactatt 540
aaccattttg caactgggtg agcagctgat gctgctgggtg tcagcattgc agatggaatg 600
atttggcgtg ttatccaatg ggttattcctt gtcggcatgt ctatttggtt tgtttacaat 660
tacgctagta agattgaaga agacccaagt aaatcattgg ttgcagacaa ggaagaagag 720
cataaggaac tcttccagtt gcaaaattct ggagaagact taaacaagcg ccaacgaaac 780
gttttgacca tttttacttt gacctttgtc attatgattc ttagtttgat tccgtgggaa 840
gattttggca tcaaattcct tactaatatc aatacttggg taaccacaat gcctatctta 900
gggggagtta ttgggaaaac catgggagca tttgggtactt ggtatttccc agaaatcacc 960
atgtctctta tcatgatggg tgtcttagtt gctattgttt atcgtatgag tgaagaagac 1020
tttttttagct cttttttgac tgggtgcagg gaatttttag gtgttgccat gatctgtgct 1080
attgcacgcg gtattcaagt tatcatgaat ggtgggtatga ttacagccac tatcttacac 1140
ttaggtgaaa caagtctttc tgggttatct tctcaagttt ttgtgatatt agcttatatt 1200
ttctacctcc caatgtcctt cttgattcca tcaacatcag gacttgctgg ggctacaatg 1260
ggaattatgg caccgcttgg acaattctca aatgtccctg ctcaccttgt tattacagcc 1320
ttccagtcag cttctggaat cttaaacaatg atttctccaa cttcagcaat cgttatggga 1380
gcacttgccg ttggtgcgct tgaccttggg acttgggtgga aattcattgg taaatttatt 1440
gtaatggtga tgcttgtaag cgtgctatta cttgtagttg caacattcct ttaa 1494

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<210> SEQ ID NO 276

<211> LENGTH: 497

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 276

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Met Thr Glu Glu Lys Arg Gly Phe Arg Ile Pro Ser Ser Tyr Thr
1      5      10      15
Val Leu Phe Ile Ile Ala Ile Met Ala Val Leu Thr Trp Phe Ile
20     25     30
Pro Ala Gly Ala Tyr Glu Thr Ala Lys Gly Gly Gly Val Ile Ser Gly
35     40     45
Thr Tyr Lys Thr Val Ala Ser Asn Pro Gln Gly Phe Phe Asp Ile Leu
50     55     60
Met Ala Pro Val Arg Gly Met Leu Gly Val Glu Gly Thr Asp Gly Ala
65     70     75     80
Ile Gln Val Ser Phe Phe Ile Leu Met Val Gly Gly Phe Leu Gly Val
85     90     95
Val Asn Lys Thr Gly Ala Leu Asp Thr Gly Ile Ala Ser Val Val Arg
100    105    110
Lys Asn Lys Gly Arg Glu Lys Met Leu Ile Ala Ile Leu Ile Pro Leu
115    120    125
Phe Ala Leu Gly Gly Thr Thr Tyr Gly Met Gly Glu Glu Thr Met Ala
130    135    140
Phe Tyr Pro Leu Leu Ile Pro Val Met Ile Ala Val Gly Phe Asp Ser
145    150    155    160
Ile Val Ala Val Ala Ile Ile Leu Ile Gly Ser Gln Ile Gly Cys Leu
165    170    175
Ala Ser Thr Ile Asn Pro Phe Ala Thr Gly Val Ala Ala Asp Ala Ala
180    185    190
Gly Val Ser Ile Ala Asp Gly Met Ile Trp Arg Val Ile Gln Trp Val
195    200    205
Ile Leu Val Gly Met Ser Ile Trp Phe Val Tyr Asn Tyr Ala Ser Lys
210    215    220
Ile Glu Glu Asp Pro Ser Lys Ser Leu Val Ala Asp Lys Glu Glu Glu
225    230    235    240

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ttttcaaacg ttatcagttt ggtagaatat gttggtatga tgtctgaagt agacgtttta	1140
gcacaaactg cagtttcagg agaagaactt ttgcgacgca agcctatcga tttcagtggc	1200
caagaatcctt atttaccaga ttatgatgat tcaagaagac cagaatcgac cattggctat	1260
gaacaacaag cgtcacaaac agcatatgat tcacaagttc cgagtgatcc taaacaaaaa	1320
atttcagaac gtgttcgtgg catatttggg agtatgtttg attaa	1365

<210> SEQ ID NO 278

<211> LENGTH: 454

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 278

Met Ala Arg Asn Gly Phe Phe Thr Gly Leu Asp Ile Gly Thr Ser Ser	
1	5 10 15
Ile Lys Val Leu Val Ala Glu Phe Ile Ser Gly Glu Met Asn Val Ile	
	20 25 30
Gly Val Ser Asn Val Pro Ser Thr Gly Val Lys Asp Gly Ile Ile Ile	
	35 40 45
Asp Ile Glu Ala Ala Ala Thr Ala Ile Lys Thr Ala Val Glu Gln Ala	
	50 55 60
Glu Glu Lys Ala Gly Met Thr Ile Glu Lys Val Asn Val Gly Leu Pro	
65	70 75 80
Ala Asn Leu Leu Gln Ile Glu Pro Thr Gln Gly Met Ile Pro Val Pro	
	85 90 95
Ser Glu Ser Lys Glu Ile Lys Asp Glu Asp Val Asp Ser Val Val Lys	
	100 105 110
Ser Ala Leu Thr Lys Ser Ile Thr Pro Glu Arg Glu Val Ile Ser Leu	
	115 120 125
Val Pro Glu Glu Phe Ile Val Asp Gly Phe Gln Gly Ile Arg Asp Pro	
	130 135 140
Arg Gly Met Met Gly Ile Arg Leu Glu Met Arg Gly Leu Ile Tyr Thr	
145	150 155 160
Gly Pro Ser Thr Ile Leu His Asn Leu Arg Lys Thr Val Glu Arg Ala	
	165 170 175
Gly Ile Lys Val Glu Asn Ile Ile Ile Ser Pro Leu Ala Met Ala Lys	
	180 185 190
Thr Ile Leu Asn Glu Gly Glu Arg Glu Phe Gly Ala Thr Val Ile Asp	
	195 200 205
Met Gly Gly Gly Gln Thr Thr Val Ala Ser Met Arg Ala Gln Glu Leu	
	210 215 220
Gln Tyr Thr Asn Ile Tyr Ala Glu Gly Gly Glu Tyr Ile Thr Lys Asp	
225	230 235 240
Ile Ser Lys Val Leu Lys Thr Ser Leu Ala Ile Ala Glu Ala Leu Lys	
	245 250 255
Phe Asn Phe Gly Gln Ala Glu Ile Ser Glu Ala Ser Ile Thr Glu Thr	
	260 265 270
Val Lys Val Asp Val Val Gly Ser Glu Glu Pro Val Glu Val Thr Glu	
	275 280 285
Arg Tyr Leu Ser Glu Ile Ile Ser Ala Arg Ile Arg His Ile Leu Asp	
	290 295 300
Arg Val Lys Gln Asp Leu Glu Arg Gly Arg Leu Leu Asp Leu Pro Gly	
305	310 315 320
Gly Ile Val Leu Ile Gly Gly Gly Ala Ile Met Pro Gly Val Val Glu	
	325 330 335
Ile Ala Gln Glu Ile Phe Gly Val Thr Val Lys Leu His Val Pro Asn	
	340 345 350
Gln Val Gly Ile Arg Asn Pro Met Phe Ser Asn Val Ile Ser Leu Val	
	355 360 365

Glu	Tyr	Val	Gly	Met	Met	Ser	Glu	Val	Asp	Val	Leu	Ala	Gln	Thr	Ala
370						375					380				
Val	Ser	Gly	Glu	Glu	Leu	Leu	Arg	Arg	Lys	Pro	Ile	Asp	Phe	Ser	Gly
385					390					395					400
Gln	Glu	Ser	Tyr	Leu	Pro	Asp	Tyr	Asp	Asp	Ser	Arg	Arg	Pro	Glu	Ser
				405					410					415	
Thr	Ile	Gly	Tyr	Glu	Gln	Gln	Ala	Ser	Gln	Thr	Ala	Tyr	Asp	Ser	Gln
			420					425					430		
Val	Pro	Ser	Asp	Pro	Lys	Gln	Lys	Ile	Ser	Glu	Arg	Val	Arg	Gly	Ile
	435						440					445			
Phe	Gly	Ser	Met	Phe	Asp										
450															

<210> SEQ ID NO 279

<211> LENGTH: 1320

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 279

atggcatttt	catttgatac	tgcattcaatt	caagggtgcaa	ttataaaaagt	aattgggagtc	60
ggcggagggtg	gcggaatgc	cattaatcgt	atgattgatg	aagggtgttgc	tggtgtcgag	120
ttcatcgag	caaacacaga	cattcaggca	ttaagctcat	caaaagctga	aacggttatt	180
caactaggcc	ctaaattaac	tcgtggactt	ggtgctggag	gacaacctga	agtaggacgt	240
aaagctgctg	aagaaagcga	agaaatttta	acagaagctc	ttacaggagc	ggacatggta	300
tttattactg	ccggtatggg	tggtggctct	gggacagggg	ctgcaccggt	tattgctcgt	360
atcgctaaaa	gtttgggagc	cttgacagta	gctgttgta	ctcgcccgtt	tggttttgaa	420
ggtaacaaac	gtggtaattt	tgctattgaa	ggtatcgaag	aactacgtga	acaagtgtat	480
actttgttaa	ttatttcaaa	taataacctt	cttgagattg	ttgataaaaa	gacaccttta	540
ttagaagcac	ttagtgaagc	tgataatggt	ttacgccagg	gagttcaagg	gataaccgac	600
ttaattacta	gtcctggcct	tatcaatctc	gattttgccc	acgtgaaaac	agttatggca	660
aataaaggga	atgccttgat	ggggattggg	attggctctg	gagaagagcg	cattgttgag	720
gcggcgcgta	aggcaatcta	ttcaccctta	ttagaaacga	ctattgatgg	tgcaacaagc	780
gttattgtga	acgttacagg	aggtctcgac	atgacactta	cagaagctga	agaagcctct	840
gaaattgttg	ggcaagctgc	tggtcaaggc	gttaacattt	ggtaggaac	atctattgat	900
gatactatga	aagatgacat	ccgtgtgact	gttgtagcaa	ctggagtgcg	ccaagaaaaa	960
gccgaacaag	tttcagggtt	tcgtcagcct	aggactttta	cccaaaccac	cgcgcagcaa	1020
gtagcgggtg	cacaatatgc	atcagatcaa	gcaaaacagt	cggttcaacc	agggtttgat	1080
cgtcgctcaa	attttgattt	tgacatgggg	gagtcctcgc	agataccaag	tgacacaaaag	1140
gtaatttcta	atcataatca	aaatcaagg	tctgcttttg	gaaattggga	tttgagacgt	1200
gataatatatt	ctcgtccaac	agaagggtgaa	ttggataacc	atcttaatat	gtcaacgttc	1260
tcagctaacg	atgacagtga	tgatgaatta	gaaacgcctc	cattctttta	aaaccgttaa	1320

<210> SEQ ID NO 280

<211> LENGTH: 439

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 280

Met	Ala	Phe	Ser	Phe	Asp	Thr	Ala	Ser	Ile	Gln	Gly	Ala	Ile	Ile	Lys
1				5					10					15	
Val	Ile	Gly	Val	Gly	Gly	Gly	Gly	Gly	Asn	Ala	Ile	Asn	Arg	Met	Ile
		20						25					30		
Asp	Glu	Gly	Val	Ala	Gly	Val	Glu	Phe	Ile	Ala	Ala	Asn	Thr	Asp	Ile
		35					40					45			
Gln	Ala	Leu	Ser	Ser	Ser	Lys	Ala	Glu	Thr	Val	Ile	Gln	Leu	Gly	Pro
	50					55					60				
Lys	Leu	Thr	Arg	Gly	Leu	Gly	Ala	Gly	Gly	Gln	Pro	Glu	Val	Gly	Arg
65				70					75					80	
Lys	Ala	Ala	Glu	Glu	Ser	Glu	Glu	Ile	Leu	Thr	Glu	Ala	Leu	Thr	Gly

				85					90					95					
Ala	Asp	Met	Val	Phe	Ile	Thr	Ala	Gly	Met	Gly	Gly	Gly	Ser	Gly	Thr				
			100					105					110						
Gly	Ala	Ala	Pro	Val	Ile	Ala	Arg	Ile	Ala	Lys	Ser	Leu	Gly	Ala	Leu				
		115					120					125							
Thr	Val	Ala	Val	Val	Thr	Arg	Pro	Phe	Gly	Phe	Glu	Gly	Asn	Lys	Arg				
	130					135					140								
Gly	Asn	Phe	Ala	Ile	Glu	Gly	Ile	Glu	Glu	Leu	Arg	Glu	Gln	Val	Asp				
145					150					155					160				
Thr	Leu	Leu	Ile	Ile	Ser	Asn	Asn	Asn	Leu	Leu	Glu	Ile	Val	Asp	Lys				
			165					170					175						
Lys	Thr	Pro	Leu	Leu	Glu	Ala	Leu	Ser	Glu	Ala	Asp	Asn	Val	Leu	Arg				
		180						185					190						
Gln	Gly	Val	Gln	Gly	Ile	Thr	Asp	Leu	Ile	Thr	Ser	Pro	Gly	Leu	Ile				
	195						200					205							
Asn	Leu	Asp	Phe	Ala	Asp	Val	Lys	Thr	Val	Met	Ala	Asn	Lys	Gly	Asn				
	210					215				220									
Ala	Leu	Met	Gly	Ile	Gly	Ile	Gly	Ser	Gly	Glu	Glu	Arg	Ile	Val	Glu				
225					230					235					240				
Ala	Ala	Arg	Lys	Ala	Ile	Tyr	Ser	Pro	Leu	Leu	Glu	Thr	Thr	Ile	Asp				
			245					250					255						
Gly	Ala	Gln	Asp	Val	Ile	Val	Asn	Val	Thr	Gly	Gly	Leu	Asp	Met	Thr				
		260						265					270						
Leu	Thr	Glu	Ala	Glu	Glu	Ala	Ser	Glu	Ile	Val	Gly	Gln	Ala	Ala	Gly				
	275						280					285							
Gln	Gly	Val	Asn	Ile	Trp	Leu	Gly	Thr	Ser	Ile	Asp	Asp	Thr	Met	Lys				
	290				295					300									
Asp	Asp	Ile	Arg	Val	Thr	Val	Val	Ala	Thr	Gly	Val	Arg	Gln	Glu	Lys				
305					310					315					320				
Ala	Glu	Gln	Val	Ser	Gly	Phe	Arg	Gln	Pro	Arg	Thr	Phe	Thr	Gln	Thr				
			325					330					335						
Asn	Ala	Gln	Gln	Val	Ala	Gly	Ala	Gln	Tyr	Ala	Ser	Asp	Gln	Ala	Lys				
		340						345					350						
Gln	Ser	Val	Gln	Pro	Gly	Phe	Asp	Arg	Arg	Ser	Asn	Phe	Asp	Phe	Asp				
	355						360					365							
Met	Gly	Glu	Ser	Arg	Glu	Ile	Pro	Ser	Ala	Gln	Lys	Val	Ile	Ser	Asn				
	370					375					380								
His	Asn	Gln	Asn	Gln	Gly	Ser	Ala	Phe	Gly	Asn	Trp	Asp	Leu	Arg	Arg				
385				390						395					400				
Asp	Asn	Ile	Ser	Arg	Pro	Thr	Glu	Gly	Glu	Leu	Asp	Asn	His	Leu	Asn				
			405					410					415						
Met	Ser	Thr	Phe	Ser	Ala	Asn	Asp	Asp	Ser	Asp	Asp	Glu	Leu	Glu	Thr				
		420					425					430							
Pro	Pro	Phe	Phe	Lys	Asn	Arg													
		435																	

<210> SEQ ID NO 281

<211> LENGTH: 687

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 281

atggatttgt	catttttgcc	caaatactgg	gcctacttta	actacggtgt	acttgtcacc	60
attatgattt	cagtcagcgt	tgtctttttt	ggaaccctta	ttggtgtctt	ggtaaccctg	120
attaagcgta	gtcatgtgaa	gccgttgacc	tggtcggtta	atctttacgt	ttggatcttt	180
cggggaacac	ctatggtggt	tcaaatacatg	attgcctttg	cttggatgca	ttttaacaat	240
atgcctacta	ttggttttgg	gggttttagac	ttggactttt	caagactact	tcctggaatt	300
attatcattt	cattgaatag	cggtgcttat	atttcagaaa	ttgttagagc	aggtattgag	360

gctgtaccaa aagggcaatt agaagcagct tattcactag gtattcgtcc tcaaaatgcc	420
atgcgttatg tgattttgcc tcaggccttt aaaaatattt tgccagcctt aggaaatgaa	480
tttattacca ttattaagga tagtgctctt ttacaaacca ttggagtgat ggaactttgg	540
aatggtgccc aatcgtgtgt aacggctact tattctccaa tttccccttt actggtggct	600
gctttttact acttaatggt cacaacagtg atggcacagt tattggcagt cttagaacgt	660
cacatggcgc aaggaggtaa tcattga	687

<210> SEQ ID NO 282
 <211> LENGTH: 228
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 282

Met Asp Leu Ser Phe Leu Pro Lys Tyr Trp Ala Tyr Phe Asn Tyr Gly	
1 5 10 15	
Val Leu Val Thr Ile Met Ile Ser Val Ser Val Val Phe Phe Gly Thr	
20 25 30	
Leu Ile Gly Val Leu Val Thr Leu Ile Lys Arg Ser His Val Lys Pro	
35 40 45	
Leu Thr Trp Val Val Asn Leu Tyr Val Trp Ile Phe Arg Gly Thr Pro	
50 55 60	
Met Val Val Gln Ile Met Ile Ala Phe Ala Trp Met His Phe Asn Asn	
65 70 75 80	
Met Pro Thr Ile Gly Phe Gly Val Leu Asp Leu Asp Phe Ser Arg Leu	
85 90 95	
Leu Pro Gly Ile Ile Ile Ile Ser Leu Asn Ser Gly Ala Tyr Ile Ser	
100 105 110	
Glu Ile Val Arg Ala Gly Ile Glu Ala Val Pro Lys Gly Gln Leu Glu	
115 120 125	
Ala Ala Tyr Ser Leu Gly Ile Arg Pro Gln Asn Ala Met Arg Tyr Val	
130 135 140	
Ile Leu Pro Gln Ala Phe Lys Asn Ile Leu Pro Ala Leu Gly Asn Glu	
145 150 155 160	
Phe Ile Thr Ile Ile Lys Asp Ser Ala Leu Leu Gln Thr Ile Gly Val	
165 170 175	
Met Glu Leu Trp Asn Gly Ala Gln Ser Val Val Thr Ala Thr Tyr Ser	
180 185 190	
Pro Ile Ser Pro Leu Leu Val Ala Ala Phe Tyr Tyr Leu Met Val Thr	
195 200 205	
Thr Val Met Ala Gln Leu Leu Ala Val Leu Glu Arg His Met Ala Gln	
210 215 220	
Gly Gly Asn His	
225	

<210> SEQ ID NO 283
 <211> LENGTH: 432
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 283

gtgccgccag ttgatccaac aatgtagct gtaactgtgg cagtttcaga cgtgtcttcc	60
agtttagctt taatgtcagc taagctatcc ttgctaaaac cggctttggc caaagcatca	120
tcaatctgct tttcatcaac ttcaaggctt ttaagagacg ttctaaattc ttcaagtttt	180
ttatcaaaat cttgctcttt agtgctcagca tcagataaaa attttttgag tcgctcatcg	240
actgccttgg ctagctcctc agcttccagc acttttagcgt taacctcagc aactttgacc	300
cttcatttag cttcagcttt ttgatgcca tcttcaatct cttcacggag tttagcttct	360
tttgtgtcaa aaatacgatt agcattatca atctgctttt gtaattttgc ttcaaatgct	420
gcgtcatggt ga	432

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<210> SEQ ID NO 284
<211> LENGTH: 143
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 284
Met Pro Pro Val Asp Pro Thr Met Leu Ala Val Thr Val Ala Val Ser
1      5      10      15
Asp Val Ser Ser Ser Leu Ala Leu Met Ser Ala Lys Leu Ser Leu Leu
20      25      30
Lys Pro Ala Leu Ala Lys Ala Ser Ser Ile Cys Phe Ser Ser Thr Ser
35      40      45
Arg Ser Leu Arg Asp Val Leu Asn Ser Ser Ser Phe Leu Ser Lys Ser
50      55      60
Cys Ser Leu Val Ser Ala Ser Asp Lys Asn Phe Leu Ser Arg Ser Ser
65      70      75      80
Thr Ala Leu Ala Ser Ser Ser Ala Ser Ser Thr Leu Ala Leu Thr Ser
85      90      95
Ala Thr Leu Thr Ser Ala Leu Ala Ser Ala Phe Leu Met Pro Ser Ser
100     105     110
Ile Ser Ser Arg Ser Leu Ala Ser Phe Val Ser Lys Ile Arg Leu Ala
115     120     125
Leu Ser Ile Cys Phe Cys Asn Phe Ala Ser Asn Ala Ala Ser Cys
130     135     140

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<210> SEQ ID NO 285
<211> LENGTH: 807
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 285
atggatatgt ctaaatacaaa tcgtcgtact tggcaagggt tagttgttat tttaatagct      60
attctcacca cttttaccac aagtactgtt acggcagcca gaaaaattag aaatttccct      120
gataccacgg aaattttgtt aggaacgaag gcgactgaga caccaggaat cttaccattc      180
actggtagct accaattagt ttggggcgat cttgacaatc tgcaaaggcc aaccttcgca      240
cacatccagc taaaagatca agatgagcct aatattaaac gaaaaggact taaattcaat      300
cctcctggct ggcataatta caaattgact gacgctaata gaaaaacaac ttggttaatg      360
gaccgtggcc atttagttgg ttaccaattt agcggcttaa atgacgagcc taaaaaccta      420
gttacaatga caaaatatct taatactggc tttagtgaac aaaatccttt aggaatgctc      480
tattatgaaa atagattaga tagctggtta gctctacacc ctaacttctg gctagactat      540
aaagttactc ctgtttatca taaaaatgag ttagttcctc gccaaagtag tctacagtat      600
gttggaattg atgaaaatgg agatctactt caaattaagt taggtagtga aaaagaaagt      660
gtagacaact ttggagtaac atcagttaca ttagataacg tatctccttt agctgaattg      720
gattacaaaa caggaatgat gctagattca actcaaaacg aagaagatag taatttagaa      780
accgaagagt ttgaagaagc ggcttaa                                807

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<210> SEQ ID NO 286
<211> LENGTH: 268
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 286
Met Asp Met Ser Lys Ser Asn Arg Arg Thr Trp Gln Gly Leu Val Val
1      5      10      15
Ile Leu Ile Ala Ile Leu Thr Thr Phe Thr Thr Ser Thr Val Thr Ala
20      25      30
Ala Arg Lys Ile Arg Asn Phe Pro Asp Thr Thr Glu Ile Leu Leu Gly
35      40      45
Thr Lys Ala Thr Glu Thr Pro Gly Ile Leu Pro Phe Thr Gly Ser Tyr
50      55      60

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Gln	Leu	Val	Leu	Gly	Asp	Leu	Asp	Asn	Leu	Gln	Arg	Pro	Thr	Phe	Ala
65					70					75					80
His	Ile	Gln	Leu	Lys	Asp	Gln	Asp	Glu	Pro	Asn	Ile	Lys	Arg	Lys	Gly
				85					90					95	
Leu	Lys	Phe	Asn	Pro	Pro	Gly	Trp	His	Asn	Tyr	Lys	Leu	Thr	Asp	Ala
			100					105					110		
Asn	Gly	Lys	Thr	Thr	Trp	Leu	Met	Asp	Arg	Gly	His	Leu	Val	Gly	Tyr
		115					120					125			
Gln	Phe	Ser	Gly	Leu	Asn	Asp	Glu	Pro	Lys	Asn	Leu	Val	Thr	Met	Thr
	130					135					140				
Lys	Tyr	Leu	Asn	Thr	Gly	Phe	Ser	Asp	Lys	Asn	Pro	Leu	Gly	Met	Leu
145					150					155					160
Tyr	Tyr	Glu	Asn	Arg	Leu	Asp	Ser	Trp	Leu	Ala	Leu	His	Pro	Asn	Phe
			165					170						175	
Trp	Leu	Asp	Tyr	Lys	Val	Thr	Pro	Val	Tyr	His	Lys	Asn	Glu	Leu	Val
			180					185					190		
Pro	Arg	Gln	Val	Val	Leu	Gln	Tyr	Val	Gly	Ile	Asp	Glu	Asn	Gly	Asp
		195					200					205			
Leu	Leu	Gln	Ile	Lys	Leu	Gly	Ser	Glu	Lys	Glu	Ser	Val	Asp	Asn	Phe
	210					215					220				
Gly	Val	Thr	Ser	Val	Thr	Leu	Asp	Asn	Val	Ser	Pro	Leu	Ala	Glu	Leu
225					230				235						240
Asp	Tyr	Gln	Thr	Gly	Met	Met	Leu	Asp	Ser	Thr	Gln	Asn	Glu	Glu	Asp
			245					250						255	
Ser	Asn	Leu	Glu	Thr	Glu	Glu	Phe	Glu	Glu	Ala	Ala				
			260					265							

<210> SEQ ID NO 287

<211> LENGTH: 1863

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 287

atgacaatca	gacaatggat	ggcagaccat	cttcatttga	tggagacttt	agcgtgtttg	60
gtattaataa	taattggcct	agccttttta	cactcatttc	cacaagtggc	ttccgctatt	120
ttcattacag	ccttccttgat	tggaggatat	gcgtctgcaa	aaacgggtat	attggatttg	180
gtgaagaaca	aacacttgtc	agtggatatt	ttgatgattt	tggcagctat	cggtgctgga	240
attatcggtc	attggctgga	gggtgctctg	cttattttta	tcttttcgtt	gtccaatacg	300
cttgaagaaa	tggccatgga	aaaaagtaag	gatgctattt	cagccttgat	gtccttgacg	360
ccagatacag	ctcgtcaata	ccaagaagat	ggccatattt	tagaagtga	gaccagatcc	420
ttgagtgttg	gtgaccgttt	acaagttcgt	aaaggcgaag	ctgttccaat	tgacgggcag	480
ttgcttagtc	cttttggtca	atttgatgaa	tctatggtca	ctggtgagcc	tatcactggt	540
gataaggcag	aaggccagga	tctgattggg	ggaaccatta	accaaggaca	aaccatagat	600
atgttggtta	ctattgaaaa	tgacgatact	ctctttgcc	agattattaa	tctggtggaa	660
tctgccccag	aaaagaaaa	caaaaccgcc	acctttatcg	aaagcttaga	agatggttat	720
gtcaaatttg	tgctcgtcct	tattcctgcc	tttatcctct	ttagccactt	tgtgctttct	780
tggacttggt	tggctgcttt	ttaccgaggg	atgattctct	taacagtagc	ttcaccatgt	840
gccctaattg	ccagttccac	acctgctagc	ttggctgcta	tttctcgtgc	agccagaaag	900
ggattgatta	tcaaaggagg	ggatattgtc	gataacatgg	gagatattaa	ggctgttgtc	960
atggataaaa	cgggaacgct	cacccaagga	aaaccttctg	ttgtgaatgc	tcattatttg	1020
gaagatgagt	tgctcgtgaa	tagactggta	aaaggagcag	agactgctag	taccatcctt	1080
atttctaaag	cccttcttga	atacactgaa	aaattggagc	cactgacctt	tgaccactta	1140
gaagaaattt	ctgggaaagg	ttttcagggc	ttctatcaag	ggcaagaatg	gcgaattggc	1200
aagaaaaacct	acattttgga	aaagggtcaa	gacctatcag	cttttgaaga	aactattcaa	1260
gtggaagaaa	atcaagggaa	aaccctaata	tttgtttcac	gtgaccatca	attgatagct	1320
tactatgccc	tcttggtatga	tatcaaaaata	gaatcaaaac	gtgctattaa	gtctcttcac	1380
gccatgggaa	tcaaaacagt	catgttaaca	ggtgaccaag	aacgaaccgc	caattatgtg	1440
gcacaaaaaac	ttggtattga	tgaagtggta	gcccaactgta	tgccctcaaga	taagggtggct	1500

aagttagcag aattaaagac taaatatggt tttgtggcta tggtaggaga tggtattaat	1560
gatgctcctg cccttgctca agcagatggt tcttatgcta ttggatcagg aacagatatt	1620
gcaatggaaa gtgcagacag tgtgattatg gatgacttga ctcgtattcc attttcgatt	1680
caactttccc gcacaatgaa gaccattatc aaacaaaata ttgtttttgc cttatctgtg	1740
attaccttat tgatttttagc caatgttttt caggtagtta acttgccgct tggtgttggt	1800
ggacacgaag gctcaacgat tttagtgttt ttaaattggct tgcgtttact ttcttttaaa	1860
taa	1863

<210> SEQ ID NO 288

<211> LENGTH: 620

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 288

Met Thr Ile Arg Gln Trp Met Ala Asp His Leu His Leu Met Glu Thr	
1 5 10 15	
Leu Ala Cys Leu Val Leu Ile Ile Ile Gly Leu Ala Phe Leu His Ser	
20 25 30	
Phe Pro Gln Val Ala Ser Ala Ile Phe Ile Thr Ala Phe Leu Ile Gly	
35 40 45	
Gly Tyr Ala Ser Ala Lys Thr Gly Ile Leu Asp Leu Val Lys Asn Lys	
50 55 60	
His Leu Ser Val Asp Ile Leu Met Ile Leu Ala Ala Ile Gly Ala Gly	
65 70 75 80	
Ile Ile Gly Tyr Trp Leu Glu Gly Ala Leu Leu Ile Phe Ile Phe Ser	
85 90 95	
Leu Ser Asn Thr Leu Glu Glu Met Ala Met Glu Lys Ser Lys Asp Ala	
100 105 110	
Ile Ser Ala Leu Met Ser Leu Thr Pro Asp Thr Ala Arg Gln Tyr Gln	
115 120 125	
Glu Asp Gly His Ile Leu Glu Val Glu Thr Arg Ser Leu Ser Val Gly	
130 135 140	
Asp Arg Leu Gln Val Arg Lys Gly Glu Ala Val Pro Ile Asp Gly Gln	
145 150 155 160	
Leu Leu Ser Pro Phe Gly Gln Phe Asp Glu Ser Met Val Thr Gly Glu	
165 170 175	
Pro Ile Thr Val Asp Lys Ala Glu Gly Gln Asp Leu Ile Gly Gly Thr	
180 185 190	
Ile Asn Gln Gly Gln Thr Ile Asp Met Leu Val Thr Ile Glu Asn Asp	
195 200 205	
Asp Thr Leu Phe Ala Lys Ile Ile Asn Leu Val Glu Ser Ala Gln Glu	
210 215 220	
Lys Lys Ser Lys Thr Ala Thr Phe Ile Glu Ser Leu Glu Asp Gly Tyr	
225 230 235 240	
Val Lys Phe Val Leu Val Leu Ile Pro Ala Phe Ile Leu Phe Ser His	
245 250 255	
Phe Val Leu Ser Trp Thr Trp Leu Ala Ala Phe Tyr Arg Gly Met Ile	
260 265 270	
Leu Leu Thr Val Ala Ser Pro Cys Ala Leu Ile Ala Ser Ser Thr Pro	
275 280 285	
Ala Ser Leu Ala Ala Ile Ser Arg Ala Ala Arg Lys Gly Leu Ile Ile	
290 295 300	
Lys Gly Gly Asp Ile Val Asp Asn Met Gly Asp Ile Lys Ala Val Val	
305 310 315 320	
Met Asp Lys Thr Gly Thr Leu Thr Gln Gly Lys Pro Ser Val Val Asn	
325 330 335	
Ala His Tyr Leu Glu Asp Glu Leu Leu Val Asn Arg Leu Val Lys Gly	
340 345 350	


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<211> LENGTH: 293
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 290
Met Ile Met Thr Ser Pro Phe Leu Leu Lys Gly Leu Ala Phe Phe Arg
1           5           10          15
Lys Ile Asp Ile Leu Lys Cys Val Phe Val Asn Thr Val Thr Lys Gly
20          25          30
Asp Ile Met Lys Thr Pro Glu Gln Ile Leu Glu Ala Thr Ile His Ile
35          40          45
Gly Glu His Lys Val Thr Lys Thr Phe Leu Ala Lys Ser Ile Leu Gly
50          55          60
Phe Ile Gly Gly Ala Met Ile Ser Leu Gly Tyr Leu Leu Tyr Val Arg
65          70          75          80
Ile Ala Ala Ser Gly Leu Glu Thr Phe Gly Ala Phe Ser Ser Ile Val
85          90          95
Gly Ala Cys Ala Phe Pro Ile Gly Leu Ile Ile Ile Leu Met Ala Gly
100         105         110
Gly Glu Leu Ile Thr Gly Asn Met Met Ala Val Ser Ala Ala Leu Leu
115         120         125
Ala Lys Lys Ile Lys Phe Ser Glu Leu Ala Lys Asn Trp Leu Ile Ile
130         135         140
Thr Leu Phe Asn Val Ile Gly Ala Val Phe Val Ala Phe Val Phe Gly
145         150         155         160
His Phe Leu Gly Leu Thr Ser Ala Gly Ile Phe Lys Glu Glu Val Ile
165         170         175
Glu Val Ala His Ala Lys Ile Ala Ala Ser Pro Leu Gln Ala Leu Val
180         185         190
Ser Gly Ile Gly Cys Asn Trp Phe Val Gly Leu Ala Leu Trp Leu Cys
195         200         205
Tyr Gly Ala Asn Asp Ala Ala Gly Lys Phe Leu Gly Thr Trp Phe Pro
210         215         220
Val Met Thr Phe Val Ala Leu Gly Phe Gln His Ser Val Ala Asn Ala
225         230         235         240
Phe Val Ile Pro Ala Ala Ile Phe Glu Gly Gly Ala Thr Trp Leu Asp
245         250         255
Phe Val Thr Asn Phe Ile Phe Val Tyr Ser Gly Asn Ile Ile Gly Gly
260         265         270
Ala Ile Phe Val Ser Phe Leu Tyr Phe Lys Val Tyr Tyr His Pro Gln
275         280         285
Lys Ser Lys Thr Gln
290

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<210> SEQ ID NO 291
<211> LENGTH: 696
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 291
atggattttt ttgcaattga ccccatcgga ctgcctcata cctcacttat cttttacttg      60
tcgtcactct tgatagcgct tttgcttggt tttttgactt ttcaagcata taggttaaaa      120
tctcatcggt attttttctt gtttttacag ttatctcagg tgattggctt atacacatgg      180
tacgtggttaa ggggggtttcc tttagatgaa gctttgccgt tgtatcattg tcgcatcgct      240
atgtagtcta tcttttttct acctgatcgt aacaagttta agcaattatt tatggttttg      300
gggtaggttg gaacattcct tgcactttta tcgccagatc tttatccgtt tagattatgg      360
catgtagcaa atgtctcggt ttattttggt cattatgctt tgtagtgtaa tggtttgatt      420
tacctcttgc gtttttacga tgccagtcag ttaagactgc tatcagtagt acgctattta      480
gcaactgtta actttcttct tctgttggtc agtttagcca cgaaaggaaa ttatggtttt      540

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gtgatggata	ttccagtgat	tcatacgcgt	catttgctac	ttaattttgt	gatcggtaca	600
agtggccttg	cttttatggt	taaaataacc	gaatattttt	accttaaatt	tggtgaagct	660
caacagctgg	cacttgcttt	ctctaaagaa	aagtag			696

<210> SEQ ID NO 292
 <211> LENGTH: 231
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 292

Met	Asp	Phe	Phe	Ala	Ile	Asp	Pro	Ile	Gly	Leu	Pro	His	Thr	Ser	Leu	
1				5					10					15		
Ile	Phe	Tyr	Leu	Ser	Ser	Leu	Leu	Ile	Ala	Leu	Leu	Leu	Val	Phe	Leu	
			20					25					30			
Thr	Phe	Gln	Ala	Tyr	Arg	Leu	Lys	Ser	His	Arg	Tyr	Phe	Phe	Leu	Phe	
			35				40					45				
Leu	Gln	Leu	Ser	Gln	Val	Ile	Gly	Leu	Tyr	Thr	Trp	Tyr	Val	Leu	Arg	
			50			55					60					
Gly	Phe	Pro	Leu	Asp	Glu	Ala	Leu	Pro	Leu	Tyr	His	Cys	Arg	Ile	Ala	
65					70				75					80		
Met	Leu	Ala	Ile	Phe	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Phe	Lys	Gln	Leu	
				85				90						95		
Phe	Met	Val	Leu	Gly	Ile	Gly	Gly	Thr	Phe	Leu	Ala	Leu	Leu	Ser	Pro	
			100				105						110			
Asp	Leu	Tyr	Pro	Phe	Arg	Leu	Trp	His	Val	Ala	Asn	Val	Ser	Phe	Tyr	
			115				120					125				
Phe	Gly	His	Tyr	Ala	Leu	Leu	Val	Asn	Gly	Leu	Ile	Tyr	Leu	Leu	Arg	
			130				135				140					
Phe	Tyr	Asp	Ala	Ser	Gln	Leu	Arg	Leu	Leu	Ser	Val	Val	Arg	Tyr	Leu	
145					150					155				160		
Ala	Thr	Val	Asn	Phe	Leu	Leu	Leu	Val	Ser	Leu	Ala	Thr	Lys	Gly		
			165					170					175			
Asn	Tyr	Gly	Phe	Val	Met	Asp	Ile	Pro	Val	Ile	His	Thr	Arg	His	Leu	
			180					185					190			
Leu	Leu	Asn	Phe	Val	Ile	Val	Thr	Ser	Gly	Leu	Thr	Phe	Met	Val	Lys	
			195				200					205				
Ile	Thr	Glu	Tyr	Phe	Tyr	Leu	Lys	Phe	Gly	Glu	Ala	Gln	Gln	Leu	Ala	
			210				215				220					
Leu	Ala	Phe	Ser	Lys	Glu	Lys										
225						230										

<210> SEQ ID NO 293
 <211> LENGTH: 663
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 293

atgtagacg	aattattaat	taaaggaaaa	tcgtttttga	gagagcggta	ttttctgcca	60
tacctaatta	gtcttttatt	aggacttttt	ctaatactaa	gcttcagttt	tttggtctgg	120
ggaaataggc	agagcaaggc	agccgttcct	gctttgagag	aaatatcgcc	tgtgaaacag	180
caggtttagtg	aagaaaaaaa	ggaaattcaa	gaagatagca	gtatttttagt	ggatttaaaa	240
ggcgccgtac	aaaaagaggg	agttttataag	ctaactgcta	gcagtcgtgt	gcgagatgtc	300
attgaactag	ctggaggcct	aacttcagaa	gctgataaac	atgctattaa	ttttgcagaa	360
aaactaactg	atgagcaagt	tgtttatgta	cctaaacaag	gagaagagat	ttctgtgcta	420
ccaagatcat	tagttttctgg	taaaaaagaa	actgccagca	aggatcagtc	aaaggttcat	480
attaataagg	ccagcttaga	agaactacaa	catatcccag	gtattggtgc	taaaagagct	540
caggatatta	ttgatatgag	agataagtta	ggtgggttta	aagcgttaga	agatctccgt	600
cagggtttcgg	ggattggcga	aaaaacgctc	gagaaaattaa	aagatgacat	tttcttggtac	660
taa						663

aaggaactgg	ctacattaca	tggttatata	ttgacagctt	gggcaatagc	tgcatctaact	1080
ggacctatgt	tattatctat	cactgttgaa	tggtactata	attatcttct	taccttatgt	1140
gtttttattg	tcttatacat	tttaggatta	atggttagcat	taagggtaaa	gaaatga	1197

<210> SEQ ID NO 296
 <211> LENGTH: 398
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 296

Met	Glu	Lys	Thr	Lys	Arg	Tyr	Ile	Ile	Ala	Thr	Ala	Gly	Ile	Leu	Leu
1				5					10					15	
His	Leu	Met	Leu	Gly	Ser	Thr	Tyr	Ala	Trp	Ser	Val	Tyr	Arg	Asn	Pro
			20					25					30		
Ile	Leu	Gln	Glu	Thr	Gly	Trp	Asp	Gln	Ala	Pro	Val	Ala	Phe	Ala	Phe
		35					40					45			
Ser	Leu	Ala	Ile	Phe	Cys	Leu	Gly	Leu	Ser	Ala	Ala	Phe	Met	Gly	Asn
	50					55					60				
Leu	Val	Glu	Gln	Tyr	Gly	Pro	Arg	Leu	Thr	Gly	Thr	Val	Ser	Ala	Ile
65					70					75					80
Leu	Tyr	Ala	Ser	Gly	Asn	Met	Leu	Thr	Gly	Leu	Ala	Ile	Asp	Arg	Lys
			85						90					95	
Glu	Ile	Trp	Leu	Leu	Tyr	Ile	Gly	Tyr	Gly	Val	Ile	Gly	Gly	Leu	Gly
			100					105					110		
Leu	Gly	Ala	Gly	Tyr	Ile	Thr	Pro	Ile	Ser	Thr	Ile	Ile	Lys	Trp	Phe
		115					120					125			
Pro	Asp	Lys	Arg	Gly	Met	Ala	Thr	Gly	Phe	Ala	Ile	Met	Gly	Phe	Gly
	130					135					140				
Phe	Ala	Ser	Leu	Leu	Thr	Ser	Pro	Ile	Ala	Gln	Trp	Leu	Ile	Glu	Thr
145					150					155					160
Glu	Gly	Leu	Val	Ala	Thr	Phe	Tyr	Leu	Leu	Gly	Leu	Ile	Tyr	Leu	Ile
			165						170					175	
Val	Met	Leu	Phe	Ala	Ser	Gln	Leu	Ile	Lys	Pro	Thr	Ala	Ala	Glu	
		180					185						190		
Ile	Ala	Ile	Leu	Asp	Lys	Lys	Arg	Leu	Gln	Asn	Asn	Ser	Tyr	Leu	Ile
		195					200					205			
Glu	Gly	Met	Thr	Ala	Lys	Glu	Ala	Leu	Lys	Thr	Lys	Ser	Phe	Tyr	Cys
	210					215					220				
Leu	Trp	Val	Ile	Leu	Phe	Ile	Asn	Ile	Thr	Cys	Gly	Leu	Gly	Leu	Ile
225					230					235					240
Ser	Val	Val	Ala	Pro	Met	Ala	Gln	Asp	Leu	Thr	Gly	Met	Ser	Pro	Glu
			245						250					255	
Met	Ser	Ala	Ile	Val	Val	Gly	Ala	Met	Gly	Ile	Phe	Asn	Gly	Phe	Gly
			260				265						270		
Arg	Leu	Val	Trp	Ala	Ser	Leu	Ser	Asp	Tyr	Ile	Gly	Arg	Arg	Val	Thr
		275					280					285			
Val	Ile	Leu	Leu	Phe	Leu	Val	Ser	Ile	Ile	Met	Thr	Ile	Ser	Leu	Ile
	290					295					300				
Phe	Ala	His	Ser	Ser	Leu	Ile	Phe	Met	Ile	Ser	Ile	Ala	Thr	Leu	Met
305					310					315					320
Thr	Cys	Tyr	Gly	Ala	Gly	Phe	Ser	Leu	Ile	Pro	Pro	Tyr	Leu	Ser	Asp
			325						330					335	
Leu	Phe	Gly	Ala	Lys	Glu	Leu	Ala	Thr	Leu	His	Gly	Tyr	Ile	Leu	Thr
		340					345						350		
Ala	Trp	Ala	Ile	Ala	Ala	Leu	Thr	Gly	Pro	Met	Leu	Leu	Ser	Ile	Thr
	355						360					365			
Val	Glu	Trp	Thr	His	Asn	Tyr	Leu	Leu	Thr	Leu	Cys	Val	Phe	Ile	Val
	370					375					380				

Leu Tyr Ile Leu Gly Leu Met Val Ala Leu Arg Leu Lys Lys
 385 390 395

<210> SEQ ID NO 297
 <211> LENGTH: 696
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 297

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atgaaaggat tcattaatta tttaaaaata gcagtgtcga ttattctggc tatgggttttc      60
aatgtccttc cgatgatttt attgcaaaaag caacacgata ttcctatggg acttaattgg      120
ggaattggta ttttctactt gggtattggt ggaagtgtcc ttattgtatt atgggggtcct      180
tatcaagcta agcaagacac ttttattaaa cagcaaaaaa tgagattggg tgactggggg      240
tatttagcat tattttgggt aatcatccgt gtgatagcta ttgtaggtac ccttggttaac      300
cagctatggg ctgggtcaaca agtgagtgtc aatgatgctg caatacatac cttagctaga      360
cttatcaaag gtgggtttccc gctttatact gccctatttg tacttgtgat agctttttatc      420
gctcctatta tggaagaact agtctttaga ggatttccta tgattgatct cttcaaagga      480
aaatcactta aggtggcagg tttagtgtacc tctcttgttt ttgctttacc acatgccacc      540
aatagtgttg aatttatcat gtacagctgt atgggcattt ttctctttgt tgcctatcaa      600
agacgaggaa acttaaaaga tgctatcttg ttacatatat ttaataactt gattgaagtc      660
attttggttaa tgtcaatagg cttaggagtc atataa      696
  
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<210> SEQ ID NO 298
 <211> LENGTH: 231
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 298

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Met Lys Gly Phe Ile Asn Tyr Leu Lys Ile Ala Val Leu Ile Ile Leu
1      5      10      15
Ala Met Val Phe Asn Val Leu Pro Met Ile Leu Leu Gln Lys Gln His
20     25     30
Asp Ile Pro Met Val Leu Asn Trp Gly Ile Gly Ile Phe Tyr Leu Val
35     40     45
Ile Val Gly Ser Val Leu Ile Val Leu Trp Gly Leu Tyr Gln Ala Lys
50     55     60
Gln Asp Thr Phe Ile Lys Gln Gln Lys Met Arg Leu Val Asp Trp Gly
65     70     75     80
Tyr Leu Ala Leu Phe Trp Leu Ile Ile Arg Val Ile Ala Ile Val Gly
85     90     95
Thr Leu Val Asn Gln Leu Trp Ser Gly Gln Gln Val Ser Ala Asn Asp
100    105    110
Ala Ala Ile His Thr Leu Ala Arg Leu Ile Lys Gly Gly Phe Pro Leu
115    120    125
Tyr Thr Ala Leu Phe Val Leu Val Ile Ala Phe Ile Ala Pro Ile Met
130    135    140
Glu Glu Leu Val Phe Arg Gly Phe Pro Met Ile Asp Leu Phe Lys Gly
145    150    155    160
Lys Ser Leu Lys Val Ala Gly Leu Val Thr Ser Leu Val Phe Ala Leu
165    170    175
Pro His Ala Thr Asn Ser Val Glu Phe Ile Met Tyr Ser Cys Met Gly
180    185    190
Ile Phe Leu Phe Val Ala Tyr Gln Arg Arg Gly Asn Leu Lys Asp Ala
195    200    205
Ile Leu Leu His Ile Phe Asn Asn Leu Ile Glu Val Ile Leu Leu Met
210    215    220
Ser Ile Gly Leu Gly Val Ile
225    230
  
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<210> SEQ ID NO 299
<211> LENGTH: 1314
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 299
    atgacgatta taattatgga ctctaatagt gctcacgaga ctgataatct atcagtctct      60
    tttcttaact tttgttataa tagtcttatg aaacgacact ttttactctt gaccttttac      120
    ctcttttttaa caggtttaac agctggcctt gttgctttta tcttaacaaa agccattcac      180
    ctgattcagt ccctcagttt tggattcagt caaggttctt ttagcactat gattgctagt      240
    gttccaccac aaagacgagc tctttcactc ctctttgctg gacttcttgc aggtccttggg      300
    tggcacctat tggctaaaaa aggaaaggac attcaatcta ttcagcaaat cattcaagat      360
    gacatctcat ttagtccctg gacacagttt tggcatgggt ggctccaatt aacgaccgta      420
    tctatgggag ctctgtgcgg ccgagaagga gcttcacggg aagtcgctgt taccttgacg      480
    tctctttgga gccaaagatg caacttgtca aaagccgatc aaaaactttt attagcctgc      540
    gcttctggcg ctgcccttgg tgcgtgtctac aatgctccct tagccactat tttatttatc      600
    ttagaagcta ttcttaaccg ttgggtccctt aaaaatatat acgctgcctg cctaacgagc      660
    tatgtggctg tggaaacagt tgctttatta caaggccgac atgagattca atacctaatg      720
    cctcagcaac attggacgct aggaaccctt attgggtccg tcttggtggg tcttatcctt      780
    tccctctttg ctacagctta caaacatctt ttgaaacacc ttcctaaggc tgatgccaaa      840
    agtcagtggg ttattccgaa agttctcatc gcttttagcc ttatcgcagg actcagcatt      900
    ttcttccag agattttagg aaatggcaaa gctggattac tcttttttct ccatgaagaa      960
    ccacatctga gctatattag ctggctactt gttgccaaag ctgtcgctat ctctttagtt     1020
    tttgcttctg gagcaaaagg gggtaaaatt gctccttcta tgatgcttgg aggtgctagt     1080
    ggcttactac tagctatcct tagtcagtac cttattccct tgtctctatc aaatacgta      1140
    gccattatgg ttggtgcaac aatcttttta ggtgtgatca ataagatacc cttggcggca      1200
    ccagtttttc tgggtgaaat tacaggccaa tcgttactaa tgattatccc ttttagcatta     1260
    gctaacctca ttttttattt tagctatcag ttttatcggt tcatccttaa atga          1314

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<210> SEQ ID NO 300
<211> LENGTH: 437
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 300
    Met Thr Ile Ile Ile Met Asp Ser Asn Ser Ala His Glu Thr Asp Asn
     1              5              10              15
    Leu Ser Val Ser Phe Leu Asn Phe Cys Tyr Asn Ser Leu Met Lys Arg
              20              25              30
    His Phe Leu Leu Leu Thr Phe Tyr Leu Phe Leu Thr Gly Leu Thr Ala
              35              40              45
    Gly Leu Val Ala Phe Ile Leu Thr Lys Ala Ile His Leu Ile Gln Ser
              50              55              60
    Leu Ser Phe Gly Phe Ser Gln Gly Ser Phe Ser Thr Met Ile Ala Ser
    65              70              75              80
    Val Pro Pro Gln Arg Arg Ala Leu Ser Leu Leu Phe Ala Gly Leu Leu
              85              90              95
    Ala Gly Leu Gly Trp His Leu Leu Ala Lys Lys Gly Lys Asp Ile Gln
              100             105             110
    Ser Ile Gln Gln Ile Ile Gln Asp Asp Ile Ser Phe Ser Pro Trp Thr
              115             120             125
    Gln Phe Trp His Gly Trp Leu Gln Leu Thr Thr Val Ser Met Gly Ala
              130             135             140
    Pro Val Gly Arg Glu Gly Ala Ser Arg Glu Val Ala Val Thr Leu Thr
    145             150             155             160
    Ser Leu Trp Ser Gln Arg Cys Asn Leu Ser Lys Ala Asp Gln Lys Leu
              165             170             175
    Leu Leu Ala Cys Ala Ser Gly Ala Ala Leu Gly Ala Val Tyr Asn Ala
              180             185             190

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<400> SEQUENCE: 302
Met Lys Gln Ile Thr Gln Gln Lys Trp Leu Arg Tyr Gly Leu Phe Ile
1      5      10      15
Ala Leu Val Leu Asn Gly Ile Glu Leu Glu Leu Leu Gly Leu Thr Ala
20     25     30
Asn Asn Leu Ser Phe Lys Glu Ala Phe Ala Leu Ile Leu Thr Ile Ser
35     40     45
Leu Leu Gly Ile Tyr Leu Ile Pro Phe Ala Ala Ala Ile Phe Tyr Leu
50     55     60
Ser Lys Lys Phe His Met Asn Leu Asn Val Ile Ile Val Ser Cys Leu
65     70     75     80
Ser Gly Leu Tyr Ile Ser Gly Phe Leu Ala Ser Cys Gly Asn His Leu
85     90     95
Val Gly Gln Phe Trp Ser Tyr Ile Ile Pro Ser Lys Asp Ala Leu Lys
100    105    110
Leu Trp Gly Asp Ala Leu Thr Ala Pro Ile Val Glu Glu Pro Ile Lys
115    120    125
Ala Ser Ser Ala Ile Leu Val Ile Thr Leu Phe Pro Arg Leu Thr Leu
130    135    140
Lys Glu Lys Leu Val Val Ala Leu Leu Ser Gly Met Gly Phe Gln Leu
145    150    155    160
Thr Glu Asp Ile Arg Tyr Leu Ile Gln Ala Lys Ser Ile Asp Ser Leu
165    170    175
Val Pro Thr Ala Ile Glu Arg Ile Ser Thr Ala Val Thr Ser His Trp
180    185    190
Val His Thr Ala Ile Phe Thr Ile Gly Ala Tyr Leu Leu Leu Lys Gly
195    200    205
Ser Asn Leu Phe Ser Lys Gln Gln Gln Ile Phe Trp Leu Leu Ser Pro
210    215    220
Leu Val Leu His Phe Ile Trp Asn Ser Pro Leu Thr Ser Ile Pro Gly
225    230    235    240
Met Thr Val Leu Leu Gly Thr Leu Ile Leu Leu Ile Phe Gly Asp Leu
245    250    255
Phe Gln Lys Ile Asn Thr Leu Asp Asp Asp Val Leu Phe
260    265

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<210> SEQ ID NO 303
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 303
ttgggagaaa aaccagcagc tttactcata atgttaccaa acatatcatt aagattatatt      60
cggctcatga cttgttctgc attaaaggca gcctcgaaag ccaaaatcgc attctcacta      120
tttgctaaga caggctcaga gcccatcaat aaggctctgt cttgggcaga aatgttatct      180
agaatttcat tccaagcatt ttttagagca tctagatatt gtcgagattg ttggctatatt      240
cgaaccgttt cttccatgat tttcaaaatg gtaaccgat caaccctgta g                291

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<210> SEQ ID NO 304
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 304
Met Gly Glu Lys Pro Ala Ala Leu Leu Ile Met Leu Pro Asn Ile Ser
1      5      10      15
Leu Arg Leu Phe Arg Leu Met Thr Cys Ser Ala Leu Lys Ala Ala Ser
20     25     30
Lys Ala Lys Ile Ala Phe Ser Leu Phe Ala Lys Thr Gly Ser Glu Pro

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ttgttgacca	gtttaattat	tttattttta	ttagcctttg	ccttaatcct	ttcaatat	480
tctaaagctg	ctattcaagt	gctggataag	cattaccatt	tgagtgataa	tatcacacg	540
atcttcttgc	tcctcattca	acctattaca	gttttgatta	tttttgttgg	cttgatgcta	600
ctatatTTTT	tattacccaa	tgTTaagatt	aaaaaaattc	gctacatttt	accaggaacc	660
ctattttacat	cttttTgtgat	gacattttttg	agTaatctgg	tTggcaatta	cgTgtgtgat	720
aatgttgagc	ggatggTtaga	tattaaaatg	tttggTtcag	tTatgatttt	tatcatcatg	780
ctatggTttta	ttttctttagc	aagaatcctg	atTTtaggag	ctatatTTaa	Tgcgacctat	840
caagaaatgt	ccttgggggaa	attagaaggT	cgtagTggTg	atatgatcgc	tatccttaaa	900
aaaacacttg	ggaatgattc	agatctatct	ccttcacagt	ctatcgaaga	tagtcacact	960
gattga						966

[illegible]

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<210> SEQ ID NO 309
<211> LENGTH: 1221
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 309
atgtcaacat tatcattgga caccacaaat aagcgagctt tagtggcagc tattgcagct    60
tcaggaacgg atgacttgaa tgtcatgttt cttgcctttt ccatgtcttc cattatgaca    120
gacttgggtc ttagtggcac tcaggggtggc tggattgcga ccattaccaa tttaggaatg    180
ttggtgggag gcctcttatt cgggttgctg gctgataggc accacaagtt taaggctcttt    240
aaatggacga ttttactgtt ttcagtagca acaggattaa tttattttac ccagtctttg    300
ccctacctgt acctgatgcg atttattgct ggcataggag ttggaggtga gtacggtgta    360
gccattgcca taatggcagg gattgtacca ccagaaaaaa tgggtcggat gtcttcttta    420
aatggtattg ctggccagct tggctctatt agttcggctc ttttagcagg gtggctggct    480
ccaagtctag gctggcgtgg cctttttctc tttggattac ttccgattct cttggtgatt    540
tggtatgactt tagccataga tgacaaaaaa atttgggatac attatgggca agaggaggaa    600
gaatgcagtc aaccaattaa aatcaatgaa ctattcaaaa caaaatcctt aacagctcaa    660
acccttgctt taatggtcat gacgactgtg cagattgcgg gctatttttg aatgatgaat    720
tggttgccaa ccattattca aacaagctta aacctttcag taaaaagttc gtccttgtgg    780
atggtggcta ctattgtcgg catgtgtttg gggatgctgt attttggtca gcttttagat    840
tgctttggtc cacgtctgat ttattccctc tttttattag catcatctat ttgtgtttac    900
ctttttcaat ttgccaattc catggcgagt atggttattg gaggtgctat tgtcggtttt    960
tttgtcaatg ggatgtttgc tggctacggg gctatgatta ccagacttta tccccatcac    1020
attcgatcca cggctaataa tgttattttg aatgttggcc gtgctctagg aggattttcg    1080
tccgttgcta ttggtagtat tttagatgcc tcaggatatt caatgggcat gattttccta    1140
gcttctctgt atgtgattag ttttgagacc atgtggtcta ttggtcagtt aaaagcagaa    1200
cgctaccaac aattgcgtta g                                     1221

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<210> SEQ ID NO 310
<211> LENGTH: 406
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 310
Met Ser Thr Leu Ser Leu Asp Thr Thr Asn Lys Arg Ala Leu Val Ala
1          5          10          15
Ala Ile Ala Ala Ser Gly Thr Asp Asp Leu Asn Val Met Phe Leu Ala
20        25        30
Phe Ser Met Ser Ser Ile Met Thr Asp Leu Gly Leu Ser Gly Thr Gln
35        40        45
Gly Gly Trp Ile Ala Thr Ile Thr Asn Leu Gly Met Leu Val Gly Gly
50        55        60
Leu Leu Phe Gly Leu Leu Ala Asp Arg His His Lys Phe Lys Val Phe
65        70        75        80
Lys Trp Thr Ile Leu Leu Phe Ser Val Ala Thr Gly Leu Ile Tyr Phe
85        90        95
Thr Gln Ser Leu Pro Tyr Leu Tyr Leu Met Arg Phe Ile Ala Gly Ile
100       105       110
Gly Val Gly Gly Glu Tyr Gly Val Ala Ile Ala Ile Met Ala Gly Ile
115       120       125
Val Pro Pro Glu Lys Met Gly Arg Met Ser Ser Leu Asn Gly Ile Ala
130       135       140
Gly Gln Leu Gly Ser Ile Ser Ser Ala Leu Leu Ala Gly Trp Leu Ala
145       150       155       160
Pro Ser Leu Gly Trp Arg Gly Leu Phe Leu Phe Gly Leu Leu Pro Ile
165       170       175
Leu Leu Val Ile Trp Met Thr Leu Ala Ile Asp Asp Gln Lys Ile Trp
180       185       190

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Val	Ile	Ile	Phe	Ser	Ile	Ile	Tyr	Ala	Tyr	Leu	Ser	Leu	Arg	Asn	Ser
65					70					75					80
Tyr	Tyr	Gly	Glu	Leu	Met	Thr	Tyr	Leu	Phe	Met	Thr	Leu	Pro	Met	Thr
				85					90					95	
Ile	Phe	Ser	Leu	Phe	Thr	Trp	Leu	Asn	His	Pro	Phe	Glu	Gly	Lys	Lys
			100					105					110		
Ser	Gln	Val	Thr	Ile	Ser	Arg	Leu	Thr	Pro	Thr	Asp	Arg	Arg	Cys	Leu
		115					120					125			
Phe	Val	Phe	Thr	Ile	Leu	Ile	Thr	Leu	Ile	Phe	Tyr	Ser	Ile	Leu	Ala
	130					135					140				
Ser	Ile	Ser	Asn	Ser	Leu	Phe	Thr	Cys	Leu	His	Phe	Ile	Asp	Cys	His
145				150						155					160
Phe	Phe	Leu	Ser	Gly	Leu	Ser	Gln	Leu							
				165											

<210> SEQ ID NO 313
 <211> LENGTH: 342
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 313

atgattaaaa	cgattaaaag	gagaaacctt	atgaaatcta	ttatgttagt	ttgtaatgcc	60
ggtatgtcaa	ctagtatggt	ggtgactaag	atgcaaaaag	cagcccaagc	gcgtgacctt	120
gaagtttcta	tttgggcagt	tcctgtgagt	gaagctgaca	acgaaatggc	tgctaatagc	180
attgacgttc	tcttggttagg	tccacaagtc	aaattcttac	taaaggattt	taaagataag	240
tttgaaccag	atattaaagt	agatgccatt	aacatggctg	attatggtct	tatgaacggt	300
gaaaaagtcc	ttgaaacagc	cctagcaatg	atggaggagt	ag		342

<210> SEQ ID NO 314
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 314

Met	Ile	Lys	Thr	Ile	Lys	Arg	Arg	Asn	Leu	Met	Lys	Ser	Ile	Met	Leu
1				5					10					15	
Val	Cys	Asn	Ala	Gly	Met	Ser	Thr	Ser	Met	Leu	Val	Thr	Lys	Met	Gln
			20					25					30		
Lys	Ala	Ala	Gln	Ala	Arg	Asp	Leu	Glu	Val	Ser	Ile	Trp	Ala	Val	Pro
		35					40					45			
Val	Ser	Glu	Ala	Asp	Asn	Glu	Met	Ala	Ala	Asn	Ser	Ile	Asp	Val	Leu
	50					55					60				
Leu	Leu	Gly	Pro	Gln	Val	Lys	Phe	Leu	Leu	Lys	Asp	Phe	Lys	Asp	Lys
65				70						75					80
Phe	Glu	Pro	Asp	Ile	Lys	Val	Asp	Ala	Ile	Asn	Met	Ala	Asp	Tyr	Gly
			85					90						95	
Leu	Met	Asn	Gly	Glu	Lys	Val	Leu	Glu	Thr	Ala	Leu	Ala	Met	Met	Glu
			100					105					110		
Glu															

<210> SEQ ID NO 315
 <211> LENGTH: 816
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 315

ttgaccaaac	gtaatattac	cattaccta	ccagataatg	taccacctgc	ggttaataaa	60
gcctttgctg	ccattattcc	aggaacagtt	gcgatttacg	cttcggcaat	tttcgcctac	120
ctcattttcg	cattaacagg	ttcttccta	agtgatgtca	tttcaaccta	tatccaatta	180
ccattgctag	gcttatcaca	gggtattggt	tcagttatct	tgtaaacctt	cttagttcaa	240

ctgctctggt	tcttcggctt	gcatggtc	cat	aatgtcttag	ccccagtgat	ggatgggtatt	300
tatatggtag	ctttaacaga	aaatacagct	gcttacaata	cagcgcatag	cgctgcta	at	360
ttaccataacc	tttgacacg	cgggtccttt	gatgcttatg	ctcaa	atggg	tggttcagga	420
gtaaccttgg	cattgattat	tgctatcttc	atattctcaa	aacgagaaga	gcataaaaacc		480
attgccaaat	tgtccgcacc	aatgggtggt	ttcaatatca	acgaaccaat	tacatttggg		540
atgccaaattg	ttttgaatcc	aacctttgtg	attccatggc	taattgtgcc	accaatttgt		600
gctagcatag	cttatttttgc	tactgcaata	ggtttgattc	caccggtatt	cttatcagta		660
ccttgatta	cccctgttgg	actttatgct	tacctagcta	ctggaggtaa	tattatggca		720
ggtttggtt	cactgtttaa	cctctttgtt	gccttcctta	tctgggcacc	atttgtcatt		780
ttggccaata	aagaaaaagc	gagtgcctt	gcatga				816

<210> SEQ ID NO 316
 <211> LENGTH: 271
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 316

Met	Thr	Lys	Arg	Asn	Ile	Thr	Ile	Thr	Leu	Pro	Asp	Asn	Val	Pro	Pro
1				5					10				15		
Ala	Val	Asn	Lys	Ala	Phe	Ala	Ala	Ile	Ile	Pro	Gly	Thr	Val	Ala	Ile
			20					25					30		
Tyr	Ala	Ser	Ala	Ile	Phe	Ala	Tyr	Leu	Ile	Phe	Ala	Leu	Thr	Gly	Ser
		35					40					45			
Ser	Leu	Ser	Asp	Val	Ile	Ser	Thr	Tyr	Ile	Gln	Leu	Pro	Leu	Leu	Gly
	50					55				60					
Leu	Ser	Gln	Gly	Ile	Gly	Ser	Val	Ile	Leu	Leu	Thr	Phe	Leu	Val	Gln
65				70					75					80	
Leu	Leu	Trp	Phe	Phe	Gly	Leu	His	Gly	His	Asn	Val	Leu	Ala	Pro	Val
			85					90					95		
Met	Asp	Gly	Ile	Tyr	Met	Val	Ala	Leu	Thr	Glu	Asn	Thr	Ala	Ala	Tyr
		100						105					110		
Asn	Thr	Ala	His	Ser	Ala	Ala	Asn	Leu	Pro	Tyr	Leu	Trp	Thr	Arg	Gly
		115					120					125			
Ser	Phe	Asp	Ala	Tyr	Ala	Gln	Met	Gly	Gly	Ser	Gly	Val	Thr	Leu	Ala
	130					135					140				
Leu	Ile	Ile	Ala	Ile	Phe	Ile	Phe	Ser	Lys	Arg	Glu	Glu	His	Lys	Thr
145				150						155				160	
Ile	Ala	Lys	Leu	Ser	Ala	Pro	Met	Gly	Val	Phe	Asn	Ile	Asn	Glu	Pro
			165					170					175		
Ile	Thr	Phe	Gly	Met	Pro	Ile	Val	Leu	Asn	Pro	Thr	Phe	Val	Ile	Pro
	180						185						190		
Trp	Leu	Ile	Val	Pro	Pro	Ile	Cys	Ala	Ser	Ile	Ala	Tyr	Phe	Ala	Thr
	195					200					205				
Ala	Ile	Gly	Leu	Ile	Pro	Pro	Val	Phe	Leu	Ser	Val	Pro	Trp	Ile	Thr
	210				215						220				
Pro	Val	Gly	Leu	Tyr	Ala	Tyr	Leu	Ala	Thr	Gly	Gly	Asn	Ile	Met	Ala
225				230					235					240	
Gly	Leu	Val	Ser	Leu	Phe	Asn	Leu	Phe	Val	Ala	Phe	Leu	Ile	Trp	Ala
			245					250					255		
Pro	Phe	Val	Ile	Leu	Ala	Asn	Lys	Glu	Lys	Ala	Ser	Asp	Leu	Ala	
		260						265					270		

<210> SEQ ID NO 317
 <211> LENGTH: 2175
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 317

atgacgcaca	aaataaaaagt	attgctgctt	gcgataatgt	ctattttttt	gacatgcaat	60
------------	-------------	------------	------------	------------	------------	----

attgcaagtg	ctgaaactat	tgctattggt	tcagatacag	cttatgcccc	atttgaattt	120
aaagactcag	atcaaattta	caaaggaatt	gacgttgata	ttattaatga	agtagccaaa	180
cgtcaatctt	gggatttcag	tatgagtttc	ccgggttttg	atgcagctgt	aaatgctgtt	240
caatctgggtc	aagcgagtgc	tctaattggcc	ggtacaacca	ttacgaatgc	tcgtaagaaa	300
gtcttttcatt	tctcagagcc	atattacgat	accaaatttg	tcattgcgac	acgtaaagcc	360
aatgccatca	aaaaatacag	tgacttaaaa	ggaaaaaacgg	tcggtgttaa	aaatggaaca	420
gcgggtcaag	ccttttttgaa	taactataaa	aaaaagtatg	attatactgt	taaaacattt	480
gacacagggtg	atcttatgta	taatagttta	tctgctgggt	ctattgccgc	tgttatggat	540
gatgaggcgg	ttatccaata	cgcaatcagc	caaaaccaag	atattgctat	taacatgaaa	600
ggagagccca	ttggaagctt	tggttttgct	gtcaaaaagg	gaagcggata	tgattatcta	660
gttaatgatt	tcaatacagc	tcttaaagct	atgaaagctg	atggtaccta	ccaagctatc	720
atgaccaagt	ggttaggcac	agatgataaa	gctaccacca	gtcaggcaac	gggaaatcca	780
tctgccaaag	ctacacctac	aaaggacagt	tataaaattg	tctctgattc	gtcttttgca	840
ccgtttgaa	ttcaaaatgg	taagggcaaa	tacgttggtg	ttgacataga	attaatcaaa	900
gctattgcta	aacaacaagg	tttcaaaatt	gaaatcgcta	atccaggttt	cgtactgcc	960
ttaaatgctg	tgcaatctag	ccaagcagat	ggggtcattg	ctggtgcaac	tattactgac	1020
gctcgtaaag	ctatctttga	tttttctgat	ccttattata	cttctaatat	catttttagct	1080
gttaaagctg	gaaaaaacat	caagaactat	gaagacttag	acagaaaaaac	agtcggtgct	1140
aaaaacggca	cttcatctta	ctcttggtta	aaagaaaacg	ctcctaaata	tggttataat	1200
gtcaaggcat	ttgatgatgg	ttctagcatg	tatgatagct	taaattcagg	ttctgtagat	1260
gctatcatgg	atgatgaggc	ggttcttaaa	tacgctatct	ctcaaggtcg	tcgctttgaa	1320
acacctcttg	agggcatttc	tactggtgaa	gttggttttg	ctgtcaagaa	aggaactaat	1380
ccagaattaa	tcgaaatggt	caacaatggc	ttagctgctc	tcaaaaaatc	tggtcagtat	1440
gatgacatta	tagataaata	ccttgactct	aagaaagctg	caactccttc	tgaaaaaggt	1500
gctgatgagt	ctactatttc	aggcctatta	tcaaataact	acaaaacaact	attggcagga	1560
cttggaacca	cgctcagttt	aacccttatt	tcatttgcta	ttgctataat	tatcgggatc	1620
atctttggga	tgatggccgt	gtcaccaact	aaatcacttc	gacttatttc	aacggctctt	1680
gtggacgttg	ttcgagggat	tcctttgatg	attgtggctg	ccttcatttt	ctggggagta	1740
ccaaacctta	tcgagagtat	gaccggccac	cagtcaccga	ttaatgattt	cttagctgct	1800
acaattgcac	tgctacttaa	tggcggagcc	tatattgctg	aaattgttcg	cgggtggtatc	1860
gaagctgttc	cagcagggca	aatggaagct	agtcgaagtc	ttggtttgtc	ttacggaacc	1920
acgatgagaa	aagtaattct	cccacaagct	gtgaaactaa	tgttacctaa	ctttatcaat	1980
cagtttggtta	tttcattgaa	ggatacaaca	atcgtctcag	caattggttt	agtggaaactc	2040
ttccaaacag	gtaaaatcat	tattgctaga	aattaccagt	cgttccgtat	gtatgctatt	2100
ttagcaatta	tttaccttat	catgattata	ctcttaacaa	gacttgcaaa	acgttttagaa	2160
aagaggctta	actaa					2175

<210> SEQ ID NO 318

<211> LENGTH: 724

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 318

Met	Thr	His	Lys	Ile	Lys	Val	Leu	Leu	Leu	Ala	Ile	Met	Ser	Ile	Phe
1			5					10						15	
Leu	Thr	Cys	Asn	Ile	Ala	Ser	Ala	Glu	Thr	Ile	Ala	Ile	Val	Ser	Asp
			20					25					30		
Thr	Ala	Tyr	Ala	Pro	Phe	Glu	Phe	Lys	Asp	Ser	Asp	Gln	Ile	Tyr	Lys
		35				40					45				
Gly	Ile	Asp	Val	Asp	Ile	Ile	Asn	Glu	Val	Ala	Lys	Arg	Gln	Ser	Trp
	50				55					60					
Asp	Phe	Ser	Met	Ser	Phe	Pro	Gly	Phe	Asp	Ala	Ala	Val	Asn	Ala	Val
65				70				75					80		
Gln	Ser	Gly	Gln	Ala	Ser	Ala	Leu	Met	Ala	Gly	Thr	Thr	Ile	Thr	Asn
			85				90						95		
Ala	Arg	Lys	Lys	Val	Phe	His	Phe	Ser	Glu	Pro	Tyr	Tyr	Asp	Thr	Lys
			100				105						110		
Ile	Val	Ile	Ala	Thr	Arg	Lys	Ala	Asn	Ala	Ile	Lys	Lys	Tyr	Ser	Asp

		115					120				125								
Leu	Lys	Gly	Lys	Thr	Val	Gly	Val	Lys	Asn	Gly	Thr	Ala	Ala	Gln	Ala				
	130					135					140								
Phe	Leu	Asn	Asn	Tyr	Lys	Lys	Lys	Tyr	Asp	Tyr	Thr	Val	Lys	Thr	Phe				
145					150					155					160				
Asp	Thr	Gly	Asp	Leu	Met	Tyr	Asn	Ser	Leu	Ser	Ala	Gly	Ser	Ile	Ala				
			165						170					175					
Ala	Val	Met	Asp	Asp	Glu	Ala	Val	Ile	Gln	Tyr	Ala	Ile	Ser	Gln	Asn				
			180					185					190						
Gln	Asp	Ile	Ala	Ile	Asn	Met	Lys	Gly	Glu	Pro	Ile	Gly	Ser	Phe	Gly				
	195						200					205							
Phe	Ala	Val	Lys	Lys	Gly	Ser	Gly	Tyr	Asp	Tyr	Leu	Val	Asn	Asp	Phe				
210						215					220								
Asn	Thr	Ala	Leu	Lys	Ala	Met	Lys	Ala	Asp	Gly	Thr	Tyr	Gln	Ala	Ile				
225				230					235						240				
Met	Thr	Lys	Trp	Leu	Gly	Thr	Asp	Asp	Lys	Ala	Thr	Thr	Ser	Gln	Ala				
			245						250					255					
Thr	Gly	Asn	Pro	Ser	Ala	Lys	Ala	Thr	Pro	Thr	Lys	Asp	Ser	Tyr	Lys				
		260					265						270						
Ile	Val	Ser	Asp	Ser	Ser	Phe	Ala	Pro	Phe	Glu	Phe	Gln	Asn	Gly	Lys				
	275					280						285							
Gly	Lys	Tyr	Val	Gly	Ile	Asp	Ile	Glu	Leu	Ile	Lys	Ala	Ile	Ala	Lys				
290					295						300								
Gln	Gln	Gly	Phe	Lys	Ile	Glu	Ile	Ala	Asn	Pro	Gly	Phe	Asp	Ala	Ala				
305				310					315					320					
Leu	Asn	Ala	Val	Gln	Ser	Ser	Gln	Ala	Asp	Gly	Val	Ile	Ala	Gly	Ala				
			325						330					335					
Thr	Ile	Thr	Asp	Ala	Arg	Lys	Ala	Ile	Phe	Asp	Phe	Ser	Asp	Pro	Tyr				
		340					345					350							
Tyr	Thr	Ser	Asn	Ile	Ile	Leu	Ala	Val	Lys	Ala	Gly	Lys	Asn	Ile	Lys				
	355					360					365								
Asn	Tyr	Glu	Asp	Leu	Asp	Arg	Lys	Thr	Val	Gly	Ala	Lys	Asn	Gly	Thr				
370					375					380									
Ser	Ser	Tyr	Ser	Trp	Leu	Lys	Glu	Asn	Ala	Pro	Lys	Tyr	Gly	Tyr	Asn				
385				390					395					400					
Val	Lys	Ala	Phe	Asp	Asp	Gly	Ser	Ser	Met	Tyr	Asp	Ser	Leu	Asn	Ser				
			405						410					415					
Gly	Ser	Val	Asp	Ala	Ile	Met	Asp	Asp	Glu	Ala	Val	Leu	Lys	Tyr	Ala				
		420					425					430							
Ile	Ser	Gln	Gly	Arg	Arg	Phe	Glu	Thr	Pro	Leu	Glu	Gly	Ile	Ser	Thr				
	435					440					445								
Gly	Glu	Val	Gly	Phe	Ala	Val	Lys	Lys	Gly	Thr	Asn	Pro	Glu	Leu	Ile				
450					455					460									
Glu	Met	Phe	Asn	Asn	Gly	Leu	Ala	Ala	Leu	Lys	Lys	Ser	Gly	Gln	Tyr				
465				470					475					480					
Asp	Asp	Ile	Ile	Asp	Lys	Tyr	Leu	Asp	Ser	Lys	Lys	Ala	Ala	Thr	Pro				
			485						490					495					
Ser	Glu	Lys	Gly	Ala	Asp	Glu	Ser	Thr	Ile	Ser	Gly	Leu	Leu	Ser	Asn				
		500					505					510							
Asn	Tyr	Lys	Gln	Leu	Leu	Ala	Gly	Leu	Gly	Thr	Thr	Leu	Ser	Leu	Thr				
	515					520					525								
Leu	Ile	Ser	Phe	Ala	Ile	Ala	Ile	Ile	Ile	Gly	Ile	Ile	Phe	Gly	Met				
530					535					540									
Met	Ala	Val	Ser	Pro	Thr	Lys	Ser	Leu	Arg	Leu	Ile	Ser	Thr	Val	Phe				
545				550					555					560					
Val	Asp	Val	Val	Arg	Gly	Ile	Pro	Leu	Met	Ile	Val	Ala	Ala	Phe	Ile				
				565					570					575					

Phe	Trp	Gly	Val	Pro	Asn	Leu	Ile	Glu	Ser	Met	Thr	Gly	His	Gln	Ser
			580					585					590		
Pro	Ile	Asn	Asp	Phe	Leu	Ala	Ala	Thr	Ile	Ala	Leu	Ser	Leu	Asn	Gly
		595					600					605			
Gly	Ala	Tyr	Ile	Ala	Glu	Ile	Val	Arg	Gly	Gly	Ile	Glu	Ala	Val	Pro
	610					615					620				
Ala	Gly	Gln	Met	Glu	Ala	Ser	Arg	Ser	Leu	Gly	Leu	Ser	Tyr	Gly	Thr
625					630					635					640
Thr	Met	Arg	Lys	Val	Ile	Leu	Pro	Gln	Ala	Val	Lys	Leu	Met	Leu	Pro
			645						650					655	
Asn	Phe	Ile	Asn	Gln	Phe	Val	Ile	Ser	Leu	Lys	Asp	Thr	Thr	Ile	Val
		660						665					670		
Ser	Ala	Ile	Gly	Leu	Val	Glu	Leu	Phe	Gln	Thr	Gly	Lys	Ile	Ile	Ile
		675					680					685			
Ala	Arg	Asn	Tyr	Gln	Ser	Phe	Arg	Met	Tyr	Ala	Ile	Leu	Ala	Ile	Ile
	690					695					700				
Tyr	Leu	Ile	Met	Ile	Ile	Leu	Leu	Thr	Arg	Leu	Ala	Lys	Arg	Leu	Glu
705					710					715					720
Lys	Arg	Leu	Asn												

<210> SEQ ID NO 319

<211> LENGTH: 825

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 319

ttggtaactt	attataataa	ggatttagtg	cctcaagcac	ctaaaagctt	tactgaatta	60
gaagtcttac	aaaaagattc	taagtttgct	tttgccctctg	aaccaggaaa	atctgtaggt	120
ttcttggcga	aatggacaga	cttctattat	ggttatgggt	taattgccgg	ttatggcggt	180
tatatctttg	gtgataaagg	aaccaaacca	agtgatttag	gcctaggtaa	cgacggaact	240
gttgaagggt	taaactacgc	gaaacagtgg	tatggcactt	ggcctcaagg	aatgcaagac	300
actaaaaaag	ctggtgattt	tatcactgaa	caatttat	ctaaaaaagc	tgggtgtcatt	360
attgatggtc	catgggcagc	tagctccttt	aaagatgctg	gtgttaactt	tggggtaatg	420
gaaattccta	ctttgacaaa	tggtaaaaaa	taccaaccgt	tcgcaggtgg	taaagcttgg	480
gttatttcaa	actattctaa	aggaaaaacg	actgctcaaa	aattccttga	ttatgtgacc	540
aatgctgaaa	accaaaaacg	tttctatgat	aaaacacaag	aaattccagc	taacttaaca	600
gcacgtaact	atgcttctaa	agagggtaat	gagttaacga	aagctgtgat	tagtcagttt	660
gagagcgcac	aaccaatgcc	aaatattcca	gaaatggctg	aagtttggga	accaggtgca	720
aatatgttct	ttaacgtggc	ttctggtaag	gaagaagcat	ctaaagctgc	aaaagaagca	780
gcaaaaacta	ttaaggaagc	tattgaacaa	aaatacgctg	aataa		825

<210> SEQ ID NO 320

<211> LENGTH: 274

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 320

Met	Val	Thr	Tyr	Tyr	Asn	Lys	Asp	Leu	Val	Pro	Gln	Ala	Pro	Lys	Ser
1				5					10					15	
Phe	Thr	Glu	Leu	Glu	Val	Leu	Gln	Lys	Asp	Ser	Lys	Phe	Ala	Phe	Ala
			20					25					30		
Ser	Glu	Pro	Gly	Lys	Ser	Val	Gly	Phe	Leu	Ala	Lys	Trp	Thr	Asp	Phe
		35					40					45			
Tyr	Tyr	Gly	Tyr	Gly	Leu	Ile	Ala	Gly	Tyr	Gly	Gly	Tyr	Ile	Phe	Gly
	50					55					60				
Asp	Lys	Gly	Thr	Lys	Pro	Ser	Asp	Leu	Gly	Leu	Gly	Asn	Asp	Gly	Thr
65					70					75					80
Val	Glu	Gly	Leu	Asn	Tyr	Ala	Lys	Gln	Trp	Tyr	Gly	Thr	Trp	Pro	Gln
				85					90						95

Gly	Met	Gln	Asp	Thr	Lys	Lys	Ala	Gly	Asp	Phe	Ile	Thr	Glu	Gln	Phe	
			100					105					110			
Ile	Ser	Lys	Lys	Ala	Gly	Val	Ile	Ile	Asp	Gly	Pro	Trp	Ala	Ala	Ser	
		115					120					125				
Ser	Phe	Lys	Asp	Ala	Gly	Val	Asn	Phe	Gly	Val	Met	Glu	Ile	Pro	Thr	
	130					135					140					
Leu	Thr	Asn	Gly	Lys	Lys	Tyr	Gln	Pro	Phe	Ala	Gly	Gly	Lys	Ala	Trp	
145					150					155					160	
Val	Ile	Ser	Asn	Tyr	Ser	Lys	Gly	Lys	Thr	Thr	Ala	Gln	Lys	Phe	Leu	
			165						170					175		
Asp	Tyr	Val	Thr	Asn	Ala	Glu	Asn	Gln	Lys	Arg	Phe	Tyr	Asp	Lys	Thr	
		180						185					190			
Gln	Glu	Ile	Pro	Ala	Asn	Leu	Thr	Ala	Arg	Asn	Tyr	Ala	Ser	Lys	Glu	
		195					200					205				
Gly	Asn	Glu	Leu	Thr	Lys	Ala	Val	Ile	Ser	Gln	Phe	Glu	Ser	Ala	Gln	
	210					215					220					
Pro	Met	Pro	Asn	Ile	Pro	Glu	Met	Ala	Glu	Val	Trp	Glu	Pro	Gly	Ala	
225					230					235					240	
Asn	Met	Phe	Phe	Asn	Val	Ala	Ser	Gly	Lys	Glu	Glu	Ala	Ser	Lys	Ala	
			245					250						255		
Ala	Lys	Glu	Ala	Ala	Lys	Thr	Ile	Lys	Glu	Ala	Ile	Glu	Gln	Lys	Tyr	
			260					265					270			
Ala	Glu															

<210> SEQ ID NO 321

<211> LENGTH: 1308

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 321

atggtagaga	accaaagaca	acagaagcct	aataaagcca	tgtggctatc	tggtatccca	60
ggtttgggac	aactatacaa	taaacaaatc	gttaaagggg	gagtccttatt	agttgttttc	120
ttcctagagc	tactagaaat	tgtagttcta	ggaattcctg	ctttaacagg	tctttacagt	180
cttggaaagt	ttccaatgca	agatcactcc	ttatttatgt	taattaaggg	ggccatgcaa	240
ttaattactc	tagtccttatt	tggatattttt	catttggttg	ctatgagaga	tgctaaatta	300
gttgccacatc	aaatgaatga	aggcaagaag	gttccgggtga	cggctaaaga	gacccttgaa	360
gcgatttatg	aaaaaggatt	tccttacttg	ctcatcattc	cggcttattt	agcaatggct	420
ttcgtatta	tttttccagt	tttagtgacc	ttgctgattg	cttttaccac	ttacgatttt	480
aggcatattc	ctccgtatcg	tttattggat	tgggtagggt	tgaagaattt	tcttaatatc	540
ttagaattaa	gcaccttcaa	aacagcattt	acatctgttt	tgatcatggac	gctgatctgg	600
acattagcag	cgacaagtct	tcaaattggt	attggaattg	caacggctgt	tattgctaata	660
caatccttta	tcagaggaaa	acgtctcttt	ggtgtgatata	tcttggtacc	atgggctggt	720
ccagcattta	tctctattat	gagttttggt	aattttcttta	atgattccat	tggggccatg	780
aatgttcagg	ttcttccttt	catcgagaaa	ttccttcctt	tcgttgactt	cggcaattgtg	840
tcctggaaga	cagacccctt	ctggacaaaa	gtggctgtta	ttatggtgca	aggttggcta	900
ggatttccct	atatctatat	tttggtatca	ggtattttac	aggcaattcc	agctgattta	960
tacgaagcag	caaccggtga	tgggtgcgaca	gtcttacaga	aattccgcca	tatcaccatg	1020
ccaatgattt	ttgcggttgc	agcaccaacc	tttatctctc	agtacacctt	taacttcaat	1080
aattttctcta	ttatttatct	gtttaataat	gggggccctg	gtactgtggg	ggcgaggact	1140
gggacaactg	atattctgat	ttcttggatt	tacaagttga	ccacacaaac	ctcgccctcaa	1200
ttttcgatgg	cgtcggcaat	gaccttaatc	atctctgtaa	taatgatttc	ggtatcattg	1260
attaccttta	agaaatttaa	agcttttgat	atggaggaga	gatcatga		1308

<210> SEQ ID NO 322

<211> LENGTH: 435

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 322

Met	Val	Glu	Asn	Gln	Arg	Gln	Gln	Lys	Pro	Asn	Lys	Ala	Met	Trp	Leu
1				5					10					15	
Ser	Val	Ile	Pro	Gly	Leu	Gly	Gln	Leu	Tyr	Asn	Lys	Gln	Ile	Val	Lys
			20					25					30		
Gly	Gly	Val	Leu	Leu	Val	Val	Phe	Phe	Leu	Glu	Leu	Leu	Glu	Ile	Val
		35					40					45			
Val	Leu	Gly	Ile	Pro	Ala	Leu	Thr	Gly	Leu	Tyr	Ser	Leu	Gly	Ser	Val
	50					55					60				
Pro	Met	Gln	Asp	His	Ser	Leu	Phe	Met	Leu	Ile	Lys	Gly	Ala	Met	Gln
65				70						75					80
Leu	Ile	Thr	Leu	Val	Leu	Phe	Gly	Ile	Phe	His	Leu	Val	Ala	Met	Arg
			85					90						95	
Asp	Ala	Lys	Leu	Val	Ala	His	Gln	Met	Asn	Glu	Gly	Lys	Lys	Val	Pro
		100						105					110		
Val	Thr	Ala	Lys	Glu	Thr	Leu	Glu	Ala	Ile	Tyr	Glu	Lys	Gly	Phe	Pro
		115					120					125			
Tyr	Leu	Leu	Ile	Ile	Pro	Ala	Tyr	Leu	Ala	Met	Ala	Phe	Ala	Ile	Ile
	130					135					140				
Phe	Pro	Val	Leu	Val	Thr	Leu	Leu	Ile	Ala	Phe	Thr	Asn	Tyr	Asp	Phe
145				150						155					160
Arg	His	Ile	Pro	Pro	Tyr	Arg	Leu	Leu	Asp	Trp	Val	Gly	Leu	Lys	Asn
			165						170					175	
Phe	Leu	Asn	Ile	Leu	Glu	Leu	Ser	Thr	Phe	Lys	Thr	Ala	Phe	Thr	Ser
		180						185					190		
Val	Leu	Ser	Trp	Thr	Leu	Ile	Trp	Thr	Leu	Ala	Ala	Thr	Ser	Leu	Gln
		195					200					205			
Ile	Val	Ile	Gly	Ile	Ala	Thr	Ala	Val	Ile	Ala	Asn	Gln	Ser	Phe	Ile
	210					215					220				
Arg	Gly	Lys	Arg	Leu	Phe	Gly	Val	Ile	Phe	Leu	Leu	Pro	Trp	Ala	Val
225				230						235					240
Pro	Ala	Phe	Ile	Ser	Ile	Met	Ser	Phe	Gly	Asn	Phe	Phe	Asn	Asp	Ser
			245						250					255	
Ile	Gly	Ala	Met	Asn	Val	Gln	Val	Leu	Pro	Phe	Ile	Glu	Lys	Phe	Leu
		260						265					270		
Pro	Phe	Val	Asp	Phe	Gly	Ile	Val	Ser	Trp	Lys	Thr	Asp	Pro	Phe	Trp
		275					280					285			
Thr	Lys	Val	Ala	Val	Ile	Met	Val	Gln	Gly	Trp	Leu	Gly	Phe	Pro	Tyr
	290					295					300				
Ile	Tyr	Ile	Leu	Val	Ser	Gly	Ile	Leu	Gln	Ala	Ile	Pro	Ala	Asp	Leu
305				310						315					320
Tyr	Glu	Ala	Ala	Thr	Val	Asp	Gly	Ala	Thr	Val	Leu	Gln	Lys	Phe	Arg
			325						330					335	
His	Ile	Thr	Met	Pro	Met	Ile	Phe	Ala	Val	Ala	Ala	Pro	Thr	Phe	Ile
			340					345					350		
Ser	Gln	Tyr	Thr	Phe											

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<210> SEQ ID NO 323
<211> LENGTH: 861
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 323
atgagaaaga cttatgtttc aatatccatg aaacgcaaac gtttcttcac ccaattattg      60
acttatctct atctaattct cttagtgatc gtgattttat tcccaatact agtgacggtc      120
agttcagctt ttagaccagg aaataccaca gccttttagtt ttcattttga tgggccatgg      180
accttgctta actttaaaac actctttcaa gataccttat acttaagatg gtattggaat      240
accttgatcg tggcattctt caccatgctc atacaagtaa cagtcacac tttgacaggt      300
tatgcgatata gccgttacaa tttctttgga cgcaaaaaaa gtttaatctt tttcctagtc      360
gtacagatgg ttcctaccat ggcggcttta acggcttact ttgttatggc gtggctcttt      420
aatgccttaa accaatactg gttcttgatt ttgatttacg tcggtggtgg tattcctatg      480
aatgcctggt tgatgaaggg ttattttgac acggtacctt atgacttga cgaatctgct      540
aagttagatg gttctggaca ctttaggacc ttctaccaa ttgtccttcc tcttggtcga      600
ccaatgattg cagtacaatc cttatgggct tttatgggct ctttcggaga cttcatgttg      660
gctaaattcc ttttaagggc gcaagaaaat tatacggtag cagttggtct tcaatcgttt      720
attacgaatg atgctagaaa tccaaggtta accttatttg ctgcgggagc tattctgatt      780
gcagtgccta tttcagttct ctttttcttc ctacagaaaa atttcgtttc cggtttaaca      840
agtggtggtta ccaaagggtta a

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<210> SEQ ID NO 324
<211> LENGTH: 286
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 324
Met Arg Lys Thr Tyr Val Ser Ile Ser Met Lys Arg Lys Arg Phe Phe
1      5      10      15
Thr Gln Leu Leu Thr Tyr Leu Tyr Leu Ile Ser Leu Val Ile Val Ile
20     25     30
Leu Phe Pro Ile Leu Val Thr Val Ser Ser Ala Phe Arg Pro Gly Asn
35     40     45
Thr Thr Ala Phe Ser Phe His Phe Asp Gly Pro Trp Thr Leu Ser Asn
50     55     60
Phe Lys Thr Leu Phe Gln Asp Thr Leu Tyr Leu Arg Trp Tyr Trp Asn
65     70     75     80
Thr Leu Ile Val Ala Phe Phe Thr Met Leu Ile Gln Val Thr Val Ile
85     90     95
Thr Leu Thr Gly Tyr Ala Tyr Ser Arg Tyr Asn Phe Phe Gly Arg Lys
100    105    110
Lys Ser Leu Ile Phe Phe Leu Val Val Gln Met Val Pro Thr Met Ala
115    120    125
Ala Leu Thr Ala Tyr Phe Val Met Ala Trp Leu Phe Asn Ala Leu Asn
130    135    140
Gln Tyr Trp Phe Leu Ile Leu Ile Tyr Val Gly Gly Gly Ile Pro Met
145    150    155    160
Asn Ala Trp Leu Met Lys Gly Tyr Phe Asp Thr Val Pro Tyr Asp Leu
165    170    175
Asp Glu Ser Ala Lys Leu Asp Gly Ser Gly His Phe Arg Thr Phe Tyr
180    185    190
Gln Ile Val Leu Pro Leu Val Arg Pro Met Ile Ala Val Gln Ser Leu
195    200    205
Trp Ala Phe Met Gly Pro Phe Gly Asp Phe Met Leu Ala Lys Phe Leu
210    215    220
Leu Arg Ala Gln Glu Asn Tyr Thr Val Ala Val Gly Leu Gln Ser Phe
225    230    235    240
Ile Thr Asn Asp Ala Arg Asn Pro Lys Val Thr Leu Phe Ala Ala Gly

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				245					250					255			
Ala	Ile	Leu	Ile	Ala	Val	Pro	Ile	Ser	Val	Leu	Phe	Phe	Phe	Leu	Gln		
			260					265						270			
Lys	Asn	Phe	Val	Ser	Gly	Leu	Thr	Ser	Gly	Gly	Thr	Lys	Gly				
		275					280						285				

<210> SEQ ID NO 325
 <211> LENGTH: 816
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 325

atgccagata	aaaaacaatt	tcctatcttct	tacattttcac	attgcctttc	tcctagggca	60
atgtttgcca	gccgagctca	gtttacttgg	tggcaaaatc	ttcttattat	tgtttttttg	120
aacgccttaa	taatgattcc	agttacgtta	cactatgcta	acatgacaac	gtatcccttg	180
gaacggattg	taactaagag	tttgtcgctt	atcacagaca	aaacctatca	agcattgacc	240
caaggaaaga	ttgagaaaga	tacgtttcag	ggccaatctc	tgattcgacg	agatgggtgaa	300
ttggtttttg	ctgtttttacc	gacaaagggtc	gatttagagc	aattggcatc	agaatcaacc	360
agacaaatta	ttgtgacaaa	aaaagaatgg	cgttttgtta	cccctgatgg	caaggaaactc	420
cgtgctcacg	ttagaggcca	gcagcagtca	ctcgctgacc	tgacaacagt	taaagcagtg	480
aaggactttg	tcaatcagca	atggatatgac	agtaataaag	ccagtgtact	tggtttttctt	540
ttgctgacgt	ttgtttctcat	ggtgtgtgtg	ggtaccctta	ttgtgattgg	tctaggcgct	600
ttctttttga	ctctgactaa	acgatcacga	ctatttatga	ttcgaaactt	ctctgaagga	660
cttggattga	tggttaattg	tttggcttgg	ccgagtctac	tggcgattgc	tcttagtttc	720
tttattcagg	atccagtact	gattatgaat	tgccaagtat	ttggtacctt	attaatgctg	780
acctgggtgt	tctacaaaac	acagtttaga	gattga			816

<210> SEQ ID NO 326
 <211> LENGTH: 271
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 326

Met	Pro	Asp	Lys	Lys	Gln	Phe	Pro	Ile	Ser	Tyr	Ile	Ser	His	Cys	Leu	
1			5						10					15		
Ser	Pro	Arg	Ala	Met	Phe	Ala	Ser	Arg	Ala	Gln	Phe	Thr	Trp	Trp	Gln	
		20						25					30			
Asn	Leu	Leu	Ile	Ile	Val	Phe	Leu	Asn	Ala	Leu	Ile	Met	Ile	Pro	Val	
	35						40					45				
Thr	Leu	His	Tyr	Ala	Asn	Met	Thr	Thr	Tyr	Pro	Leu	Glu	Arg	Ile	Val	
	50					55					60					
Thr	Lys	Ser	Leu	Ser	Pro	Ile	Thr	Asp	Lys	Thr	Tyr	Gln	Ala	Leu	Thr	
65					70				75					80		
Gln	Gly	Lys	Ile	Glu	Lys	Asp	Thr	Phe	Gln	Gly	Gln	Ser	Leu	Ile	Arg	
			85						90					95		
Arg	Asp	Gly	Glu	Leu	Val	Leu	Ala	Val	Leu	Pro	Thr	Lys	Val	Asp	Leu	
		100						105					110			
Glu	Gln	Leu	Ala	Ser	Glu	Ser	Thr	Arg	Gln	Ile	Ile	Val	Thr	Lys	Lys	
	115						120					125				
Glu	Trp	Arg	Phe	Val	Thr	Pro	Asp	Gly	Lys	Glu	Leu	Arg	Ala	His	Val	
	130					135				140						
Arg	Gly	Gln	Gln	Gln	Ser	Leu	Ala	Asp	Leu	Thr	Thr	Val	Lys	Ala	Val	
145					150				155					160		
Lys	Asp	Phe	Val	Asn	Gln	Gln	Trp	Tyr	Asp	Ser	Asn	Lys	Ala	Ser	Val	
			165						170					175		
Leu	Gly	Phe	Leu	Leu	Leu	Thr	Phe	Val	Leu	Met	Val	Cys	Val	Gly	Thr	
		180						185					190			
Leu	Ile	Val	Ile	Gly	Leu	Gly	Ala	Phe	Phe	Leu	Thr	Leu	Thr	Lys	Arg	
	195						200						205			

Ser	Arg	Leu	Phe	Met	Ile	Arg	Asn	Phe	Ser	Glu	Gly	Leu	Gly	Leu	Met
210						215					220				
Val	Asn	Cys	Leu	Ala	Trp	Pro	Ser	Leu	Leu	Ala	Ile	Ala	Leu	Ser	Phe
225					230					235					240
Phe	Ile	Gln	Asp	Pro	Val	Leu	Ile	Met	Asn	Cys	Gln	Val	Phe	Gly	Thr
				245					250					255	
Leu	Leu	Met	Leu	Thr	Trp	Val	Phe	Tyr	Lys	Thr	Gln	Phe	Arg	Asp	
			260					265						270	

<210> SEQ ID NO 327

<211> LENGTH: 837

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 327

atgaaaaaca aacgtcgatt tcaacttgga cttgtttatg ctactttaat catcctctca	60
atcatttggc tcttcccaat cgcttggggtt attcttacta gcttccgtag cgaaggaact	120
gcttacgtca attattttat tcctaagact tttacattaa atcactacat taatcttttt	180
actaatgaaa ccttttccttt tggaaaatgg tttatgaata ctcttattgt agccactttt	240
acatgtatta tttcaacctt cataactggt gccatagcct actctcttag ccgaattaag	300
tttaagtttc gcaatggctt tttaaaacta gcccttattt taaatatggt ccctgggttc	360
atgagcatga ttgccatcta ctatatctta aaggccttag gtttgacgca aaccctaaca	420
gcacttgtcc ttgtttattc ctcaggtgca gcccttgggt tttacattgc aaaaggattt	480
tttgatacca ttccttattc acttgatgaa tcagctatga ttgatggcgc tactcgtatg	540
gatattttct ttaaaataac ccttccttta gcaaaaccaa tcattgtcta tactgccctt	600
cttgctttta tggggccttg gattgacttt atctttgcac aagttatttt aggtgatgct	660
acaagtaaat ataccgttgc tattggacta ttttcaatgc ttcagccaga taccattaac	720
aactggttta tggccttcac tgctggttct gtcttaattg ccgtcccaat cactctcctc	780
ttcatgttta tgcaaaaata ctatgttgaa ggcatcacag gtggttctgt taaataa	837

<210> SEQ ID NO 328

<211> LENGTH: 278

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 328

Met	Lys	Asn	Lys	Arg	Arg	Phe	Gln	Leu	Gly	Leu	Val	Tyr	Ala	Thr	Leu
1			5						10					15	
Ile	Ile	Leu	Ser	Ile	Ile	Trp	Leu	Phe	Pro	Ile	Ala	Trp	Val	Ile	Leu
			20					25					30		
Thr	Ser	Phe	Arg	Ser	Glu	Gly	Thr	Ala	Tyr	Val	Asn	Tyr	Phe	Ile	Pro
			35				40					45			
Lys	Thr	Phe	Thr	Leu	Asn	His	Tyr	Ile	Asn	Leu	Phe	Thr	Asn	Glu	Thr
			50			55					60				
Phe	Pro	Phe	Gly	Lys	Trp	Phe	Met	Asn	Thr	Leu	Ile	Val	Ala	Thr	Phe
65					70					75				80	
Thr	Cys	Ile	Ile	Ser	Thr	Phe	Ile	Thr	Val	Ala	Ile	Ala	Tyr	Ser	Leu
				85					90					95	
Ser	Arg	Ile	Lys	Phe	Lys	Phe	Arg	Asn	Gly	Phe	Leu	Lys	Leu	Ala	Leu
			100					105					110		
Ile	Leu	Asn	Met	Phe	Pro	Gly	Phe	Met	Ser	Met	Ile	Ala	Ile	Tyr	Tyr
		115				120						125			
Ile	Leu	Lys	Ala	Leu	Gly	Leu	Thr	Gln	Thr	Leu	Thr	Ala	Leu	Val	Leu
		130				135						140			
Val	Tyr	Ser	Ser	Gly	Ala	Ala	Leu	Gly	Phe	Tyr	Ile	Ala	Lys	Gly	Phe
145					150					155					160
Phe	Asp	Thr	Ile	Pro	Tyr	Ser	Leu	Asp	Glu	Ser	Ala	Met	Ile	Asp	Gly
				165					170					175	
Ala	Thr	Arg	Met	Asp	Ile	Phe	Phe	Lys	Ile	Thr	Leu	Pro	Leu	Ala	Lys

			180					185				190					
Pro	Ile	Ile	Val	Tyr	Thr	Ala	Leu	Leu	Ala	Phe	Met	Gly	Pro	Trp	Ile		
		195					200					205					
Asp	Phe	Ile	Phe	Ala	Gln	Val	Ile	Leu	Gly	Asp	Ala	Thr	Ser	Lys	Tyr		
	210					215					220						
Thr	Val	Ala	Ile	Gly	Leu	Phe	Ser	Met	Leu	Gln	Pro	Asp	Thr	Ile	Asn		
225					230					235					240		
Asn	Trp	Phe	Met	Ala	Phe	Thr	Ala	Gly	Ser	Val	Leu	Ile	Ala	Val	Pro		
			245						250					255			
Ile	Thr	Leu	Leu	Phe	Met	Phe	Met	Gln	Lys	Tyr	Tyr	Val	Glu	Gly	Ile		
		260						265					270				
Thr	Gly	Gly	Ser	Val	Lys												
		275															

<210> SEQ ID NO 329

<211> LENGTH: 1362

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 329

atgactcagt	caaacttgac	accaaata	tctgtaatag	aagccttaaa	aagaggcagt	60
tgggatatta	aactttcgag	tattatcatg	ggatttgcca	actttgctaa	caaacagttt	120
atcaaaggaa	tcttattttt	aataagtga	cttatctttc	tagtagcttt	tgtctcccaa	180
atcatccctg	ctatccgtgg	ccttgctact	cttggtactc	aaactcaggg	aatgactaca	240
aaaactattg	atgggattaa	catccaagtt	gctggtgatg	gcgataactc	tatgttaatg	300
cttatttttg	gttttagcatc	actcattttc	tgccatagtct	ttgcttacat	ttactgggtgt	360
aatctcaaaa	gtgctcgtaa	cctttatctt	ttcaaacaaa	aagggtcagaa	gataccaagc	420
ttcaaagaag	atcttgccac	acttacaaat	ggtcgctttc	atatgacttt	aatggctatc	480
ccactgattg	gtgtgctttt	attcaccatt	cttcctttga	tttacatgat	ctgtttggcc	540
tttaccaatt	ttgatcataa	tcacttgctt	ccaaaatctt	tatttgattg	gggtgggactt	600
gctaactttg	gaaatgtttt	aagcggccgt	atggcaggaa	ccttttttcc	tatctttctca	660
tggactttga	tttgggctgt	ttttgccaca	gtaactaatt	tcttctttgg	tattattctt	720
gctttgttaa	tcaataccaa	aggattaaag	tggaaaaaaa	tgtggcgaac	catctttgtt	780
atcaccattg	cagttccaca	attcatctca	ttattgatta	tgcggaactt	actcaatgac	840
gaaggcccac	taaatgctct	tctcaataaa	atcgggcttga	ttaatggctc	actgccattt	900
ttatctgata	ctctttgggc	aaaattctca	atcatttttg	tcaacatgtg	gatcgggtatt	960
ccatttacca	tgctgattgc	gactgggtatt	atcatgaacc	ttccaagtga	acaaattgag	1020
gctgctgaaa	ttgatggcgc	tagcaaatc	caagtcttca	agtctatcac	gttccctcaa	1080
attctcttga	tcatgacacc	aaacttgatt	caacaattta	tcggaaaatat	caataacttt	1140
aacgtcattt	acctccttac	tggtgggtgt	ccaacaaatt	cagaatacta	tcaggcagga	1200
acaacagact	tgctggtcac	ttggctttat	aaattaaccg	tcacagctgc	tgactacaat	1260
ttagcttctg	ttatcggtat	cttaatcttt	acagtttcag	ctatctttag	cttacttgct	1320
tatacaagga	cagcatccta	caaggaagga	gcggctaaat	aa		1362

<210> SEQ ID NO 330

<211> LENGTH: 453

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 330

Met	Thr	Gln	Ser	Asn	Leu	Thr	Pro	Asn	Ile	Ser	Val	Ile	Glu	Ala	Leu
1			5						10					15	
Lys	Arg	Gly	Ser	Trp	Asp	Ile	Lys	Leu	Ser	Ser	Ile	Ile	Met	Gly	Phe
		20						25					30		
Ala	Asn	Phe	Ala	Asn	Lys	Gln	Phe	Ile	Lys	Gly	Ile	Leu	Phe	Leu	Ile
		35					40					45			
Ser	Glu	Leu	Ile	Phe	Leu	Val	Ala	Phe	Val	Ser	Gln	Ile	Ile	Pro	Ala
	50					55					60				
Ile	Arg	Gly	Leu	Val	Thr	Leu	Gly	Thr	Gln	Thr	Gln	Gly	Met	Thr	Thr

65					70					75					80
Lys	Thr	Ile	Asp	Gly	Ile	Asn	Ile	Gln	Val	Ala	Val	Asp	Gly	Asp	Asn
				85					90					95	
Ser	Met	Leu	Met	Leu	Ile	Phe	Gly	Leu	Ala	Ser	Leu	Ile	Phe	Cys	Leu
			100					105					110		
Val	Phe	Ala	Tyr	Ile	Tyr	Trp	Cys	Asn	Leu	Lys	Ser	Ala	Arg	Asn	Leu
	115						120					125			
Tyr	Leu	Phe	Lys	Gln	Lys	Gly	Gln	Lys	Ile	Pro	Ser	Phe	Lys	Glu	Asp
	130					135					140				
Leu	Ala	Thr	Leu	Thr	Asn	Gly	Arg	Phe	His	Met	Thr	Leu	Met	Ala	Ile
145					150					155					160
Pro	Leu	Ile	Gly	Val	Leu	Leu	Phe	Thr	Ile	Leu	Pro	Leu	Ile	Tyr	Met
			165						170					175	
Ile	Cys	Leu	Ala	Phe	Thr	Asn	Phe	Asp	His	Asn	His	Leu	Pro	Pro	Lys
			180					185					190		
Ser	Leu	Phe	Asp	Trp	Val	Gly	Leu	Ala	Asn	Phe	Gly	Asn	Val	Leu	Ser
		195				200						205			
Gly	Arg	Met	Ala	Gly	Thr	Phe	Phe	Pro	Ile	Phe	Ser	Trp	Thr	Leu	Ile
	210					215						220			
Trp	Ala	Val	Phe	Ala	Thr	Val	Thr	Asn	Phe	Phe	Phe	Gly	Ile	Ile	Leu
225					230					235					240
Ala	Leu	Leu	Ile	Asn	Thr	Lys	Gly	Leu	Lys	Trp	Lys	Lys	Met	Trp	Arg
			245					250					255		
Thr	Ile	Phe	Val	Ile	Thr	Ile	Ala	Val	Pro	Gln	Phe	Ile	Ser	Leu	Leu
			260					265					270		
Ile	Met	Arg	Asn	Leu	Leu	Asn	Asp	Glu	Gly	Pro	Leu	Asn	Ala	Leu	Leu
		275				280						285			
Asn	Lys	Ile	Gly	Leu	Ile	Asn	Gly	Ser	Leu	Pro	Phe	Leu	Ser	Asp	Pro
	290					295					300				
Leu	Trp	Ala	Lys	Phe	Ser	Ile	Ile	Phe	Val	Asn	Met	Trp	Ile	Gly	Ile
305					310					315					320
Pro	Phe	Thr	Met	Leu	Ile	Ala	Thr	Gly	Ile	Ile	Met	Asn	Leu	Pro	Ser
			325					330					335		
Glu	Gln	Ile	Glu	Ala	Ala	Glu	Ile	Asp	Gly	Ala	Ser	Lys	Phe	Gln	Val
			340					345					350		
Phe	Lys	Ser	Ile	Thr	Phe	Pro	Gln	Ile	Leu	Leu	Ile	Met	Thr	Pro	Asn
		355					360					365			
Leu	Ile	Gln	Gln	Phe	Ile	Gly	Asn	Ile	Asn	Asn	Phe	Asn	Val	Ile	Tyr
	370					375					380				
Leu	Leu	Thr	Gly	Gly	Gly	Pro	Thr	Asn	Ser	Glu	Tyr	Tyr	Gln	Ala	Gly
385					390					395					400
Thr	Thr	Asp	Leu	Leu	Val	Thr	Trp	Leu	Tyr	Lys	Leu	Thr	Val	Thr	Ala
			405					410					415		
Ala	Asp	Tyr	Asn	Leu	Ala	Ser	Val	Ile	Gly	Ile	Leu	Ile	Phe	Thr	Val
			420					425					430		
Ser	Ala	Ile	Phe	Ser	Leu	Leu	Ala	Tyr	Thr	Arg	Thr	Ala	Ser	Tyr	Lys
		435					440					445			
Glu	Gly	Ala	Ala	Lys											
	450														

<210> SEQ ID NO 331

<211> LENGTH: 786

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 331

atgttttgga	aattattaaa	atacgaattt	agatctattg	gaaaatggta	ctttgcgctt	60
aatgctttcg	ttattgccat	cgctgccatt	ttgtcattta	cgataaaact	gtttgctcaa	120

```

agcaatagtg atggactatt tggagtacta accaataaga tgttgccctct gacattaggt 180
ttaacttttg gctccctgat cgctgggtcc ctcttatcaa cattacttat cattatcaaa 240
cgtttcagca aaagtgtttt tggatgggaa ggatacttaa cgttgacttt acccgtaaat 300
tcgcatcaaaa ttattttatc aaaactacta gcttctttta tttgcagtgt tttcaatact 360
atcatccttg catttgctat cgctattgta attgtaccaa tgtttaacat caacgaacta 420
ttagaaggat tctttaatag ttttaagatg gattatttca tcaatatgct aactgtacta 480
gcctatgtcc tattatcaac atttacgagt atcttattaa tttatctttc catttctata 540
ggccaacttt tttccaatcg gcgaggcttg atggccttta ttgcatatth tatattagtt 600
attctgatta gcgttgctgc aacatatgtt cacagtcaca tctttaatat taatacaagt 660
gccgatagtt tcccattttac tgagcaaaaa acaattttatc ttcttatttt ggaacaattt 720
attgaaatga taatgtttta cctcgccact aattttatta tcaaaaataa actcaaccta 780
cagtaa 786

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<210> SEQ ID NO 332
 <211> LENGTH: 261
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 332

```

Met Phe Gly Lys Leu Leu Lys Tyr Glu Phe Arg Ser Ile Gly Lys Trp
1      5      10      15
Tyr Phe Ala Leu Asn Ala Phe Val Ile Ala Ile Ala Ala Ile Leu Ser
20      25      30
Phe Thr Ile Lys Leu Phe Ala Gln Ser Asn Ser Asp Gly Leu Phe Gly
35      40      45
Val Leu Thr Asn Lys Met Leu Pro Leu Thr Leu Gly Leu Thr Phe Gly
50      55      60
Ser Leu Ile Ala Gly Ser Leu Leu Ser Thr Leu Leu Ile Ile Ile Lys
65      70      75      80
Arg Phe Ser Lys Ser Val Phe Gly Trp Glu Gly Tyr Leu Thr Leu Thr
85      90      95
Leu Pro Val Asn Ser His Gln Ile Ile Leu Ser Lys Leu Leu Ala Ser
100     105     110
Phe Ile Cys Ser Val Phe Asn Thr Ile Ile Leu Ala Phe Ala Ile Ala
115     120     125
Ile Val Ile Val Pro Met Phe Asn Ile Asn Glu Leu Leu Glu Gly Phe
130     135     140
Phe Asn Ser Phe Lys Met Asp Tyr Phe Ile Asn Met Leu Thr Val Leu
145     150     155     160
Ala Tyr Val Leu Leu Ser Thr Phe Thr Ser Ile Leu Leu Ile Tyr Leu
165     170     175
Ser Ile Ser Ile Gly Gln Leu Phe Ser Asn Arg Arg Gly Leu Met Ala
180     185     190
Phe Ile Ala Tyr Phe Ile Leu Val Ile Leu Ile Ser Val Ala Ala Thr
195     200     205
Tyr Val His Ser His Ile Phe Asn Ile Asn Thr Ser Ala Asp Ser Phe
210     215     220
Pro Phe Thr Glu Gln Lys Thr Ile Tyr Leu Leu Ile Leu Glu Gln Phe
225     230     235     240
Ile Glu Met Ile Met Phe Tyr Leu Ala Thr Asn Phe Ile Ile Lys Asn
245     250     255
Lys Leu Asn Leu Gln
260

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<210> SEQ ID NO 333
 <211> LENGTH: 558
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes

```

<400> SEQUENCE: 333
atggttaaagc gagattttat aagaaatata ttattgttat taattgtgat tattggggct      60
attttggtga gaatctttgt tttttcaact tttaaagttt ctccagaaac agctaatact      120
tatttaaaga gtggtgattt agtcacaatc aaaaaaataa ttcagcccaa atataaagat      180
tttgtgggtt atagagttgg aaaaaaagat tatgtcagtc gagtcattgc tgttgaaggc      240
gatagcgtga cttatatgga cgatatTTTTT tacctcaata atatggtaga gtcacaggct      300
taccttgaaa agatgaaagc acattacttg aatcatgcac cgtttggcac attgtataca      360
gatgatttta cagttgctac catcacagct gataagtatc aaaaagtcc taaggggaag      420
tatcttcttt tgaatgataa ccggaaaaat acgaatgaca gtcgtcgatt tgggttaata      480
aatgcctcgc agattaaagg tttagtgacc tttagagttt tgcctctcag cgattttgga      540
tttgtagaag tagagtag                                     558

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```

<210> SEQ ID NO 334
<211> LENGTH: 185
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 334

```

```

Met Val Lys Arg Asp Phe Ile Arg Asn Ile Leu Leu Leu Ile Val
1           5           10          15
Ile Ile Gly Ala Ile Leu Leu Arg Ile Phe Val Phe Ser Thr Phe Lys
20          25          30
Val Ser Pro Glu Thr Ala Asn Thr Tyr Leu Lys Ser Gly Asp Leu Val
35          40          45
Thr Ile Lys Lys Asn Ile Gln Pro Lys Tyr Lys Asp Phe Val Val Tyr
50          55          60
Arg Val Gly Lys Lys Asp Tyr Val Ser Arg Val Ile Ala Val Glu Gly
65          70          75          80
Asp Ser Val Thr Tyr Met Asp Asp Ile Phe Tyr Leu Asn Asn Met Val
85          90          95
Glu Ser Gln Ala Tyr Leu Glu Lys Met Lys Ala His Tyr Leu Asn His
100         105         110
Ala Pro Phe Gly Thr Leu Tyr Thr Asp Asp Phe Thr Val Ala Thr Ile
115         120         125
Thr Ala Asp Lys Tyr Gln Lys Val Pro Lys Gly Lys Tyr Leu Leu Leu
130         135         140
Asn Asp Asn Arg Lys Asn Thr Asn Asp Ser Arg Arg Phe Gly Leu Ile
145         150         155         160
Asn Ala Ser Gln Ile Lys Gly Leu Val Thr Phe Arg Val Leu Pro Leu
165         170         175
Ser Asp Phe Gly Phe Val Glu Val Glu
180         185

```

```

<210> SEQ ID NO 335
<211> LENGTH: 642
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 335

```

```

atgacctata ttcagcaagt tttacccagc ttattagatg gtgccttggt gactttacaa      60
gtattcttta ttgttatcat tctttctata cccttagggg ctatttttagc tttcttgatg      120
aagattccct ttaaaccgct acagtgggtt ttgaccctat acgtgtggat gatgcgaggg      180
acaccattac tacttcaatt gatttttttc tattatgttt tgccaagtgt ggggattagt      240
tttgatcgaa tgccagctgc tattttggcg tttactttga attatgctgc ctactttgct      300
gaaattttta gaggtgggat tgaggctatt ccaaagggtc aatatgaagc agctaaaagta      360
ttaaagttaa aacctcttca aaccattcgt tatattattt tgcctcaagt gtttaaaatt      420
gtgttaccaa gtgttttcaa tgaagtcatt aatttgggtc aagattcttc cttgtctat      480
gtactcgggtg taggagatct tttattagca agtaagacgg cagccaatag ggatgcaacc      540
ttagccccta tgtttatcgc tggcttatc tatttgcttt taattggact ggtcacgatt      600

```

atttcaaaac aagttgaaaa acggtttaat tattatcagt aa

642

<210> SEQ ID NO 336
<211> LENGTH: 213
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 336

Met	Thr	Tyr	Ile	Gln	Gln	Val	Leu	Pro	Ser	Leu	Leu	Asp	Gly	Ala	Leu
1			5						10					15	
Val	Thr	Leu	Gln	Val	Phe	Phe	Ile	Val	Ile	Ile	Leu	Ser	Ile	Pro	Leu
		20						25				30			
Gly	Ala	Ile	Leu	Ala	Phe	Leu	Met	Lys	Ile	Pro	Phe	Lys	Pro	Leu	Gln
		35					40					45			
Trp	Phe	Leu	Thr	Leu	Tyr	Val	Trp	Met	Met	Arg	Gly	Thr	Pro	Leu	Leu
	50					55					60				
Leu	Gln	Leu	Ile	Phe	Phe	Tyr	Tyr	Val	Leu	Pro	Ser	Val	Gly	Ile	Ser
65				70						75				80	
Phe	Asp	Arg	Met	Pro	Ala	Ala	Ile	Leu	Ala	Phe	Thr	Leu	Asn	Tyr	Ala
			85						90					95	
Ala	Tyr	Phe	Ala	Glu	Ile	Phe	Arg	Gly	Gly	Ile	Glu	Ala	Ile	Pro	Lys
			100					105					110		
Gly	Gln	Tyr	Glu	Ala	Ala	Lys	Val	Leu	Lys	Leu	Lys	Pro	Leu	Gln	Thr
		115					120					125			
Ile	Arg	Tyr	Ile	Ile	Leu	Pro	Gln	Val	Phe	Lys	Ile	Val	Leu	Pro	Ser
	130					135					140				
Val	Phe	Asn	Glu	Val	Ile	Asn	Leu	Val	Lys	Asp	Ser	Ser	Leu	Val	Tyr
145				150						155				160	
Val	Leu	Gly	Val	Gly	Asp	Leu	Leu	Leu	Ala	Ser	Lys	Thr	Ala	Ala	Asn
			165						170					175	
Arg	Asp	Ala	Thr	Leu	Ala	Pro	Met	Phe	Ile	Ala	Gly	Leu	Ile	Tyr	Leu
		180						185					190		
Leu	Leu	Ile	Gly	Leu	Val	Thr	Ile	Ser	Lys	Gln	Val	Glu	Lys	Arg	
		195					200				205				
Phe	Asn	Tyr	Tyr	Gln											
	210														

<210> SEQ ID NO 337
<211> LENGTH: 774
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 337

atgaaaccca	aacaccttct	ctgtctttca	acagttgttg	ctggattagc	tttattttca	60
actatgacgc	actcagtttt	agctgatgat	gcttcaaadc	ccgatgctat	tttaaatgaat	120
aacaaccaag	caaattttca	aagagatgct	ctagtgcaca	agcttgatga	gggacatcaa	180
caattagaag	ctattaaaca	tgaagctaaa	ggtactgata	ttgagactac	tgtaacaaa	240
gctatcgatg	ctgttgatca	catgaagagt	tctatacgct	tcaatactga	aacgatctat	300
gatttttagtt	caattggggc	aagagtagaa	gcattatcag	atgctatcaa	agcaatcgta	360
ttttccacaa	cccaattaac	tcataaagta	gaaaaagcgc	atactgatat	ggggtttgct	420
attactaaat	tagtcattcg	tattatagat	ccatttgcac	ctgttgacgc	tatcaaagct	480
caagtacaag	aaattaaagc	acttgaggaa	aaagttatca	attatcctga	tttacagcca	540
acagaccgtg	ctactatcta	tactaaagct	aaactaaata	aagctatttg	gaacactcgt	600
ttagaaagag	ataaaaaggt	tttgggaatc	aaaccatttg	acgtttacaa	tagacttaac	660
aaagctatca	cacatgcggt	tggtgtccaa	ctaaatccga	caaccactgt	tcaacaagtt	720
gacgatgaag	ttattgctgt	gcaagatgct	ttggaaacag	ctcttaagtc	atag	774

<210> SEQ ID NO 338
<211> LENGTH: 257

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 338

```
Met Lys Pro Lys His Leu Leu Cys Leu Ser Thr Val Val Ala Gly Leu
 1          5          10          15
Ala Leu Phe Ser Thr Met Thr His Ser Val Leu Ala Asp Asp Ala Ser
 20          25          30
Asn Pro Asp Ala Ile Leu Met Asn Asn Asn Gln Ala Asn Phe Gln Arg
 35          40          45
Asp Ala Leu Val Gln Lys Leu Asp Glu Gly His Gln Gln Leu Glu Ala
 50          55          60
Ile Lys His Glu Ala Lys Gly Thr Asp Ile Glu Thr Thr Val Asn Lys
 65          70          75          80
Ala Ile Asp Ala Val Asp His Met Lys Ser Ser Ile Arg Phe Asn Thr
 85          90          95
Glu Thr Ile Tyr Asp Phe Ser Ser Ile Gly Ala Arg Val Glu Ala Leu
100          105          110
Ser Asp Ala Ile Lys Ala Ile Val Phe Ser Thr Thr Gln Leu Thr His
115          120          125
Lys Val Glu Lys Ala His Thr Asp Met Gly Phe Ala Ile Thr Lys Leu
130          135          140
Val Ile Arg Ile Ile Asp Pro Phe Ala Ser Val Asp Ala Ile Lys Ala
145          150          155          160
Gln Val Gln Glu Ile Lys Ala Leu Glu Glu Lys Val Ile Asn Tyr Pro
165          170          175
Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Thr Lys Ala Lys Leu
180          185          190
Asn Lys Ala Ile Trp Asn Thr Arg Leu Glu Arg Asp Lys Lys Val Leu
195          200          205
Gly Ile Lys Pro Phe Asp Val Tyr Asn Arg Leu Asn Lys Ala Ile Thr
210          215          220
His Ala Val Gly Val Gln Leu Asn Pro Thr Thr Thr Val Gln Gln Val
225          230          235          240
Asp Asp Glu Val Ile Ala Val Gln Asp Ala Leu Glu Thr Ala Leu Lys
245          250          255
Ser
```

<210> SEQ ID NO 339

<211> LENGTH: 1236

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 339

```
atgacacagg atccgattgc aaatttaaaa ctagccagaa agggcccaat cgtttagtatt      60
attgtctact tgtcgcttag tgttgccaaa ttattagctg gttatttggt aaatgcaagt      120
tcccttattg ctgatggatt taacaattta tcggatattg tgggaaatgt agccctgctt      180
attggtcttc acttagctag ccaaccagcc gatgccaatc ataaatttgg tcattggaaa      240
attgaagact tatccagcct tgtcacttct tttattatgt ttctttaggt tttccaagta      300
ctgattcaca caattaaaag tatcttttagt ggtcagcaag ttgatattga ccctcttggg      360
gctattgtcg gtatcgtttc agcttttggt atggttagggg tttatgtctt taacaaacgt      420
ctttccaaac gtgtaaaatc cagtgcctta gtcgctgctt ctaaggataa tctagctgat      480
gctgttactt ctatcggaac atcaattgct attatagcag cttctttgca tttaccagtt      540
atcgatcata tagctgctat gatcattacg ttctttattc ttaaaacagc ttttgatata      600
tttatggaaa gttcgttttag tttatctgat ggatttgata gccgtcattt gaaaaaatatc      660
gaaaaagcca ttttagaaat ccctaaaatt gtcgccgtta agtctcaacg agctaggacc      720
tatggttagca atgtctatct tgatattgta cttgaaatga atcctgatct ttcagtctat      780
gaaagtcact ctattacaga gaaagtggag cagttattga gtgaccaatt ttctatttat      840
gacattgaca ttcacgttga gcctgccatg attcccgaag aagagatttt tgataatgtc      900
```


gccaaaaagc tctaccgcta cgaaaaatta attttgagta aggttcctga ctatgaccac	960
tacattgcta agtctttcca actgattgat gcgaatggcc aaacagttaa ctatgaacaa	1020
tttttgaacc aagaaattta ttatccaagt aacttcaacc attttcagat tgaatccatt	1080
agtcaaaaaa cgatgttggt aacttaccaa ttaaattggca atcaacgtac cagtatttgg	1140
aggcgtcatg aatcttggtc cttactcttc caccaaatta cccctatcgc taagaaacaa	1200
ttacatcaca cacactatcg tattgtaaaa atgtaa	1236

<210> SEQ ID NO 340

<211> LENGTH: 411

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 340

Met Thr Gln Asp Pro Ile Ala Asn Leu Lys Leu Ala Arg Lys Gly Pro	
1 5 10 15	
Ile Val Ser Ile Ile Val Tyr Leu Ser Leu Ser Val Ala Lys Leu Leu	
20 25 30	
Ala Gly Tyr Leu Leu Asn Ala Ser Ser Leu Ile Ala Asp Gly Phe Asn	
35 40 45	
Asn Leu Ser Asp Ile Val Gly Asn Val Ala Leu Leu Ile Gly Leu His	
50 55 60	
Leu Ala Ser Gln Pro Ala Asp Ala Asn His Lys Phe Gly His Trp Lys	
65 70 75 80	
Ile Glu Asp Leu Ser Ser Leu Val Thr Ser Phe Ile Met Phe Leu Val	
85 90 95	
Gly Phe Gln Val Leu Ile His Thr Ile Lys Ser Ile Phe Ser Gly Gln	
100 105 110	
Gln Val Asp Ile Asp Pro Leu Gly Ala Ile Val Gly Ile Val Ser Ala	
115 120 125	
Phe Val Met Leu Gly Val Tyr Val Phe Asn Lys Arg Leu Ser Lys Arg	
130 135 140	
Val Lys Ser Ser Ala Leu Val Ala Ala Ser Lys Asp Asn Leu Ala Asp	
145 150 155 160	
Ala Val Thr Ser Ile Gly Thr Ser Ile Ala Ile Ile Ala Ala Ser Leu	
165 170 175	
His Leu Pro Val Ile Asp His Ile Ala Ala Met Ile Ile Thr Phe Phe	
180 185 190	
Ile Leu Lys Thr Ala Phe Asp Ile Phe Met Glu Ser Ser Phe Ser Leu	
195 200 205	
Ser Asp Gly Phe Asp Ser Arg His Leu Lys Lys Tyr Glu Lys Ala Ile	
210 215 220	
Leu Glu Ile Pro Lys Ile Val Ala Val Lys Ser Gln Arg Ala Arg Thr	
225 230 235 240	
Tyr Gly Ser Asn Val Tyr Leu Asp Ile Val Leu Glu Met Asn Pro Asp	
245 250 255	
Leu Ser Val Tyr Glu Ser His Ser Ile Thr Glu Lys Val Glu Gln Leu	
260 265 270	
Leu Ser Asp Gln Phe Ser Ile Tyr Asp Ile Asp Ile His Val Glu Pro	
275 280 285	
Ala Met Ile Pro Glu Glu Glu Ile Phe Asp Asn Val Ala Lys Lys Leu	
290 295 300	
Tyr Arg Tyr Glu Lys Leu Ile Leu Ser Lys Val Pro Asp Tyr Asp His	
305 310 315 320	
Tyr Ile Ala Lys Ser Phe Gln Leu Ile Asp Ala Asn Gly Gln Thr Val	
325 330 335	
Asn Tyr Glu Gln Phe Leu Asn Gln Glu Ile Tyr Tyr Pro Ser Asn Phe	
340 345 350	
Asn His Phe Gln Ile Glu Ser Ile Ser Gln Lys Thr Met Leu Val Thr	

Asn	Glu	Gly	Leu	Leu	Ile	Lys	Asn	Leu	Asp	Lys	Ile	Leu	Asp	Glu	Ala
			180					185					190		
Leu	Lys	Leu	Val	Tyr	Arg	Glu	Arg	His	Asn	Gln	Leu	Phe	Gln	Gln	Thr
		195					200					205			
Asn	Tyr	Gln	Val	His	Tyr	Phe	Glu	Met	Arg	Arg	Gln	Gln	Asn	Arg	Leu
	210					215					220				
Leu	Gly	Gln	Met	Ala	Ile	Asn	Val	Asn	Thr	Leu	Met	Arg	Gln	Ser	Lys
225					230					235					240
Glu	Ser	Ile	Leu	Leu	Ser	His	Leu	Phe	His	Glu	Thr	Ala	Cys	Gln	Leu
			245						250					255	
Ser	Glu	Gln	Asn	Pro	Ala	Leu	Thr	Leu	Ile	Asp	Asp	Ile	Glu	Gln	Leu
		260						265					270		
Leu	Glu	Thr	Phe	Arg	His	Gly	Asp	Leu	Pro	Gln	Thr	Arg	Glu	Glu	Phe
		275				280						285			
Glu	Arg	Arg	Ala	Val	Leu	Phe	Gln	Leu	Leu	Gln	Asp	Leu	Glu	Arg	Phe
	290					295					300				
Ile	Leu	Leu	Lys	Val	Glu	Phe	Tyr	Gln	Asp	Tyr	Gln	Asn	Asp		
305					310					315					

<210> SEQ ID NO 343

<211> LENGTH: 936

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 343

atggaaaatc	aggaattggc	taaaaaatta	gcctcaccat	caaagaattc	aaggcttgaa	60
acctttggcc	gcaccattac	gttttttgtgt	ctggctttga	ttgtttttat	cgttgcgatg	120
attctgatct	tcgttgctca	aaaaggggtg	tcaaccttct	ttgttgacaa	ggttaatcct	180
tttgatttct	tgtttgaaaa	ggagtggcaa	ccaagtgtaa	aaaatgcggc	cggcattcct	240
tatcttggtg	ctctgccaat	gattacagga	tccttttttg	ttaccatttt	atctgctatt	300
attgccaccc	catttgccat	tggcgagcc	gtttttatga	ctgaaatctc	acctaaatat	360
ggcgctaaat	tattacagcc	tgcggttgag	cttttggttg	gaattccttc	ggttgtttat	420
gggtttatcg	gtttgcaagt	gattgttcct	tttatgcgct	ctatcttttg	tggcacaggt	480
tttgaatcc	tatctggggt	ctgtgtcttg	tttgttatga	ttttaccaac	agtgactttt	540
atgacaacag	acagtctgcg	ggcggtgcct	cgtcattacc	gcgaagcgtc	tatggctatg	600
ggagcaaac	gttgcaaac	catttggcgt	gtgttcctta	atgcagctcg	tccaggaatt	660
tttaccgctg	ttatttttg	aatggcaaga	gcttttgag	aagccttggc	tatccaaatg	720
gtagtcggta	actctgctgt	aatgccaaagt	tcactaacga	caccagccgc	aaccttaacg	780
tctgtcttga	caatgggtat	tggtaacacg	gttatgggaa	cgggtccaaaa	taatgtgctt	840
tgggcccttg	ccctagtctt	attattaatg	agtctggcct	tcaattccct	tgtcaaatta	900
atcacgaaag	aaagaaagag	aaattatgaa	cgctaa			936

<210> SEQ ID NO 344

<211> LENGTH: 311

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 344

Met	Glu	Asn	Gln	Glu	Leu	Ala	Lys	Lys	Leu	Ala	Ser	Pro	Ser	Lys	Asn
1				5					10					15	
Ser	Arg	Leu	Glu	Thr	Phe	Gly	Arg	Thr	Ile	Thr	Phe	Leu	Cys	Leu	Ala
		20						25				30			
Leu	Ile	Val	Phe	Ile	Val	Ala	Met	Ile	Leu	Ile	Phe	Val	Ala	Gln	Lys
		35				40					45				
Gly	Leu	Ser	Thr	Phe	Phe	Val	Asp	Lys	Val	Asn	Leu	Phe	Asp	Phe	Leu
	50					55				60					
Phe	Gly	Lys	Glu	Trp	Gln	Pro	Ser	Val	Lys	Asn	Ala	Ala	Gly	Ile	Pro
65					70					75				80	
Tyr	Leu	Gly	Ala	Leu	Pro	Met	Ile	Thr	Gly	Ser	Phe	Leu	Val	Thr	Ile

				85					90					95					
Leu	Ser	Ala	Ile	Ile	Ala	Thr	Pro	Phe	Ala	Ile	Gly	Ala	Ala	Val	Phe				
			100					105					110						
Met	Thr	Glu	Ile	Ser	Pro	Lys	Tyr	Gly	Ala	Lys	Leu	Leu	Gln	Pro	Ala				
		115					120					125							
Val	Glu	Leu	Leu	Val	Gly	Ile	Pro	Ser	Val	Val	Tyr	Gly	Phe	Ile	Gly				
	130					135					140								
Leu	Gln	Val	Ile	Val	Pro	Phe	Met	Arg	Ser	Ile	Phe	Gly	Gly	Thr	Gly				
145					150					155					160				
Phe	Gly	Ile	Leu	Ser	Gly	Val	Cys	Val	Leu	Phe	Val	Met	Ile	Leu	Pro				
			165					170					175						
Thr	Val	Thr	Phe	Met	Thr	Thr	Asp	Ser	Leu	Arg	Ala	Val	Pro	Arg	His				
		180					185					190							
Tyr	Arg	Glu	Ala	Ser	Met	Ala	Met	Gly	Ala	Thr	Arg	Trp	Gln	Thr	Ile				
	195					200					205								
Trp	Arg	Val	Val	Leu	Asn	Ala	Ala	Arg	Pro	Gly	Ile	Phe	Thr	Ala	Val				
	210				215					220									
Ile	Phe	Gly	Met	Ala	Arg	Ala	Phe	Gly	Glu	Ala	Leu	Ala	Ile	Gln	Met				
225				230				235						240					
Val	Val	Gly	Asn	Ser	Ala	Val	Met	Pro	Ser	Ser	Leu	Thr	Thr	Pro	Ala				
			245				250						255						
Ala	Thr	Leu	Thr	Ser	Val	Leu	Thr	Met	Gly	Ile	Gly	Asn	Thr	Val	Met				
		260				265						270							
Gly	Thr	Val	Gln	Asn	Asn	Val	Leu	Trp	Ser	Leu	Ala	Leu	Val	Leu	Leu				
	275					280					285								
Leu	Met	Ser	Leu	Ala	Phe	Asn	Ser	Leu	Val	Lys	Leu	Ile	Thr	Lys	Glu				
	290				295					300									
Arg	Lys	Arg	Asn	Tyr	Glu	Arg													
305				310															

<210> SEQ ID NO 345

<211> LENGTH: 888

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 345

atgaacgcta	aaaaagtcga	taaagtagca	actggtactc	tttataccat	tgctggaatt	60
attgtagcta	ttttagcttc	cttaattcta	tatatccttg	tccgtggctt	gccacacatc	120
agctggctct	ttttaacagg	aaaatcgtct	tcgtacgaag	ctggtggggg	aattgggtatc	180
cagttgtata	attccttctt	cctattgatt	gttactttta	ttattttccat	tccttttatca	240
actggagcgg	ggattttactt	ggctgaatat	gccaaaaaag	gacctgttac	caactttatt	300
agaacctgta	ttgagattct	gtcttcccta	ccatctgtgg	ttgtggggct	ctttgggttac	360
ttgattttcg	ttgtgcagtt	tgaatatggc	ttttctatta	tttcaggggc	tcttgctttg	420
acggctctta	atcttctcta	aatgacccgt	aatgttgaag	atagtttact	gcatgttcac	480
catacccaaa	gagaagcagg	attagcttta	ggcctgtcac	gctgggaaac	ggttttttat	540
gtggttatcc	cagaagctct	cccgggaatg	gtaacaggta	ttgtcttagc	ttcaggctcg	600
atTTTTGGTG	aagcggcagc	gcttatctat	actgctggtc	aatcagcacc	agctctggat	660
tggtcaaatt	ggaatccact	tagtgttact	agtccaatct	ctattttccg	tcaatctgag	720
acccttgctg	ttcatatttg	gaaagtcaat	agcgaaggga	caattccaga	tgctactctt	780
gtatccgcag	gaagtgcagc	agtgtctatta	atttttatcc	ttattttcaa	cttttcagct	840
cactttattg	ggaagaaact	tcattctaaa	atgacagcag	cgaaataa		888

<210> SEQ ID NO 346

<211> LENGTH: 295

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 346

Met Asn Ala Lys Lys Val Asp Lys Val Ala Thr Gly Thr Leu Tyr Thr

1				5					10					15			
Ile	Ala	Gly	Ile	Ile	Val	Ala	Ile	Leu	Ala	Ser	Leu	Ile	Leu	Tyr	Ile		
			20					25					30				
Leu	Val	Arg	Gly	Leu	Pro	His	Ile	Ser	Trp	Ser	Phe	Leu	Thr	Gly	Lys		
		35					40					45					
Ser	Ser	Ser	Tyr	Glu	Ala	Gly	Gly	Gly	Ile	Gly	Ile	Gln	Leu	Tyr	Asn		
	50					55					60						
Ser	Phe	Phe	Leu	Leu	Ile	Val	Thr	Leu	Ile	Ile	Ser	Ile	Pro	Leu	Ser		
65					70					75					80		
Thr	Gly	Ala	Gly	Ile	Tyr	Leu	Ala	Glu	Tyr	Ala	Lys	Lys	Gly	Pro	Val		
			85					90					95				
Thr	Asn	Phe	Ile	Arg	Thr	Cys	Ile	Glu	Ile	Leu	Ser	Ser	Leu	Pro	Ser		
		100						105					110				
Val	Val	Val	Gly	Leu	Phe	Gly	Tyr	Leu	Ile	Phe	Val	Val	Gln	Phe	Glu		
		115					120					125					
Tyr	Gly	Phe	Ser	Ile	Ile	Ser	Gly	Ala	Leu	Ala	Leu	Thr	Val	Phe	Asn		
	130					135					140						
Leu	Pro	Gln	Met	Thr	Arg	Asn	Val	Glu	Asp	Ser	Leu	Leu	His	Val	His		
145					150				155						160		
His	Thr	Gln	Arg	Glu	Ala	Gly	Leu	Ala	Leu	Gly	Leu	Ser	Arg	Trp	Glu		
			165					170						175			
Thr	Val	Phe	Tyr	Val	Val	Ile	Pro	Glu	Ala	Leu	Pro	Gly	Met	Val	Thr		
			180					185					190				
Gly	Ile	Val	Leu	Ala	Ser	Gly	Arg	Ile	Phe	Gly	Glu	Ala	Ala	Ala	Leu		
	195						200					205					
Ile	Tyr	Thr	Ala	Gly	Gln	Ser	Ala	Pro	Ala	Leu	Asp	Trp	Ser	Asn	Trp		
	210					215					220						
Asn	Pro	Leu	Ser	Val	Thr	Ser	Pro	Ile	Ser	Ile	Phe	Arg	Gln	Ser	Glu		
225					230					235					240		
Thr	Leu	Ala	Val	His	Ile	Trp	Lys	Val	Asn	Ser	Glu	Gly	Thr	Ile	Pro		
			245					250						255			
Asp	Ala	Thr	Leu	Val	Ser	Ala	Gly	Ser	Ala	Ala	Val	Leu	Leu	Ile	Phe		
			260					265					270				
Ile	Leu	Ile	Phe	Asn	Phe	Ser	Ala	His	Phe	Ile	Gly	Lys	Lys	Leu	His		
		275					280					285					
Ser	Lys	Met	Thr	Ala	Ala	Lys											
	290					295											

<210> SEQ ID NO 347

<211> LENGTH: 312

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 347

ttgatatatg	cattaagggc	ttcttctacc	atctgtttca	cagcttttcc	cataaggttg	60
atttggttctt	caaccactgg	aatacgtcc	tcacctttca	tacgaatagt	ggccttgga	120
atcgaagcag	catggtcacc	catacgttca	atatcacttg	atgcctttaa	aacagtaata	180
accattctaa	gatcattcga	aactggctgt	tgtagggcaa	taatttccag	cgatttcttt	240
tcaagctttg	tctcaaaatt	attaatagt	tcattcttctt	cgataacttc	tttggccaat	300
tcacgatcat	ga					312

<210> SEQ ID NO 348

<211> LENGTH: 103

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 348

Met	Ile	Tyr	Ala	Leu	Arg	Ala	Ser	Ser	Thr	Ile	Cys	Phe	Thr	Ala	Phe
1				5					10					15	

```

Pro Ile Arg Leu Ile Cys Ser Ser Thr Thr Gly Ile Arg Ser Ser Pro
      20              25              30
Phe Ile Arg Ile Val Ala Leu Ala Ile Glu Ala Ala Trp Ser Pro Ile
      35              40              45
Arg Ser Ile Ser Leu Asp Ala Phe Lys Thr Val Ile Thr Ile Leu Arg
      50              55              60
Ser Phe Glu Thr Gly Cys Cys Arg Ala Ile Ile Ser Ser Asp Phe Phe
      65              70              75              80
Ser Ser Phe Val Ser Lys Leu Leu Ile Val Ser Ser Ser Ser Ile Thr
      85              90              95
Ser Leu Ala Asn Ser Arg Ser
      100

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<210> SEQ ID NO 349
 <211> LENGTH: 1311
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 349

```

atgaataaat taaaaaaaga gattttatca gataactata accacttttt tcattttttt      60
gcggttttta cagggtatttt tgtcattatg actattatta tcttacagat tatgcggttt      120
ggcgtttatt cgtcagttga cagtagttta gtttctgtta gtaataatgc aagtagctat      180
gctaatacgt cgatggctag aatatcttct ttttactttg atactgaaaa taacattatt      240
aaggcgctgc ctgattcaga tagttctaag ttattaggaa cgctgcagc taatacagat      300
atcattttgt ttagtgctaa tggaacaatt ttaaagtctt ttgatgcgtt ttctaactat      360
caaaattttc atttagataa acgccggttg gggagtattg aaaccaccag tttaatgaat      420
ttttatggac aagaagaaaa ataccatacg ataactgtag gggttcatat caaaaattat      480
cctgcagttg cctatatgat ggcagtagta aatgtggaac aattagaccg cgtaaatgaa      540
cgttatgagc gcattattat tatagttatg agtggttttt ggctaatttc tatttttagca      600
agtattttatt tagccaagtg gagcagaaaa cctattttag aaagctatga aaaacaaaaa      660
atgtttgttg aaaatgctag tcatgaatta aggaccctt tggcggctct acagaatcgt      720
ctggaatcgc tttttcgtaa gcccaacgaa acgatattag aaaatagtga gcatctcgct      780
tctagtttag acgaggttcg caacatgcgc atcttaacaa ctaatttatt aaatttagca      840
agacgagatg atggcattaa tccacagtgg actcatttag atacagattt ttttaatgct      900
atttttgaga attatgaact agttgctaaa gaatatggaa aaatatttta ttttcagaac      960
caagtcaata gatcgtaag aatggataag gctttactaa aacaattaat aacgatttta      1020
tttgacaatg ctattaaata tacagataaa aatgggtatta ttgaaattat agtgaaaaca      1080
acggacaaaa atttattaat ttctgttatt gataatggtc cagggataac agatgaagaa      1140
aagaaaaaga tttttgatcg tttttatcga gttgacaaag ctagaacacg gcaaacaggt      1200
ggatttggct tggggttggc tttagctcag caaatcgtga tgtctttaaa aggaaatatt      1260
acagtaaagg ataatgatcc taaaggtagt atttttgaag tcaaactata a      1311

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<210> SEQ ID NO 350
 <211> LENGTH: 436
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 350

```

Met Asn Lys Leu Lys Lys Glu Ile Leu Ser Asp Asn Tyr Asn His Phe
1              5              10              15
Phe His Phe Phe Ala Val Phe Thr Gly Ile Phe Val Ile Met Thr Ile
      20              25              30
Ile Ile Leu Gln Ile Met Arg Phe Gly Val Tyr Ser Ser Val Asp Ser
      35              40              45
Ser Leu Val Ser Val Ser Asn Asn Ala Ser Ser Tyr Ala Asn Arg Thr
      50              55              60
Met Ala Arg Ile Ser Ser Phe Tyr Phe Asp Thr Glu Asn Asn Ile Ile
      65              70              75              80
Lys Ala Leu Pro Asp Ser Asp Ser Ser Lys Leu Leu Gly Thr Pro Ala

```

				85					90					95			
Ala	Asn	Thr	Asp	Ile	Ile	Leu	Phe	Ser	Ala	Asn	Gly	Thr	Ile	Leu	Asn		
			100					105					110				
Ala	Phe	Asp	Ala	Phe	Ser	Asn	Tyr	Gln	Asn	Phe	His	Leu	Asp	Lys	Arg		
		115					120					125					
Arg	Leu	Gly	Ser	Ile	Glu	Thr	Thr	Ser	Leu	Met	Asn	Phe	Tyr	Gly	Gln		
	130					135					140						
Glu	Glu	Lys	Tyr	His	Thr	Ile	Thr	Val	Gly	Val	His	Ile	Lys	Asn	Tyr		
145					150					155				160			
Pro	Ala	Val	Ala	Tyr	Met	Met	Ala	Val	Val	Asn	Val	Glu	Gln	Leu	Asp		
			165					170						175			
Arg	Ala	Asn	Glu	Arg	Tyr	Glu	Arg	Ile	Ile	Ile	Ile	Val	Met	Ser	Val		
		180						185					190				
Phe	Trp	Leu	Ile	Ser	Ile	Leu	Ala	Ser	Ile	Tyr	Leu	Ala	Lys	Trp	Ser		
	195					200					205						
Arg	Lys	Pro	Ile	Leu	Glu	Ser	Tyr	Glu	Lys	Gln	Lys	Met	Phe	Val	Glu		
210					215					220							
Asn	Ala	Ser	His	Glu	Leu	Arg	Thr	Pro	Leu	Ala	Val	Leu	Gln	Asn	Arg		
225				230					235					240			
Leu	Glu	Ser	Leu	Phe	Arg	Lys	Pro	Asn	Glu	Thr	Ile	Leu	Glu	Asn	Ser		
			245					250					255				
Glu	His	Leu	Ala	Ser	Ser	Leu	Asp	Glu	Val	Arg	Asn	Met	Arg	Ile	Leu		
		260					265					270					
Thr	Thr	Asn	Leu	Leu	Asn	Leu	Ala	Arg	Arg	Asp	Asp	Gly	Ile	Asn	Pro		
	275					280						285					
Gln	Trp	Thr	His	Leu	Asp	Thr	Asp	Phe	Phe	Asn	Ala	Ile	Phe	Glu	Asn		
290					295					300							
Tyr	Glu	Leu	Val	Ala	Lys	Glu	Tyr	Gly	Lys	Ile	Phe	Tyr	Phe	Gln	Asn		
305				310					315					320			
Gln	Val	Asn	Arg	Ser	Leu	Arg	Met	Asp	Lys	Ala	Leu	Leu	Lys	Gln	Leu		
			325					330					335				
Ile	Thr	Ile	Leu	Phe	Asp	Asn	Ala	Ile	Lys	Tyr	Thr	Asp	Lys	Asn	Gly		
		340					345					350					
Ile	Ile	Glu	Ile	Ile	Val	Lys	Thr	Asp	Lys	Asn	Leu	Leu	Ile	Ser			
	355				360					365							
Val	Ile	Asp	Asn	Gly	Pro	Gly	Ile	Thr	Asp	Glu	Glu	Lys	Lys	Lys	Ile		
	370				375					380							
Phe	Asp	Arg	Phe	Tyr	Arg	Val	Asp	Lys	Ala	Arg	Thr	Arg	Gln	Thr	Gly		
385				390					395					400			
Gly	Phe	Gly	Leu	Gly	Leu	Ala	Leu	Ala	Gln	Gln	Ile	Val	Met	Ser	Leu		
		405					410					415					
Lys	Gly	Asn	Ile	Thr	Val	Lys	Asp	Asn	Asp	Pro	Lys	Gly	Ser	Ile	Phe		
		420					425					430					
Glu	Val	Lys	Leu														
		435															

<210> SEQ ID NO 351

<211> LENGTH: 969

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 351

gtggtaaata	agatgagttt	agtaacaatt	tttgccttat	tgatgtcatc	tatgcttatt	60
tatgcaacac	cactcatttt	cacaagtatt	ggaggaactt	tctcagagcg	ctcaggcggt	120
gtaaatggtg	gtttagaagg	tatcatgggtc	atgggagcgt	tctctgggat	tgttttcaac	180
ttagagtttg	ctgaaacatt	tggaaaagca	acgccttgga	tagccgtttt	agtcggtggt	240
attggtgggt	tgattttttc	tttgattcac	gctgtagcaa	ccatcaactt	tcgagctgac	300
cacattgtca	gtggtacagt	gttgaaacttg	ttagcacctt	cttttgctgt	cttcttggtt	360

aaagctatgt	acggtaaggg	acaaacagac	aacattcaac	aatcttttgg	gaagtttgat	420
ttcccagggt	tatcacaaat	tcctgtgatt	ggtgatattt	tctttaaaaa	tactagcctt	480
attggttact	tcgccattgc	tttttcgttc	tttgcttggt	ttttgcttta	taaaaccagg	540
tttggctctgc	gtttacgatc	agttggggaa	caccctcagg	cagctgacac	acttggtatt	600
aacgtctatt	tgatgaaata	ctatgggtgtg	atgatctcag	gttttcttgg	tggaataggt	660
ggagctgttt	atgctcagtc	aatctccgtt	aactttgctg	taacaactat	cttaggtcct	720
ggattttattg	ctttggcagc	tatgatcttt	ggtaaatgga	atccagttgg	cgccatgcta	780
tctagtcttt	tctttggctt	atcgcaaaagt	ttagccgtta	ttggtgctca	attaccatta	840
ctagaaaaga	ttccaacggt	ttacttacag	attgcacctt	atatggtaac	gattattatt	900
ttagctgctt	tctttggtca	agcagttgca	ccaaaagctg	atggaatcaa	ctatattaaa	960
tctaaataa						969

<210> SEQ ID NO 352

<211> LENGTH: 322

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 352

Met	Val	Asn	Lys	Met	Ser	Leu	Val	Thr	Ile	Phe	Ala	Leu	Leu	Met	Ser	
1				5					10					15		
Ser	Met	Leu	Ile	Tyr	Ala	Thr	Pro	Leu	Ile	Phe	Thr	Ser	Ile	Gly	Gly	
			20					25					30			
Thr	Phe	Ser	Glu	Arg	Ser	Gly	Val	Val	Asn	Val	Gly	Leu	Glu	Gly	Ile	
			35				40					45				
Met	Val	Met	Gly	Ala	Phe	Ser	Gly	Ile	Val	Phe	Asn	Leu	Glu	Phe	Ala	
	50					55				60						
Glu	Thr	Phe	Gly	Lys	Ala	Thr	Pro	Trp	Ile	Ala	Val	Leu	Val	Gly	Gly	
65				70					75					80		
Ile	Val	Gly	Leu	Ile	Phe	Ser	Leu	Ile	His	Ala	Val	Ala	Thr	Ile	Asn	
			85					90					95			
Phe	Arg	Ala	Asp	His	Ile	Val	Ser	Gly	Thr	Val	Leu	Asn	Leu	Leu	Ala	
			100					105					110			
Pro	Ser	Phe	Ala	Val	Phe	Leu	Val	Lys	Ala	Met	Tyr	Gly	Lys	Gly	Gln	
			115				120					125				
Thr	Asp	Asn	Ile	Gln	Gln	Ser	Phe	Gly	Lys	Phe	Asp	Phe	Pro	Gly	Leu	
	130					135				140						
Ser	Gln	Ile	Pro	Val	Ile	Gly	Asp	Ile	Phe	Phe	Lys	Asn	Thr	Ser	Leu	
145				150					155						160	
Ile	Gly	Tyr	Phe	Ala	Ile	Ala	Phe	Ser	Phe	Phe	Ala	Trp	Phe	Leu	Leu	
			165					170					175			
Tyr	Lys	Thr	Arg	Phe	Gly	Leu	Arg	Leu	Arg	Ser	Val	Gly	Glu	His	Pro	
			180				185					190				
Gln	Ala	Ala	Asp	Thr	Leu	Gly	Ile	Asn	Val	Tyr	Leu	Met	Lys	Tyr	Tyr	
			195			200				205						
Gly	Val	Met	Ile	Ser	Gly	Phe	Leu	Gly	Gly	Ile	Gly	Gly	Ala	Val	Tyr	
	210				215					220						
Ala	Gln	Ser	Ile	Ser	Val	Asn	Phe	Ala	Val	Thr	Thr	Ile	Leu	Gly	Pro	
225				230					235					240		
Gly	Phe	Ile	Ala	Leu	Ala	Ala	Met	Ile	Phe	Gly	Lys	Trp	Asn	Pro	Val	
			245					250					255			
Gly	Ala	Met	Leu	Ser	Ser	Leu	Phe	Phe	Gly	Leu	Ser	Gln	Ser	Leu	Ala	
			260				265					270				
Val	Ile	Gly	Ala	Gln	Leu	Pro	Leu	Leu	Glu	Lys	Ile	Pro	Thr	Val	Tyr	
		275			280						285					
Leu	Gln	Ile	Ala	Pro	Tyr	Met	Val	Thr	Ile	Ile	Ile	Leu	Ala	Ala	Phe	
	290				295					300						
Phe	Gly	Gln	Ala	Val	Ala	Pro	Lys	Ala	Asp	Gly	Ile	Asn	Tyr	Ile	Lys	
305				310					315					320		

Ser Lys

<210> SEQ ID NO 353

<211> LENGTH: 1578

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 353

```
atgattatca aaaagaaaagc aaaagtaaaa tatttgctcc ataaagggaa acatggattt      60
ttaagaggaa ttttttagtag aacaacaatc attgtattat taattatttt gcaattagtt      120
ttcttatttc aatcttatgc ctggatggag cagtaccgtg tttggataac gattccttgaa      180
agtgtctttg ctattactat tgttttatat ttagttaata gtgatatgga tgctatttca      240
agaatgacgt ggtaattttt gattatgatt gctccattac cagtgtcact gtttttaatt      300
tatacaaaat tggattgggg ttacagaggg ctaaaacaaa gaataaatca tctttagatag      360
ctgtctgcac cttaccttag cgatgatgac gctatattag aggtattaaa ggatagcaca      420
tcaaccacat atcattttagt acagtactta gaaagaagtc gtggcaactt tccgatttat      480
aataatacaa gggtaactta cttccaaca ggtgaaactt tttttgatag tttaaaagaa      540
cagttattct tagctaaaaa gtacattttt ttggaatttt ttattattgc agaaggccaa      600
atgtggggag aaatccttag tattctagaa aaaaaagtca gtgaagggtg agaagttagg      660
gtgttggttg atggcatgaa cgaactatca acgctatcat cagattacgc caagagatta      720
gaacaaatag ggattaaagc taaatcattt ttaccgattt caccctttat ctctacctat      780
tacaattatc gagatcaccg aaaaattgtc gttattgatg gggaggtatc attcactgga      840
ggtattaatc tagcagatga gtacattaat gaagtagagc gttttggcca ctggaaagat      900
gctgggttaa tgcttgaggg tgaagcaaca gacagctttt taattttgtt tttacaaatg      960
tgggtctatca cagaaaaaga actgattatt gatccttatt tttcagatca ttcttttaaaa    1020
cttccttcag atggctatgt tattccctac ggtgattccc cgcttgatac tgataaaaata    1080
ggtaaaaaatg tttatataga catttttaaat catgctaaag agtacgttta tatcatgaca    1140
ccttacctta ttttagatag cgagatggaa cacgctttac ggtttgcatc agaacgtgga    1200
gtagatatcc gaattattat gccaggagtg ccagataaag gggtaaccata tgccttagct    1260
aaaacctatt ataaagcttt gatgtcttct ggagtaaaaa tttatgagta tcaaccaggg    1320
ttcgttcatt caaaggattt tatctctgat aatacaaaaag cagttgtcgg aacaattaac    1380
ttagactatc gtagccttta tcatcatttt gaatgcgcga cttatttata tcgtgtgtca    1440
gttattgctg atattgtgaa tgactttaat gaagctcaaa agcaatcact attgatgaca    1500
tcagatcatt tgacgcaacg tccttggtat caaaaattga taggattatt agtacgaata    1560
attgccccctc tcttgtaa                                     1578
```

<210> SEQ ID NO 354

<211> LENGTH: 525

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 354

```
Met Ile Ile Lys Lys Lys Ala Lys Val Lys Tyr Leu Leu His Lys Gly
 1             5             10             15
Lys His Gly Phe Leu Arg Gly Ile Phe Ser Arg Thr Thr Ile Ile Val
 20             25             30
Leu Leu Ile Ile Leu Gln Leu Val Phe Leu Phe Gln Ser Tyr Ala Trp
 35             40             45
Met Glu Gln Tyr Arg Val Trp Ile Thr Ile Leu Glu Ser Val Phe Ala
 50             55             60
Ile Thr Ile Val Leu Tyr Leu Val Asn Ser Asp Met Asp Ala Ile Ser
 65             70             75             80
Arg Met Thr Trp Leu Ile Leu Ile Met Ile Ala Pro Leu Pro Val Ser
 85             90             95
Leu Phe Leu Ile Tyr Thr Lys Leu Asp Trp Gly Tyr Arg Gly Leu Lys
100            105            110
Gln Arg Ile Asn His Leu Val Asp Leu Ser Ala Pro Tyr Leu Ser Asp
115            120            125
Asp Asp Ala Ile Leu Glu Val Leu Lys Asp Ser Thr Ser Thr Thr Tyr
```

130	135	140
His Leu Val Gln Tyr	Leu Glu Arg Ser Arg Gly Asn Phe Pro Ile Tyr	
145	150	155
Asn Asn Thr Arg Val Thr Tyr Phe Pro Thr Gly Glu Thr Phe Phe Asp		160
	165	170
Ser Leu Lys Glu Gln Leu Phe Leu Ala Lys Lys Tyr Ile Phe Leu Glu		175
	180	185
Phe Phe Ile Ile Ala Glu Gly Gln Met Trp Gly Glu Ile Leu Ser Ile		190
	195	200
Leu Glu Lys Lys Val Ser Glu Gly Val Glu Val Arg Val Leu Phe Asp		205
	210	215
Gly Met Asn Glu Leu Ser Thr Leu Ser Ser Asp Tyr Ala Lys Arg Leu		220
225	230	235
Glu Gln Ile Gly Ile Lys Ala Lys Ser Phe Leu Pro Ile Ser Pro Phe		240
	245	250
Ile Ser Thr Tyr Tyr Asn Tyr Arg Asp His Arg Lys Ile Val Val Ile		255
	260	265
Asp Gly Glu Val Ser Phe Thr Gly Gly Ile Asn Leu Ala Asp Glu Tyr		270
	275	280
Ile Asn Glu Val Glu Arg Phe Gly His Trp Lys Asp Ala Gly Leu Met		285
	290	295
Leu Glu Gly Glu Ala Thr Asp Ser Phe Leu Ile Leu Phe Leu Gln Met		300
305	310	315
Trp Ser Ile Thr Glu Lys Glu Leu Ile Ile Asp Pro Tyr Leu Ser Asp		320
	325	330
His Ser Leu Lys Leu Pro Ser Asp Gly Tyr Val Ile Pro Tyr Gly Asp		335
	340	345
Ser Pro Leu Asp Thr Asp Lys Ile Gly Lys Asn Val Tyr Ile Asp Ile		350
	355	360
Leu Asn His Ala Lys Glu Tyr Val Tyr Ile Met Thr Pro Tyr Leu Ile		365
	370	375
Leu Asp Ser Glu Met Glu His Ala Leu Arg Phe Ala Ser Glu Arg Gly		380
385	390	395
Val Asp Ile Arg Ile Ile Met Pro Gly Val Pro Asp Lys Gly Val Pro		400
	405	410
Tyr Ala Leu Ala Lys Thr Tyr Tyr Lys Ala Leu Met Ser Ser Gly Val		415
	420	425
Lys Ile Tyr Glu Tyr Gln Pro Gly Phe Val His Ser Lys Val Phe Ile		430
	435	440
Ser Asp Asn Thr Lys Ala Val Val Gly Thr Ile Asn Leu Asp Tyr Arg		445
	450	455
Ser Leu Tyr His His Phe Glu Cys Ala Thr Tyr Leu Tyr Arg Val Ser		460
465	470	475
Val Ile Ala Asp Ile Val Asn Asp Phe Asn Glu Ala Gln Lys Gln Ser		480
	485	490
Leu Leu Met Thr Ser Asp His Leu Thr Gln Arg Pro Trp Tyr Gln Lys		495
	500	505
Leu Ile Gly Leu Leu Val Arg Ile Ile Ala Pro Leu Leu		510
	515	520
		525

<210> SEQ ID NO 355

<211> LENGTH: 1224

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 355

atgacgaatt taacgtttta tgcaaaaatc ggtatttcag aagaagagca tgactctttt
gttaaagaac atcagcaa at tagcgtttta caaggtagtg attgggcaaa aatcaaaaat

60
120

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caatggcaga atgagcgaat tggatatctat aaagaggaaa agcaggttgc ctctttatca 180
cttttgatta agctattgcc acttgggaaga agcattatct atattccaag agggccagtc 240
atggattatc ttgaccgtga tttggtggca ttaccatga aaacactaaa ggattatggt 300
aaaactaaaa aggccctctt tatcaaatat gatccagcta tcctgttaaa acaatacgca 360
ctgggacagg aagaagaaga aaaaccttta gctttagcag ctattaagaa tctccaagaa 420
gctggtgttc attggactgg ttttaacaatg gagattgcag atagtatcca acctcgtttc 480
caagctaata tttacactca agaaaacctt gagatgcaat ttcctaagca taccagacgt 540
ttaataaaaag atgctaagca gcgtgggtgta aaaacatatc gtgtcagtca atcagaactt 600
cacaaatctt ccaagattgt ctccttaaca gaaaaacgta aaaatatttc tttgcgtaac 660
gaagcttact ttcaaaagtt gatgactact tatggggata aggcctactt acatctagca 720
aaagtgaata ttcctcaaaa actagatcaa taccgccagc aattaattct tattaaccaa 780
gatattactc gcacccaagc tcatcaaaaag aagcgtttaa aaaaattaga agatcaaaaa 840
gcttcttttag aacgttatat aactgaattt gaaggcttta cagaccaata tcctgaggaa 900
gttggttag caggtatatt atctatttct tatggaaatg ttatggaaat gctttatgct 960
gggatgaatg atgattttta gaagttttat cctcagatc tgctgtatcc taatgttttt 1020
caggatgctt atcaagatgg tattattttg gctaacatgg gaggagtaga aggtcgctt 1080
gatgatggac ttaccaaatt taaggccaac tttgctccga caatagaaga atttatagga 1140
gaatttaatc tccctgtcag cccactttat catattgcta ataccatgta caaaatacga 1200
aaacagttta agaataaaca ttaa 1224

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<210> SEQ ID NO 356

<211> LENGTH: 407

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 356

```

Met Thr Asn Leu Thr Phe Tyr Ala Lys Ile Gly Ile Ser Glu Glu Glu
1           5           10           15
His Asp Ser Phe Val Lys Glu His Gln Gln Ile Ser Val Leu Gln Gly
20          25          30
Ser Asp Trp Ala Lys Ile Lys Asn Gln Trp Gln Asn Glu Arg Ile Gly
35          40          45
Ile Tyr Lys Glu Glu Lys Gln Val Ala Ser Leu Ser Leu Leu Ile Lys
50          55          60
Leu Leu Pro Leu Gly Arg Ser Ile Ile Tyr Ile Pro Arg Gly Pro Val
65          70          75          80
Met Asp Tyr Leu Asp Arg Asp Leu Val Ala Phe Thr Met Lys Thr Leu
85          90          95
Lys Asp Tyr Gly Lys Thr Lys Lys Ala Leu Phe Ile Lys Tyr Asp Pro
100         105         110
Ala Ile Leu Leu Lys Gln Tyr Ala Leu Gly Gln Glu Glu Glu Glu Lys
115         120         125
Pro Leu Ala Leu Ala Ala Ile Lys Asn Leu Gln Glu Ala Gly Val His
130         135         140
Trp Thr Gly Leu Thr Met Glu Ile Ala Asp Ser Ile Gln Pro Arg Phe
145         150         155         160
Gln Ala Asn Ile Tyr Thr Gln Glu Asn Leu Glu Met Gln Phe Pro Lys
165         170         175
His Thr Arg Arg Leu Ile Lys Asp Ala Lys Gln Arg Gly Val Lys Thr
180         185         190
Tyr Arg Val Ser Gln Ser Glu Leu His Lys Phe Ser Lys Ile Val Ser
195         200         205
Leu Thr Glu Lys Arg Lys Asn Ile Ser Leu Arg Asn Glu Ala Tyr Phe
210         215         220
Gln Lys Leu Met Thr Thr Tyr Gly Asp Lys Ala Tyr Leu His Leu Ala
225         230         235         240
Lys Val Asn Ile Pro Gln Lys Leu Asp Gln Tyr Arg Gln Gln Leu Ile
245         250         255

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Leu	Ile	Asn	Gln	Asp	Ile	Thr	Arg	Thr	Gln	Ala	His	Gln	Lys	Lys	Arg
		260					265					270			
Leu	Lys	Lys	Leu	Glu	Asp	Gln	Lys	Ala	Ser	Leu	Glu	Arg	Tyr	Ile	Thr
	275					280					285				
Glu	Phe	Glu	Gly	Phe	Thr	Asp	Gln	Tyr	Pro	Glu	Glu	Val	Val	Val	Ala
	290				295					300					
Gly	Ile	Leu	Ser	Ile	Ser	Tyr	Gly	Asn	Val	Met	Glu	Met	Leu	Tyr	Ala
305				310				315						320	
Gly	Met	Asn	Asp	Asp	Phe	Lys	Lys	Phe	Tyr	Pro	Gln	Tyr	Leu	Leu	Tyr
			325					330					335		
Pro	Asn	Val	Phe	Gln	Asp	Ala	Tyr	Gln	Asp	Gly	Ile	Ile	Trp	Ala	Asn
		340					345						350		
Met	Gly	Gly	Val	Glu	Gly	Ser	Leu	Asp	Asp	Gly	Leu	Thr	Lys	Phe	Lys
	355					360					365				
Ala	Asn	Phe	Ala	Pro	Thr	Ile	Glu	Glu	Phe	Ile	Gly	Glu	Phe	Asn	Leu
	370				375					380					
Pro	Val	Ser	Pro	Leu	Tyr	His	Ile	Ala	Asn	Thr	Met	Tyr	Lys	Ile	Arg
385				390					395						400
Lys	Gln	Leu	Lys	Asn	Lys	His									
				405											

<210> SEQ ID NO 357

<211> LENGTH: 1434

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 357

atgctaagaa	aaaagagaat	tttgggttta	tttcgacttg	ttgaattaat	tttcctagga	60
ttattgttga	gtttagttgt	ttcgtacctt	gcgtaggacca	atagttttgc	aacacttcat	120
aatatattag	caactgtcgg	aatagtggaa	cgaagcaaag	atcaacagcc	tcgctatcac	180
attggacaag	ctattcaagt	acaaaaaagt	ggtccatata	atcaatggat	tggaactatt	240
aataaacagg	tagaagatat	agccgaaaat	taccgagtga	gttatcatta	tgaagtggta	300
ttccaatag	gaaaagtcac	tgtttctttg	ccagaacata	acctgaaaga	gcctgataaa	360
ccgaggttta	aaaaaggaga	tatcggttaa	ttatcttcat	taactaaaaa	gccacatata	420
aaagtatatc	aagggtcaatt	agcgactatt	aaacaagtta	aaaaatgcta	tgactattcg	480
ttaggaggat	atcagtacga	tattaatctg	aaagataatc	taagattaga	tggaatttca	540
gagcaagatt	ttgttaaacc	ttattatatt	aggttcaata	aaggaaaattc	ccctgagcaa	600
aacaatcgtc	ttttgcgaaa	agctttcgct	tatgcaaagc	agcatccaaa	tagcgttata	660
tcttttccaa	aggggcaatt	tcacattggc	tctttgcctt	cacaaaaaga	ttattttgag	720
cttccatctg	atacagctat	tattgggtcat	cagacagagt	tcattattca	cggtaaaatg	780
ttgtggtttg	gattccctac	aggaccaaag	gctgaacaag	gtgttcgtaa	tctcgtgttg	840
actggagtg	atttcaaagc	aatgatttg	aaaaaaggag	accactttat	gattatggct	900
gatcatggta	ctgattggca	tatttacgat	aacaaaattta	ctatggttca	taagcgtaat	960
agtcataattt	ttgatttagg	atctctacaa	aattcattgt	ttgagaaaaa	ccaattttatt	1020
ggctatgcgc	cagaattagt	acaagaccaa	cagctgctat	caaaggctca	agggcatgat	1080
tttttttcag	aagtcattca	gtttgatgct	gctgttcata	attttgcatg	ggatggagggt	1140
ctacttagta	atattgctcc	aaactatgaa	gcattttaacc	aaactcgaca	tctatgtcac	1200
aatattactg	taagccaaaa	tcaattttta	ccttatatag	atccgactgg	ttgcctgaga	1260
gcctatagt	gttctattgg	tcagcattcc	tcaaaaagtag	gagttattag	ggttttaaat	1320
aatgttttta	cctcatccat	tgttactaaa	gcgaagctca	ctagtgtgtt	tatggaacct	1380
attcattttc	caccaaattc	accggttatt	gtcgcaggta	atatcattaa	ttga	1434

<210> SEQ ID NO 358

<211> LENGTH: 477

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 358

Met Leu Arg Lys Lys Arg Ile Leu Gly Leu Phe Arg Leu Val Glu Leu

1				5				10				15			
Ile	Phe	Leu	Gly	Leu	Leu	Leu	Ser	Leu	Val	Val	Ser	Tyr	Leu	Ala	Trp
			20					25					30		
Thr	Asn	Ser	Phe	Ala	Thr	Leu	His	Asn	Ile	Leu	Ala	Thr	Val	Gly	Ile
		35					40					45			
Val	Glu	Arg	Ser	Lys	Asp	Gln	Gln	Pro	Arg	Tyr	His	Ile	Gly	Gln	Ala
	50				55						60				
Ile	Gln	Val	Gln	Lys	Ser	Gly	Pro	Tyr	His	Gln	Trp	Ile	Gly	Thr	Ile
65				70					75					80	
Asn	Lys	Gln	Val	Glu	Asp	Ile	Ala	Glu	Asn	Tyr	Arg	Val	Ser	Tyr	His
			85						90				95		
Tyr	Glu	Val	Val	Phe	Pro	Ile	Gly	Lys	Val	Thr	Val	Ser	Leu	Pro	Glu
		100					105						110		
His	Asn	Leu	Lys	Glu	Pro	Asp	Lys	Pro	Arg	Phe	Lys	Lys	Gly	Asp	Ile
	115				120						125				
Val	Lys	Leu	Ser	Ser	Leu	Thr	Lys	Lys	Pro	His	Ile	Lys	Val	Tyr	Gln
	130				135						140				
Gly	Gln	Leu	Ala	Thr	Ile	Lys	Gln	Val	Lys	Lys	Cys	Tyr	Asp	Tyr	Ser
145				150					155					160	
Leu	Gly	Gly	Tyr	Gln	Tyr	Asp	Ile	Asn	Leu	Lys	Asp	Asn	Leu	Arg	Leu
		165					170						175		
Asp	Gly	Ile	Ser	Glu	Gln	Asp	Phe	Val	Lys	Pro	Tyr	Tyr	Ile	Arg	Phe
	180				185							190			
Asn	Lys	Gly	Asn	Ser	Pro	Glu	Gln	Asn	Asn	Arg	Leu	Leu	Arg	Lys	Ala
	195				200						205				
Phe	Ala	Tyr	Ala	Lys	Gln	His	Pro	Asn	Ser	Val	Ile	Ser	Phe	Pro	Lys
	210				215						220				
Gly	Gln	Phe	His	Ile	Gly	Ser	Leu	Pro	Ser	Gln	Lys	Asp	Tyr	Phe	Glu
225				230					235					240	
Leu	Pro	Ser	Asp	Thr	Ala	Ile	Ile	Gly	His	Gln	Thr	Glu	Phe	Ile	Ile
		245					250						255		
His	Gly	Lys	Met	Leu	Trp	Phe	Gly	Phe	Pro	Thr	Gly	Pro	Lys	Ala	Glu
	260				265							270			
Gln	Gly	Val	Arg	Asn	Leu	Val	Leu	Thr	Gly	Val	His	Phe	Lys	Ala	Asn
	275				280						285				
Asp	Leu	Lys	Lys	Gly	Asp	His	Phe	Met	Ile	Met	Ala	Asp	His	Gly	Thr
	290			295							300				
Asp	Trp	His	Ile	Tyr	Asp	Asn	Lys	Phe	Thr	Met	Val	His	Lys	Arg	Asn
305				310					315					320	
Ser	His	Ile	Phe	Asp	Leu	Gly	Ser	Leu	Gln	Asn	Ser	Leu	Phe	Glu	Lys
		325					330						335		
Asn	Gln	Phe	Ile	Gly	Tyr	Ala	Pro	Glu	Leu	Val	Gln	Asp	Gln	Gln	Leu
		340					345					350			
Leu	Ser	Lys	Ala	Gln	Gly	His	Asp	Phe	Phe	Ser	Glu	Val	Ile	Gln	Phe
	355				360						365				
Asp	Ala	Ala	Val	His	His	Phe	Ala	Trp	Asp	Gly	Gly	Leu	Leu	Ser	Asn
	370				375						380				
Ile	Ala	Pro	Asn	Tyr	Glu	Ala	Phe	Asn	Gln	Thr	Arg	His	Leu	Cys	His
385				390					395					400	
Asn	Ile	Thr	Val	Ser	Gln	Asn	Gln	Phe	Leu	Pro	Tyr	Ile	Asp	Pro	Thr
		405					410						415		
Gly	Cys	Leu	Arg	Ala	Tyr	Ser	Gly	Ser	Ile	Gly	Gln	His	Ser	Ser	Lys
		420					425					430			
Val	Gly	Val	Ile	Arg	Val	Leu	Asn	Val	Phe	Thr	Ser	Ser	Ile	Val	
	435					440					445				
Thr	Lys	Ala	Lys	Leu	Thr	Ser	Trp	Phe	Met	Glu	Pro	Ile	His	Phe	Pro
	450				455						460				

Pro Asn Ser Pro Val Ile Val Ala Gly Asn Ile Ile Asn
 465 470 475

<210> SEQ ID NO 359
 <211> LENGTH: 666
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 359
 ttggcacacc tgagcgtatt caatatgggtg ataaggttgt tgctcttatt gaataccgtg 60
 acggtagcct catggatgtg gtttacaatg tgtaaagaca cttatttttc aggcgaagct 120
 atccaactta gtgatatgtt aagagcccg cgaagaaagag ctctgcgtca gctgcattta 180
 ttaaaggagt acccagaagg tagcttatta tcggtcacca tgaatatccc tggaccaatt 240
 aaaacctctc ctaaacttct tgaagctttt gatatagtga ttaaggccat tcaaactgcc 300
 ttagctgacg ataagatttg ttaccagttg cgattactgc ctacaacggg ttatgagtat 360
 tacctcatca caagtctacc tagccgcgac ctgaagttaa aaatgatagc cttagagaca 420
 gagttgccaa taggtcgtct catggattta gatgtcttgg tcttgcaaaa tgatctgcct 480
 cattcaatta gcagaaccgt attaggaggc tcccctaggc aatgttttat ctgttctaaa 540
 gaggccaaag tctgcggtcg cctacgtaag cacagtgtcg aggagatgca gactgctatt 600
 tcaaaattac tccattcatt tttcaataaa gacaaccaat catcgtcatc agataagaca 660
 ggttga 666

<210> SEQ ID NO 360
 <211> LENGTH: 221
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 360
 Met Ala His Leu Ser Val Phe Asn Met Val Ile Arg Leu Leu Leu Leu
 1 5 10 15
 Leu Asn Thr Val Thr Val Ala Ser Trp Met Trp Phe Thr Met Cys Lys
 20 25 30
 Asp Thr Tyr Phe Ser Gly Glu Ala Ile Gln Leu Ser Asp Met Leu Arg
 35 40 45
 Ala Arg Glu Glu Arg Ala Leu Arg Gln Leu His Leu Leu Lys Glu Tyr
 50 55 60
 Pro Glu Gly Ser Leu Leu Ser Val Thr Met Asn Ile Pro Gly Pro Ile
 65 70 75 80
 Lys Thr Ser Pro Lys Leu Leu Glu Ala Phe Asp Ile Val Ile Lys Ala
 85 90 95
 Ile Gln Thr Ala Leu Ala Asp Asp Lys Ile Cys Tyr Gln Leu Arg Leu
 100 105 110
 Leu Pro Thr Thr Gly Tyr Glu Tyr Tyr Leu Ile Thr Ser Leu Pro Ser
 115 120 125
 Arg Asp Leu Lys Leu Lys Met Ile Ala Leu Glu Thr Glu Leu Pro Ile
 130 135 140
 Gly Arg Leu Met Asp Leu Asp Val Leu Val Leu Gln Asn Asp Leu Pro
 145 150 155 160
 His Ser Ile Ser Arg Thr Val Leu Gly Gly Ser Pro Arg Gln Cys Phe
 165 170 175
 Ile Cys Ser Lys Glu Ala Lys Val Cys Gly Arg Leu Arg Lys His Ser
 180 185 190
 Val Glu Glu Met Gln Thr Ala Ile Ser Lys Leu Leu His Ser Phe Phe
 195 200 205
 Asn Lys Asp Asn Gln Ser Ser Ser Asp Lys Thr Gly
 210 215 220

<210> SEQ ID NO 361
 <211> LENGTH: 1053

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 361

```
gtggacactt taatcgcagg aataacctcc atcaccattc ctcaaattgt tatgatggtc      60
attggtgccc tcttaatgta tctaggaatt aaaaaagaat acgaaccaac cttacttgtc      120
cccatgggac ttggaaccat tctcgtaaac ttccctgggt caggagtttt aacacaagtg      180
gttaacggag tcgagcaaga aggggttttt gaggctctct tcaattttgg gattggaaca      240
gaacttttcc cactgttgat tttcattggg ataggagcca tgattgactt tggccccttg      300
cttcaaaacc cattcatgct cttgtttggg gatgcagctc aattcggaat tttctttggt      360
gtggttggtg ccgtactggc tggctttgac attaaagaag cagcttcaat cggcattatc      420
ggagcagcag acggaccgac ttctatcttt gttgccaaac aactggccaa ggatttactg      480
ggtccaatta cggttgacgc ctattcttac atggctctgg ttcctattat ccaaccattt      540
gccattaaat tagtgacaac gaaaaaagag cgccgtatcc gtatgactta caaagctgag      600
aatgtatctc aaatgactaa aatcttattc ccaatcatca ttaccttagt agcagggttc      660
atcgcccaa tttctctacc tttagtggc tttttgatgt tcggtaaact attacgggag      720
tgtgggtgtg tcgatcgctt gtcacaaact gtcacaaatg aattggtaaa cattattagt      780
atcttgcttg gattgaccat ctctattaaa atgcaggcag acctgttctt aaatgtacag      840
acactcttaa tcatcgctct tggtttactt gcttttatca tggattctat cgggtggggtc      900
atgtttgcca aattttctca tctcttccga aaagagaaga ttaatccaat gattggcgct      960
gcgggtattt cagcttttcc aatgtcaagt cgtgtcattc aaaaaatggc acagatgaag     1020
accgcgaaaa ctttatcctc atgtatgctg tag                               1053
```

<210> SEQ ID NO 362

<211> LENGTH: 350

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 362

```
Met Asp Thr Leu Ile Ala Gly Ile Thr Ser Ile Thr Ile Pro Gln Ile
1           5           10           15
Val Met Met Val Ile Gly Ala Leu Leu Met Tyr Leu Gly Ile Lys Lys
20          25          30
Glu Tyr Glu Pro Thr Leu Leu Val Pro Met Gly Leu Gly Thr Ile Leu
35          40          45
Val Asn Phe Pro Gly Ser Gly Val Leu Thr Gln Val Val Asn Gly Val
50          55          60
Glu Gln Glu Gly Val Phe Glu Ala Leu Phe Asn Phe Gly Ile Gly Thr
65          70          75          80
Glu Leu Phe Pro Leu Leu Ile Phe Ile Gly Ile Gly Ala Met Ile Asp
85          90          95
Phe Gly Pro Leu Leu Gln Asn Pro Phe Met Leu Leu Phe Gly Asp Ala
100         105         110
Ala Gln Phe Gly Ile Phe Phe Val Val Val Val Ala Val Leu Ala Gly
115         120         125
Phe Asp Ile Lys Glu Ala Ala Ser Ile Gly Ile Ile Gly Ala Ala Asp
130         135         140
Gly Pro Thr Ser Ile Phe Val Ala Asn Gln Leu Ala Lys Asp Leu Leu
145         150         155         160
Gly Pro Ile Thr Val Ala Ala Tyr Ser Tyr Met Ala Leu Val Pro Ile
165         170         175
Ile Gln Pro Phe Ala Ile Lys Leu Val Thr Thr Lys Lys Glu Arg Arg
180         185         190
Ile Arg Met Thr Tyr Lys Ala Glu Asn Val Ser Gln Met Thr Lys Ile
195         200         205
Leu Phe Pro Ile Ile Ile Thr Leu Val Ala Gly Phe Ile Ala Pro Ile
210         215         220
Ser Leu Pro Leu Val Gly Phe Leu Met Phe Gly Asn Leu Leu Arg Glu
225         230         235         240
```

Cys	Gly	Val	Leu	Asp	Arg	Leu	Ser	Gln	Thr	Ala	Gln	Asn	Glu	Leu	Val
				245					250					255	
Asn	Ile	Ile	Ser	Ile	Leu	Leu	Gly	Leu	Thr	Ile	Ser	Ile	Lys	Met	Gln
			260					265					270		
Ala	Asp	Leu	Phe	Leu	Asn	Val	Gln	Thr	Leu	Leu	Ile	Ile	Val	Phe	Gly
		275					280					285			
Leu	Leu	Ala	Phe	Ile	Met	Asp	Ser	Ile	Gly	Gly	Val	Met	Phe	Ala	Lys
	290				295						300				
Phe	Leu	Asn	Leu	Phe	Arg	Lys	Glu	Lys	Ile	Asn	Pro	Met	Ile	Gly	Ala
305					310					315					320
Ala	Gly	Ile	Ser	Ala	Phe	Pro	Met	Ser	Ser	Arg	Val	Ile	Gln	Lys	Met
			325					330						335	
Ala	Gln	Met	Lys	Thr	Arg	Lys	Thr	Leu	Ser	Ser	Cys	Met	Leu		
			340					345					350		

<210> SEQ ID NO 363
 <211> LENGTH: 1425
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 363

ttgaaaaagg	agataacaat	gatgttatta	acaatgctgg	cttatgccat	gattattgtc	60
tttatgtacg	tggtaatgaa	gaaaaaaatg	acccttttta	ctgctttggt	catgattcca	120
ttaatcatga	cgattgctgt	tatactgact	ggttcagctg	acttcaatgc	agatgccaaa	180
tttgttgcct	ttgttggtga	cggtggaatt	gctaaagacc	taacagctat	cggaccaatg	240
gttatgtatg	gtatcaacaa	tactgctaaa	acaggatatca	tgttgctatt	tgccattttg	300
ttctttctctg	tcatgttaga	tgcaggattg	tttgatccga	ttactgaaaa	gatgattcgc	360
tttgctaaag	gtgatccaat	gaagggtgctt	atcgcaacag	ctgtcgttgc	tgctgcagta	420
tctcttaatg	gtgatggaac	aaccactact	ttaattttgtt	gctctgcttt	cttacctatc	480
tataaaaaat	tggacatgaa	aatcatgaac	ctaggtgtct	tgattattct	tcaaaatact	540
attatgaact	tactgccatg	gggtggccct	actgctcgtg	cgatgtctgt	tcttggtgtc	600
ggtcctgaaa	ttcttggtga	tcttgccaccg	ggtatgatgtt	tatctcttct	ttatgtgatt	660
tgttggtgtg	ctccaagcat	ggggcgtaaa	gaacgtgcaa	gacttggtgt	tattgacttg	720
tctgaagaag	acatgcgtca	actcacagac	attactgacc	cagataccct	ttttattcgt	780
cgctcctaaaa	actttgtttt	caatgctatc	ttaaccattg	gattaatcac	ttggttagtt	840
gctgggtcctt	tcaacaaaatc	tattgctatg	gcaccgcttc	ttctttttgc	ggtgggaact	900
tgtatcgctt	tgatgggtcaa	ttaccagtg	cttaaagatc	aatcaaaaacg	cattggtgac	960
aatgctgggtg	atgcggttca	agtgggttatt	ctcgtctttg	ctgctggtat	ctttatgggt	1020
ctttttcaag	gttctgggtat	ggctagcgct	cttgcacaaa	gtttttgcaac	cattattcca	1080
aaacaactgg	cagggtttctg	gggtctcggt	attgccttag	tttctgcacc	tggtaccttc	1140
tttatctcca	atgatgggtt	ttactatggt	atcttgcttg	ttcttgacaga	agctgggtgct	1200
gaatatgggt	tcagtaacat	ggctatggca	cttgcttccc	tcattgggaca	agccttccac	1260
ttacttagtc	cattagttgc	cttcatttat	cttcttcttc	gcttgacagg	tcttgacatg	1320
ggggaatggc	aaaaagaggc	tgctaaatat	gcccttatca	tctttgttat	ctttgtggta	1380
accattattg	ccatgggaca	aatgccactt	tacattccac	aataa		1425

<210> SEQ ID NO 364
 <211> LENGTH: 474
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 364

Met	Lys	Lys	Glu	Ile	Thr	Met	Met	Leu	Leu	Thr	Met	Leu	Ala	Tyr	Ala
1				5					10					15	
Met	Ile	Ile	Val	Phe	Met	Tyr	Val	Val	Met	Lys	Lys	Lys	Met	Thr	Pro
			20					25					30		
Phe	Thr	Ala	Leu	Val	Met	Ile	Pro	Leu	Ile	Met	Thr	Ile	Ala	Val	Ile
		35					40					45			
Leu	Thr	Gly	Ser	Ala	Asp	Phe	Asn	Ala	Asp	Ala	Lys	Phe	Val	Ala	Phe

50	55	60													
Val Gly Asp Gly Gly Ile Ala Lys Asp Leu Thr Ala Ile Gly Pro Met															
65	70	75	80												
Val Met Tyr Gly Ile Asn Asn Thr Ala Lys Thr Gly Ile Met Leu Leu															
	85	90	95												
Phe Ala Ile Leu Phe Phe Ser Val Met Leu Asp Ala Gly Leu Phe Asp															
	100	105	110												
Pro Ile Thr Glu Lys Met Ile Arg Phe Ala Lys Gly Asp Pro Met Lys															
	115	120	125												
Val Leu Ile Ala Thr Ala Val Val Ala Ala Ala Val Ser Leu Asn Gly															
	130	135	140												
Asp Gly Thr Thr Thr Thr Leu Ile Cys Cys Ser Ala Phe Leu Pro Ile															
145	150	155	160												
Tyr Lys Lys Leu Asp Met Lys Ile Met Asn Leu Gly Val Leu Ile Ile															
	165	170	175												
Leu Gln Asn Thr Ile Met Asn Leu Leu Pro Trp Gly Gly Pro Thr Ala															
	180	185	190												
Arg Ala Met Ser Val Leu Gly Val Gly Pro Glu Ile Leu Gly Tyr Leu															
	195	200	205												
Ala Pro Gly Met Ile Leu Ser Leu Leu Tyr Val Ile Cys Trp Val Ala															
	210	215	220												
Pro Ser Met Gly Arg Lys Glu Arg Ala Arg Leu Gly Val Ile Asp Leu															
225	230	235	240												
Ser Glu Glu Asp Met Arg Gln Leu Thr Asp Ile Thr Asp Pro Asp Thr															
	245	250	255												
Leu Phe Ile Arg Arg Pro Lys Asn Phe Val Phe Asn Ala Ile Leu Thr															
	260	265	270												
Ile Gly Leu Ile Thr Trp Leu Val Ala Gly Ser Phe Asn Lys Ser Ile															
	275	280	285												
Ala Met Ala Pro Leu Leu Leu Phe Ala Val Gly Thr Cys Ile Ala Leu															
	290	295	300												
Met Val Asn Tyr Pro Val Leu Lys Asp Gln Ser Lys Arg Ile Gly Asp															
305	310	315	320												
Asn Ala Gly Asp Ala Val Gln Val Val Ile Leu Val Phe Ala Ala Gly															
	325	330	335												
Ile Phe Met Gly Leu Phe Gln Gly Ser Gly Met Ala Ser Ala Leu Ala															
	340	345	350												
Gln Ser Phe Ala Thr Ile Ile Pro Lys Gln Leu Ala Gly Phe Trp Gly															
	355	360	365												
Leu Val Ile Ala Leu Val Ser Ala Pro Gly Thr Phe Phe Ile Ser Asn															
	370	375	380												
Asp Gly Phe Tyr Tyr Gly Ile Leu Pro Val Leu Ala Glu Ala Gly Ala															
385	390	395	400												
Glu Tyr Gly Phe Ser Asn Met Ala Met Ala Leu Ala Ser Leu Met Gly															
	405	410	415												
Gln Ala Phe His Leu Leu Ser Pro Leu Val Ala Phe Ile Tyr Leu Leu															
	420	425	430												
Leu Arg Leu Thr Gly Leu Asp Met Gly Glu Trp Gln Lys Glu Ala Ala															
	435	440	445												
Lys Tyr Ala Leu Ile Ile Phe Val Ile Phe Val Val Thr Ile Ile Ala															
	450	455	460												
Met Gly Gln Met Pro Leu Tyr Ile Pro Gln															
465	470														

<210> SEQ ID NO 365

<211> LENGTH: 651

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 365

```
atgaacaaaa cctttaaaca aagtttacc cttatctttta gtgaggaagt agcaaacagc      60
gtgacacacg ctatcggagc atttgctatg ctcattctac ttcctatttc agccagctat      120
gcttatcaaa cttatgacct taaagccgct attggtatct ccatctttgt catcagtcctc      180
tttttgatgt ttttgtcctc tacgatttac cactccatgg cttatgggtc gggtcacaaa      240
tacattctac gcattattga tcacagtatg atttatattg ctatcgcagg aagttataca      300
cctgttgcct tatcccttgt ttctggttgg ctaggctata tcattattgt tttgcagtgg      360
ggcattacgc tttttgggat tttatacaaa atttttgcc aacgtatcaa tgaaaaattc      420
agtttgatgc tttatatcgt tatgggctgg ctcgttgtgt ttatcttgcc agtcatcatt      480
caaaaaacta gtcttgcttt tggctttctc atgttatattg gtggcttgct ttataccatt      540
ggagcgggat tttatgccaa aaaaagaccc tacttccaca tgatttggca tctctttatt      600
ttattggcct ctgccctcca atttatcgct atcactttct ttatgcttta a          651
```

<210> SEQ ID NO 366

<211> LENGTH: 216

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 366

```
Met Asn Gln Thr Phe Lys Gln Ser Leu Pro Leu Ser Phe Ser Glu Glu
 1          5          10          15
Val Ala Asn Ser Val Thr His Ala Ile Gly Ala Phe Ala Met Leu Ile
          20          25          30
Leu Leu Pro Ile Ser Ala Ser Tyr Ala Tyr Gln Thr Tyr Asp Leu Lys
          35          40          45
Ala Ala Ile Gly Ile Ser Ile Phe Val Ile Ser Leu Phe Leu Met Phe
          50          55          60
Leu Ser Ser Thr Ile Tyr His Ser Met Ala Tyr Gly Ser Val His Lys
          65          70          75          80
Tyr Ile Leu Arg Ile Ile Asp His Ser Met Ile Tyr Ile Ala Ile Ala
          85          90          95
Gly Ser Tyr Thr Pro Val Ala Leu Ser Leu Val Ser Gly Trp Leu Gly
          100          105          110
Tyr Ile Ile Ile Val Leu Gln Trp Gly Ile Thr Leu Phe Gly Ile Leu
          115          120          125
Tyr Lys Ile Phe Ala Lys Arg Ile Asn Glu Lys Phe Ser Leu Met Leu
          130          135          140
Tyr Ile Val Met Gly Trp Leu Val Val Phe Ile Leu Pro Val Ile Ile
          145          150          155          160
Gln Lys Thr Ser Leu Ala Phe Gly Leu Leu Met Leu Phe Gly Gly Leu
          165          170          175
Ser Tyr Thr Ile Gly Ala Val Phe Tyr Ala Lys Lys Arg Pro Tyr Phe
          180          185          190
His Met Ile Trp His Leu Phe Ile Leu Leu Ala Ser Ala Leu Gln Phe
          195          200          205
Ile Ala Ile Thr Phe Phe Met Leu
          210          215
```

<210> SEQ ID NO 367

<211> LENGTH: 369

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 367

```
atgactaaaa aaaatcatgg cggttttttgg gggttggtgc ttggatcagc agcagctagc      60
attgcttact taagtttatc gtcttccaaa aaagatcaac tcttgaaaaga tagtgctaaa      120
aaaatagatg atctcaacgc ttacttgcaa gataaaaagta agcaagttct ggatgcagta      180
tcggaaaaaag tccaagaatc caaagatgct gttgaagttt acggtgggtat cgccgcagaa      240
```

acagttgaag aatctttggg acaggctaaa gaaaaggtag aaggaattgg cgaagctact	300
agccaaacta tccaatctaa aatggaaaaa ctactagcg ataagacaga tgctgatgat	360
gaaaaatag	369

<210> SEQ ID NO 368
 <211> LENGTH: 122
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 368

Met Thr Lys Lys Asn His Gly Val Phe Trp Gly Leu Leu Leu Gly Ser	
1 5 10 15	
Ala Ala Ala Ser Ile Ala Tyr Leu Ser Leu Ser Ser Ser Lys Lys Asp	
20 25 30	
Gln Leu Leu Lys Asp Ser Ala Lys Lys Ile Asp Asp Leu Asn Ala Tyr	
35 40 45	
Leu Gln Asp Lys Ser Lys Gln Val Leu Asp Ala Val Ser Glu Lys Val	
50 55 60	
Gln Glu Ser Lys Asp Ala Val Glu Val Tyr Gly Gly Ile Ala Ala Glu	
65 70 75 80	
Thr Val Glu Glu Ser Leu Gly Gln Ala Lys Glu Lys Val Glu Gly Ile	
85 90 95	
Gly Glu Ala Thr Ser Gln Thr Ile Gln Ser Lys Met Glu Lys Leu Thr	
100 105 110	
Ser Asp Lys Thr Asp Ala Asp Asp Glu Lys	
115 120	

<210> SEQ ID NO 369
 <211> LENGTH: 918
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 369

atggctggac ttttttcagt aggtcagcta accacttttt taaatgttgt tgtccaatat	60
accaaacatt tcaacgatat ttcactctgtc ttggcagaga tacagagttc tttagcttgt	120
gcgcaaaggc tttatgacct tttagatatt gaaataaaaag agcaagagca ctttctaaca	180
tttaaggcat cagcggttaa ggggcaaatt gactttgaag aagtaagttt ttcttatcaa	240
aaagacaggc ccttactgaa agatattaat ttttctgttc ctgcgggttc caaggtagcg	300
attgtagggc ctacaggtgc aggtaaatca actttaatca atttactcat gcgcttttat	360
gaacttgatg ctggtagcat caagttagat aaagttccta ttaagtgtta tgctaaggaa	420
gaacttaggt ccattactgg catagtattg caagaaacct ggttgaaaga tgcgactgtt	480
catgagttga ttgcttacgg cagtgaagag gctagccgtg atgaagtagt ggcagcagcc	540
aaagcagctc atgcacactt ctttattatg caacttccta agacttatga tacttactta	600
agtgcttctg atgatgcttt gtccaaggc cagctccagt tattagctat tgccagaatg	660
tttttgaaaa aaccaaaggt cttggttcta gatgaagcca cctcctctat tgatattaga	720
acagaagctg ttattcaaga ggcactaaaa gaactcatga gaggaaggac cagctttatc	780
attgcccatac gtttatcaac gattcaatca gctgatttga ttcttgttat ggatcaaggt	840
cgattgggtg agtggggaac acatgccagc ttaatgtcaa aaaacgcctg ttatgctaga	900
ttacaaaaga tagaataa	918

<210> SEQ ID NO 370
 <211> LENGTH: 305
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 370

Met Ala Gly Leu Phe Ser Val Gly Gln Leu Thr Thr Phe Leu Asn Val	
1 5 10 15	
Val Val Gln Tyr Thr Lys Pro Phe Asn Asp Ile Ser Ser Val Leu Ala	
20 25 30	

Glu	Ile	Gln	Ser	Ser	Leu	Ala	Cys	Ala	Gln	Arg	Leu	Tyr	Asp	Leu	Leu
		35					40					45			
Asp	Ile	Glu	Ile	Lys	Glu	Gln	Glu	His	Phe	Leu	Thr	Phe	Lys	Ala	Ser
	50					55					60				
Ala	Val	Lys	Gly	Gln	Ile	Asp	Phe	Glu	Glu	Val	Ser	Phe	Ser	Tyr	Gln
65					70					75				80	
Lys	Asp	Arg	Pro	Leu	Leu	Lys	Asp	Ile	Asn	Phe	Ser	Val	Pro	Ala	Gly
			85					90					95		
Ser	Lys	Val	Ala	Ile	Val	Gly	Pro	Thr	Gly	Ala	Gly	Lys	Ser	Thr	Leu
		100						105					110		
Ile	Asn	Leu	Leu	Met	Arg	Phe	Tyr	Glu	Leu	Asp	Ala	Gly	Ser	Ile	Lys
	115						120					125			
Leu	Asp	Lys	Val	Pro	Ile	Lys	Cys	Tyr	Ala	Lys	Glu	Glu	Leu	Arg	Ser
	130					135					140				
Ile	Thr	Gly	Ile	Val	Leu	Gln	Glu	Thr	Trp	Leu	Lys	Asp	Ala	Thr	Val
145					150					155					160
His	Glu	Leu	Ile	Ala	Tyr	Gly	Ser	Glu	Glu	Ala	Ser	Arg	Asp	Glu	Val
			165							170				175	
Val	Ala	Ala	Ala	Lys	Ala	Ala	His	Ala	His	Phe	Phe	Ile	Met	Gln	Leu
		180						185					190		
Pro	Lys	Thr	Tyr	Asp	Thr	Tyr	Leu	Ser	Ala	Ser	Asp	Asp	Ala	Leu	Ser
	195						200				205				
Gln	Gly	Gln	Leu	Gln	Leu	Leu	Ala	Ile	Ala	Arg	Met	Phe	Leu	Lys	Lys
	210					215					220				
Pro	Lys	Val	Leu	Val	Leu	Asp	Glu	Ala	Thr	Ser	Ser	Ile	Asp	Ile	Arg
225					230					235					240
Thr	Glu	Ala	Val	Ile	Gln	Glu	Ala	Leu	Lys	Glu	Leu	Met	Arg	Gly	Arg
			245							250				255	
Thr	Ser	Phe	Ile	Ile	Ala	His	Arg	Leu	Ser	Thr	Ile	Gln	Ser	Ala	Asp
		260						265					270		
Leu	Ile	Leu	Val	Met	Asp	Gln	Gly	Arg	Leu	Val	Glu	Trp	Gly	Thr	His
	275						280					285			
Ala	Ser	Leu	Met	Ser	Lys	Asn	Ala	Cys	Tyr	Ala	Arg	Leu	Gln	Lys	Ile
	290					295					300				
Glu															
305															

<210> SEQ ID NO 371

<211> LENGTH: 1725

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 371

atgaaacgat	tacgtccata	tgtgaaaggg	tacctaaaag	aaagtatctt	aggctcctctt	60
tttaaattat	tagaagcttt	atttgaatta	ttagtccctt	tgттаattgc	taacatgatt	120
gatatatcga	ttagtcaaca	caacagccag	ggaattttga	gggttggttt	aacattattt	180
ggtttagcaa	ccattggctt	attgctttcc	gttacagccc	agtatttttc	ttcgaaagca	240
gctgttggtt	ttacaagaca	aatgacagat	gacttggtta	aaaaaatcat	gtttttgagc	300
aaggaggacc	aagaccatct	tggttatgct	agtctgttat	cacgattgac	cagtgatagt	360
tttcaaattc	aaactgggat	caatcaattt	ttgcgtcttt	ttctaagggc	ccctattatc	420
gtatgtggtg	ctatggtaat	ggcttattgg	attagtccaa	gtctaaccct	atggtttgtg	480
atgatggtga	ttgtcttact	aacacttggt	tttgttatgt	cacatttatt	aggccccctt	540
tatctcttaa	tccgccgaga	aacagatcac	ttggttcggt	tgactagcca	acagttacaa	600
ggaatccgag	taattaaggc	ttttaatcaa	acccaaaaag	aactccaagc	atttaagcag	660
caaaatatgc	tcttaagtcg	ccaccaatat	caagctgcta	ccctagccaa	tgtcttgaat	720
cctatgactt	ttttagtggt	caatcttacc	ctgttaatct	tgatttggca	aggaagttgg	780
caagtagctc	atagatcgct	tagtcagggc	atgttggttg	ctttaattaa	ttacctcttg	840
cagattttgg	cagaactttt	gaaaatgacc	atgttgatgg	gaaccatcaa	tcaaagtgtg	900

acagccgcaa	aacggattaa	tcaggtgttt	gttttagctg	atgaagcgcc	tttgcctta	960
cttaaagatg	gtcctatttc	aactcatctg	ttgaccatcc	ggcacttgac	ctttacttat	1020
ccaggagcag	cagagccaag	tctgtatgat	attcagttaa	gtgctgatca	gggagaatgg	1080
attggcatca	ttggtggtac	tggagcaggc	aaaacgactt	tgattgactt	gatctgccaa	1140
acttattcac	aatatagtg	tgagattagt	cttaattggc	aaggagaagt	gccaaaaaca	1200
ctaaccgagt	ggcgaaatgt	gattgctcct	gttcctcaaa	aagctcaatt	atttaaagga	1260
acgattagaa	gtaacctcct	actgggacaa	tcaatgccta	ttagtgatga	ggaactgtgg	1320
cgggctcttg	aattggctca	agcaaaagag	tttgtcgctg	ccttaccaga	acaattagag	1380
gcacctgttg	aagccttcgg	ccgtcatttt	tcaggagggc	aacggcaacg	tctagctatt	1440
gccagagcac	ttctgaagcc	aaaacccatt	ttgatttttg	atgatgccag	ttccgcctta	1500
gacaatgaga	ctcgaggacg	actttttaaa	gctctaaaag	aagagttatc	agatgtttta	1560
gtgattctag	tcacgcaatc	tattaagaat	ttgcagtttg	ctgataagat	tttagtgttg	1620
gaacagggcc	atcaattgga	ttttgccagt	catgaccagt	taaaagtaag	caatgcactt	1680
tatcaagaaa	tgctagcgct	ttacgtgaag	ggggagcaaa	aatga		1725

<210> SEQ ID NO 372

<211> LENGTH: 574

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 372

Met	Lys	Arg	Leu	Arg	Pro	Tyr	Val	Lys	Gly	Tyr	Leu	Lys	Glu	Ser	Ile
1				5					10					15	
Leu	Gly	Pro	Leu	Phe	Lys	Leu	Leu	Glu	Ala	Leu	Phe	Glu	Leu	Leu	Val
			20					25				30			
Pro	Leu	Leu	Ile	Ala	Asn	Met	Ile	Asp	Ile	Ser	Ile	Ser	Gln	His	Asn
			35				40					45			
Ser	Gln	Gly	Ile	Leu	Arg	Val	Val	Leu	Thr	Leu	Phe	Gly	Leu	Ala	Thr
	50					55				60					
Ile	Gly	Leu	Leu	Leu	Ser	Val	Thr	Ala	Gln	Tyr	Phe	Ser	Ser	Lys	Ala
65					70				75					80	
Ala	Val	Gly	Phe	Thr	Arg	Gln	Met	Thr	Asp	Asp	Leu	Phe	Lys	Lys	Ile
			85					90					95		
Met	Phe	Leu	Ser	Lys	Glu	Asp	Gln	Asp	His	Leu	Gly	Tyr	Ala	Ser	Leu
			100					105					110		
Leu	Ser	Arg	Leu	Thr	Ser	Asp	Ser	Phe	Gln	Ile	Gln	Thr	Gly	Ile	Asn
			115				120					125			
Gln	Phe	Leu	Arg	Leu	Phe	Leu	Arg	Ala	Pro	Ile	Ile	Val	Cys	Gly	Ala
	130					135					140				
Met	Val	Met	Ala	Tyr	Trp	Ile	Ser	Pro	Ser	Leu	Thr	Leu	Trp	Phe	Val
145				150					155					160	
Met	Met	Val	Ile	Val	Leu	Leu	Thr	Leu	Val	Phe	Val	Met	Ser	His	Leu
			165					170					175		
Leu	Gly	Pro	Leu	Tyr	Leu	Leu	Ile	Arg	Arg	Glu	Thr	Asp	His	Leu	Val
			180					185					190		
Arg	Leu	Thr	Ser	Gln	Gln	Leu	Gln	Gly	Ile	Arg	Val	Ile	Lys	Ala	Phe
		195				200						205			
Asn	Gln	Thr	Gln	Lys	Glu	Leu	Gln	Ala	Phe	Lys	Gln	Gln	Asn	Met	Leu
	210					215					220				
Leu	Ser	Arg	His	Gln	Tyr	Gln	Ala	Ala	Thr	Leu	Ala	Asn	Val	Leu	Asn
225				230					235					240	
Pro	Met	Thr	Phe	Leu	Val	Val	Asn	Leu	Thr	Leu	Leu	Ile	Leu	Ile	Trp
			245					250					255		
Gln	Gly	Ser	Trp	Gln	Val	Ala	His	Arg	Ser	Leu	Ser	Gln	Gly	Met	Leu
			260				265					270			
Val	Ala	Leu	Ile	Asn	Tyr	Leu	Leu	Gln	Ile	Leu	Ala	Glu	Leu	Leu	Lys
	275					280					285				
Met	Thr	Met	Leu	Met	Gly	Thr	Ile	Asn	Gln	Ser	Val	Thr	Ala	Ala	Lys

290	295	300
Arg Ile Asn Gln Val Phe Val Leu Ala Asp Glu Ala Pro Leu Pro Leu		
305	310	315
Leu Lys Asp Gly Pro Ile Ser Thr His Leu Leu Thr Ile Arg His Leu		
	325	330
Thr Phe Thr Tyr Pro Gly Ala Ala Glu Pro Ser Leu Tyr Asp Ile Gln		
	340	345
Leu Ser Ala Asp Gln Gly Glu Trp Ile Gly Ile Ile Gly Gly Thr Gly		
	355	360
Ala Gly Lys Thr Thr Leu Ile Asp Leu Ile Cys Gln Thr Tyr Ser Gln		
	370	375
Tyr Ser Gly Glu Ile Ser Leu Asn Trp Gln Gly Glu Val Pro Lys Thr		
385	390	395
Leu Thr Glu Trp Arg Asn Val Ile Ala Leu Val Pro Gln Lys Ala Gln		
	405	410
Leu Phe Lys Gly Thr Ile Arg Ser Asn Leu Leu Leu Gly Gln Ser Met		
	420	425
Pro Ile Ser Asp Glu Glu Leu Trp Arg Ala Leu Glu Leu Ala Gln Ala		
	435	440
Lys Glu Phe Val Ala Ala Leu Pro Glu Gln Leu Glu Ala Pro Val Glu		
	450	455
Ala Phe Gly Arg His Phe Ser Gly Gly Gln Arg Gln Arg Leu Ala Ile		
465	470	475
Ala Arg Ala Leu Leu Lys Pro Lys Pro Ile Leu Ile Leu Asp Asp Ala		
	485	490
Ser Ser Ala Leu Asp Asn Glu Thr Arg Gly Arg Leu Phe Lys Ala Leu		
	500	505
Lys Glu Glu Leu Ser Asp Val Leu Val Ile Leu Val Thr Gln Ser Ile		
	515	520
Lys Asn Leu Gln Phe Ala Asp Lys Ile Leu Val Leu Glu Gln Gly His		
	530	535
Gln Leu Asp Phe Ala Ser His Asp Gln Leu Lys Val Ser Asn Ala Leu		
545	550	555
Tyr Gln Glu Met Leu Ala Leu Tyr Val Lys Gly Glu Gln Lys		
	565	570

<210> SEQ ID NO 373

<211> LENGTH: 600

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 373

atgttttagac ttttaaagcg tgccctgcagt tttcttcttc tttttgtcat ttatcaatcc	60
tttgttattc atcacaatgt tcaacgtggt ttggcatata agcctatggt tgagaaaaca	120
ttagcagaaa atgatacaaa ggcaaagtga gacttagtct tagctatgat atacaccgag	180
acaaaaggag gagaagcaga tgtcatgcaa tccagtgaag gcagttcagg acaaaaaaac	240
tcgattacag atagtcaggc cagtattgag cacggggtga atttactgtc tcataatctt	300
gctctagctg aggaagcagg agtagattct tggacggctg ttcaggccta taatttttgg	360
acagcttata ttgattatat tgctgaacat ggagggtcaaa ataccgttga tttagcgcact	420
acctattcca aaaccgttgt ggcgccaagc ctaggcaaca ctagtggtca aacctatttt	480
tattaccacc ccctgcctt gatttctgga ggtaagcttt ataagaatgg cggcaatatc	540
tattactcac gagaagttca tttcaatctt tatttaattg aactgatgag ccttttttag	600

<210> SEQ ID NO 374

<211> LENGTH: 199

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 374

Met	Phe	Arg	Leu	Leu	Lys	Arg	Ala	Cys	Ser	Phe	Leu	Leu	Leu	Phe	Val
1			5					10						15	
Ile	Tyr	Gln	Ser	Phe	Val	Ile	His	His	Asn	Val	Gln	Arg	Val	Leu	Ala
		20						25					30		
Tyr	Lys	Pro	Met	Val	Glu	Lys	Thr	Leu	Ala	Glu	Asn	Asp	Thr	Lys	Ala
		35					40					45			
Asn	Val	Asp	Leu	Val	Leu	Ala	Met	Ile	Tyr	Thr	Glu	Thr	Lys	Gly	Gly
	50					55					60				
Glu	Ala	Asp	Val	Met	Gln	Ser	Ser	Glu	Ser	Ser	Ser	Gly	Gln	Lys	Asn
65					70					75				80	
Ser	Ile	Thr	Asp	Ser	Gln	Ala	Ser	Ile	Glu	His	Gly	Val	Asn	Leu	Leu
			85						90				95		
Ser	His	Asn	Leu	Ala	Leu	Ala	Glu	Glu	Ala	Gly	Val	Asp	Ser	Trp	Thr
		100					105						110		
Ala	Val	Gln	Ala	Tyr	Asn	Phe	Gly	Thr	Ala	Tyr	Ile	Asp	Tyr	Ile	Ala
		115					120					125			
Glu	His	Gly	Gly	Gln	Asn	Thr	Val	Asp	Leu	Ala	Thr	Thr	Tyr	Ser	Lys
	130					135					140				
Thr	Val	Val	Ala	Pro	Ser	Leu	Gly	Asn	Thr	Ser	Gly	Gln	Thr	Tyr	Phe
145					150					155					160
Tyr	Tyr	His	Pro	Leu	Ala	Leu	Ile	Ser	Gly	Gly	Lys	Leu	Tyr	Lys	Asn
			165						170					175	
Gly	Gly	Asn	Ile	Tyr	Tyr	Ser	Arg	Glu	Val	His	Phe	Asn	Leu	Tyr	Leu
		180						185					190		
Ile	Glu	Leu	Met	Ser	Leu	Phe									
		195													

<210> SEQ ID NO 375

<211> LENGTH: 1284

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 375

atgacacatt	caacaaagca	ggaacattct	cactcgcaat	cagctgtcct	tggcttacag	60
catgtgcttt	cgatgtatgc	cggatctatt	ttagtaccaa	ttatgatcgc	aggtgcttta	120
ggttattccg	ctagagagtt	gacctacctg	atttcgacag	atattttcat	gtgtggtgtg	180
gctactttct	tacagttaaa	gttaaccaag	catacgggag	tgggattacc	agttgtttta	240
ggatgtgctt	ttcaatcagt	ggcacctcta	tccattattg	gagcgcaca	aggttcaggt	300
gccatgtttg	gagccctcat	tgcgtcagga	atztatgtca	ttttagtggc	aggtattttt	360
tctaagattg	ctcgtttctt	cccaccaatt	gttacaggat	cggtcattac	cgttattggc	420
ttaagtctcg	taggtgttgc	tatggggaat	atgggagata	acgtcaaaga	gcctacggca	480
caaagcatga	tgttatcatt	gttgacgatt	gtcattattc	ttttagtcca	aaaatttacc	540
aaagggtttg	tgaaatccat	ttccattttg	attgggcttg	tagcgggaac	tttggtttca	600
gctatgatgg	gattagtaga	tacaactcct	gtttagagag	cttcttggat	tcattgtgcca	660
accccattht	atthtggcat	gccaaacttht	gaaatcactt	ctattgtgat	gatgtgtatc	720
atcgcaacgg	tttctatggg	tgaatcaaca	ggtgtctact	tagcgttttc	agatttgact	780
aatgatcaat	tagatgaaaa	acgtttgcgc	aatgggttatc	gctcagaagg	gatcgagtc	840
tttctcggtg	ggttatttta	caccttccct	tacactgggt	tttctcaaaa	cgttggactt	900
gtccaaatct	caggtattaa	aacccgctcg	ccgatttact	acgcagcagg	tatccttgtg	960
gtcattggcc	tactccctaa	atthtagagca	atggcacaaa	tgattccaag	cccagttctt	1020
gggtggagcca	tgcttggtct	ctttgggtatg	gttgctcttc	aaggaatgca	aatgcttaat	1080
cgtgttgatt	tccaaaagaa	cgagtataat	tttattattg	ctgccgtttc	catctcagca	1140
ggtttaggct	ttaatggcac	taatcttttt	gccagcttac	cagagacagc	tcaaagtgtc	1200
ttaacgaatg	gtattgtgat	tgccactttg	acatctgttg	tcttaaattht	agttttaaat	1260
ggcaaaagaca	aacaagatga	ataa				1284

<210> SEQ ID NO 376

<211> LENGTH: 427

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 376

```
Met Thr His Ser Thr Lys Gln Glu His Ser His Ser Gln Ser Ala Val
1      5      10      15
Leu Gly Leu Gln His Val Leu Ser Met Tyr Ala Gly Ser Ile Leu Val
20      25      30
Pro Ile Met Ile Ala Gly Ala Leu Gly Tyr Ser Ala Arg Glu Leu Thr
35      40      45
Tyr Leu Ile Ser Thr Asp Ile Phe Met Cys Gly Val Ala Thr Phe Leu
50      55      60
Gln Leu Lys Leu Thr Lys His Thr Gly Val Gly Leu Pro Val Val Leu
65      70      75      80
Gly Cys Ala Phe Gln Ser Val Ala Pro Leu Ser Ile Ile Gly Ala Gln
85      90      95
Gln Gly Ser Gly Ala Met Phe Gly Ala Leu Ile Ala Ser Gly Ile Tyr
100      105      110
Val Ile Leu Val Ala Gly Ile Phe Ser Lys Ile Ala Arg Phe Phe Pro
115      120      125
Pro Ile Val Thr Gly Ser Val Ile Thr Val Ile Gly Leu Ser Leu Val
130      135      140
Gly Val Ala Met Gly Asn Met Gly Asp Asn Val Lys Glu Pro Thr Ala
145      150      155      160
Gln Ser Met Met Leu Ser Leu Leu Thr Ile Val Ile Ile Leu Leu Val
165      170      175
Gln Lys Phe Thr Lys Gly Phe Val Lys Ser Ile Ser Ile Leu Ile Gly
180      185      190
Leu Val Ala Gly Thr Leu Val Ser Ala Met Met Gly Leu Val Asp Thr
195      200      205
Thr Pro Val Val Glu Ala Ser Trp Ile His Val Pro Thr Pro Phe Tyr
210      215      220
Phe Gly Met Pro Thr Phe Glu Ile Thr Ser Ile Val Met Met Cys Ile
225      230      235      240
Ile Ala Thr Val Ser Met Val Glu Ser Thr Gly Val Tyr Leu Ala Leu
245      250      255
Ser Asp Leu Thr Asn Asp Gln Leu Asp Glu Lys Arg Leu Arg Asn Gly
260      265      270
Tyr Arg Ser Glu Gly Ile Ala Val Phe Leu Gly Gly Leu Phe Asn Thr
275      280      285
Phe Pro Tyr Thr Gly Phe Ser Gln Asn Val Gly Leu Val Gln Ile Ser
290      295      300
Gly Ile Lys Thr Arg Arg Pro Ile Tyr Tyr Ala Ala Gly Ile Leu Val
305      310      315      320
Val Ile Gly Leu Leu Pro Lys Phe Arg Ala Met Ala Gln Met Ile Pro
325      330      335
Ser Pro Val Leu Gly Gly Ala Met Leu Val Leu Phe Gly Met Val Ala
340      345      350
Leu Gln Gly Met Gln Met Leu Asn Arg Val Asp Phe Gln Lys Asn Glu
355      360      365
Tyr Asn Phe Ile Ile Ala Ala Val Ser Ile Ser Ala Gly Leu Gly Phe
370      375      380
Asn Gly Thr Asn Leu Phe Ala Ser Leu Pro Glu Thr Ala Gln Met Phe
385      390      395      400
Leu Thr Asn Gly Ile Val Ile Ala Thr Leu Thr Ser Val Val Leu Asn
405      410      415
Leu Val Leu Asn Gly Lys Asp Lys Gln Asp Glu
420      425
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<210> SEQ ID NO 377
<211> LENGTH: 1563
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 377
atgcttttgt ggtcaattta tttggaggtg atgagcatgc ctagtttgtt tgtaactttc      60
caaaaccggt ttaatgaatg gctggcggct ctgggggaac acctgcaa atccctttta      120
tctcttatga tcgccttgct aatagggtgt ccttttagcag cccttctcag tcgcagcaaa      180
cgttgggtcag acattatggt acaggtaaca ggtgtttttc aaaccattcc ctcactggct      240
ttgcttggtc ttttcatccc tttaatggga attggaacgt tgacctgcagt gacagcttta      300
gttatctatg cgatttttcc gattttacaa aacaccatca caggattaaa tgggtattgac      360
ccaagtctcg tggaagcagg aatagctttt gggatgacca aatgggagcg attgaaaaca      420
tttgagattc caattgccat gcctgttatt atgtcagggtg tgcggacgtc agcagtcagt      480
attatcggga cagctacttt agcttccttg ataggagccg gtggacttgg ctctttcatc      540
ttattagggg ttgatcgtaa taatgctaac ctgattctga taggggctat ttcttcagct      600
ctgctagcta ttattttcaa tagtttggtt cagtaccttg agaaaagcttc cttgcgacgg      660
attatgatta gttttggaat taccttactt gcactgctag catcgatac tcctatggcg      720
cttagtcagt tttcaaaagg aaaagataca gtggttattg ccggtaaaatt gggagcagag      780
cccgatattc tgattaatct ctataaggaa ttaattgaag accaatcaga tataagtgtt      840
gagttgaaat ctaatttttg gaaaactagc ttcttatatg aagcccttaa atctggagat      900
attgatattg atcctgaatt tacaggaacc ataacatcaa gtcttttacg cgacaaacca      960
cctttgtcta atgaccctaa gcaggcttat gaggatgcta aaaaaggcat tgctaagcaa      1020
gataaactga cccttctcaa gccatttgct taccaaaata cgtatgctgt tgctatgcca      1080
gaaaaattgg ctaaggaata tcagattgaa accatttctg atttaaaagc gcatgctgat      1140
actttaaagg ccggttttac tttggaattt aaggacagag cagatggcta taagggaatg      1200
caatctcaat atggattaca gctatctgtg gcgacgatgg agccagctct tcgttatcaa      1260
gcaattcaat caggagatat ccaagtaaca gatgcttact ctacggatgc tgaaattacg      1320
aaataccatt tgaaagtttt aaaggatgat aaacagttgt ttccacctta tcaggagct      1380
cctttgatga aaacttcctt attaacaaaa catccagaat taaaaggcat tcttaatcaa      1440
ttagcgggaa aaattactga aaaagagatg caggacatga actacgaggt atctgttaaa      1500
ggagcagatg ctaataaggt cgctcgagat tatctgttga aaacaggctt aatccagaaa      1563
taa

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<210> SEQ ID NO 378
<211> LENGTH: 520
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 378
Met Leu Leu Trp Ser Ile Tyr Leu Glu Val Met Ser Met Pro Ser Leu
1           5           10           15
Phe Val Thr Phe Gln Asn Arg Phe Asn Glu Trp Leu Ala Ala Leu Gly
20          25          30
Glu His Leu Gln Ile Ser Leu Leu Ser Leu Met Ile Ala Leu Leu Ile
35          40          45
Gly Val Pro Leu Ala Ala Leu Leu Ser Arg Ser Lys Arg Trp Ser Asp
50          55          60
Ile Met Leu Gln Val Thr Gly Val Phe Gln Thr Ile Pro Ser Leu Ala
65          70          75          80
Leu Leu Gly Leu Phe Ile Pro Leu Met Gly Ile Gly Thr Leu Pro Ala
85          90          95
Val Thr Ala Leu Val Ile Tyr Ala Ile Phe Pro Ile Leu Gln Asn Thr
100         105         110
Ile Thr Gly Leu Asn Gly Ile Asp Pro Ser Leu Val Glu Ala Gly Ile
115         120         125
Ala Phe Gly Met Thr Lys Trp Glu Arg Leu Lys Thr Phe Glu Ile Pro
130         135         140

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Ile	Ala	Met	Pro	Val	Ile	Met	Ser	Gly	Val	Arg	Thr	Ser	Ala	Val	Met	145	150	155	160
Ile	Ile	Gly	Thr	Ala	Thr	Leu	Ala	Ser	Leu	Ile	Gly	Ala	Gly	Gly	Leu	165	170	175	
Gly	Ser	Phe	Ile	Leu	Leu	Gly	Ile	Asp	Arg	Asn	Asn	Ala	Asn	Leu	Ile	180	185	190	
Leu	Ile	Gly	Ala	Ile	Ser	Ser	Ala	Leu	Leu	Ala	Ile	Ile	Phe	Asn	Ser	195	200	205	
Leu	Leu	Gln	Tyr	Leu	Glu	Lys	Ala	Ser	Leu	Arg	Arg	Ile	Met	Ile	Ser	210	215	220	
Phe	Gly	Ile	Thr	Leu	Leu	Ala	Leu	Leu	Ala	Ser	Tyr	Thr	Pro	Met	Ala	225	230	235	240
Leu	Ser	Gln	Phe	Ser	Lys	Gly	Lys	Asp	Thr	Val	Val	Ile	Ala	Gly	Lys	245	250	255	
Leu	Gly	Ala	Glu	Pro	Asp	Ile	Leu	Ile	Asn	Leu	Tyr	Lys	Glu	Leu	Ile	260	265	270	
Glu	Asp	Gln	Ser	Asp	Ile	Ser	Val	Glu	Leu	Lys	Ser	Asn	Phe	Gly	Lys	275	280	285	
Thr	Ser	Phe	Leu	Tyr	Glu	Ala	Leu	Lys	Ser	Gly	Asp	Ile	Asp	Met	Tyr	290	295	300	
Pro	Glu	Phe	Thr	Gly	Thr	Ile	Thr	Ser	Ser	Leu	Leu	Arg	Asp	Lys	Pro	305	310	315	320
Pro	Leu	Ser	Asn	Asp	Pro	Lys	Gln	Val	Tyr	Glu	Asp	Ala	Lys	Lys	Gly	325	330	335	
Ile	Ala	Lys	Gln	Asp	Lys	Leu	Thr	Leu	Leu	Lys	Pro	Phe	Ala	Tyr	Gln	340	345	350	
Asn	Thr	Tyr	Ala	Val	Ala	Met	Pro	Glu	Lys	Leu	Ala	Lys	Glu	Tyr	Gln	355	360	365	
Ile	Glu	Thr	Ile	Ser	Asp	Leu	Lys	Ala	His	Ala	Asp	Thr	Leu	Lys	Ala	370	375	380	
Gly	Phe	Thr	Leu	Glu	Phe	Lys	Asp	Arg	Ala	Asp	Gly	Tyr	Lys	Gly	Met	385	390	395	400
Gln	Ser	Gln	Tyr	Gly	Leu	Gln	Leu	Ser	Val	Ala	Thr	Met	Glu	Pro	Ala	405	410	415	
Leu	Arg	Tyr	Gln	Ala	Ile	Gln	Ser	Gly	Asp	Ile	Gln	Val	Thr	Asp	Ala	420	425	430	
Tyr	Ser	Thr	Asp	Ala	Glu	Ile	Thr	Lys	Tyr	His	Leu	Lys	Val	Leu	Lys	435	440	445	
Asp	Asp	Lys	Gln	Leu	Phe	Pro	Pro	Tyr	Gln	Gly	Ala	Pro	Leu	Met	Lys	450	455	460	
Thr	Ser	Leu	Leu	Thr	Lys	His	Pro	Glu	Leu	Lys	Gly	Ile	Leu	Asn	Gln	465	470	475	480
Leu	Ala	Gly	Lys	Ile	Thr	Glu	Lys	Glu	Met	Gln	Asp	Met	Asn	Tyr	Glu	485	490	495	
Val	Ser	Val	Lys	Gly	Ala	Asp	Ala	Asn	Lys	Val	Ala	Arg	Asp	Tyr	Leu	500	505	510	
Leu	Lys	Thr	Gly	Leu	Ile	Gln	Lys									515	520		

<210> SEQ ID NO 379

<211> LENGTH: 1149

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 379

atgataatta aaggagttac catgaaattt gaaaaaaaaac aagtcttcta tttagtcctt	60
acgtttatct tatgctatgg gatcctagca aactggcgaa atggaacggc tatcgtcacg	120
actattttaca aaacaagcct tccttttttt tatggagcag caggtgccta tattgttaat	180

attgtaatga	gcgcttacga	aaaggtatat	gtttatatct	ttaaagactg	gtcacatgtc	240
ttaaaagtaa	aacgggggat	ttgtttactg	ttagcgtatt	tgacattttt	tattttaatt	300
acttggatta	tttccattgt	cattccagac	ttaattacaa	gtatttagtac	tctaacaaaa	360
tttgatacta	taacgataca	agaagttggt	aacaatcttg	agcacaataa	actgtttagca	420
cgtactattc	agtatattgg	tggcgatggc	aaacttacag	agacgattgc	taactatagt	480
caacagttat	taaagcaatt	tcttactggt	ttgacaaaata	ttttaacatc	tgtcacgggt	540
attgcttctg	caattattaa	tctttttatt	agttttgttt	tttcggtata	cgtttttagca	600
agtaaagaag	atctttgtcg	tcagggaaat	actttagtag	atacttatac	tggttaagtac	660
gctaaacgca	ttcattactt	gtagagttg	ttgcatcagc	gttttcacgg	attttttggt	720
agtcagacct	tagaagctat	gatttttaggt	tcgctgactg	ctagtggcat	gtttatatta	780
agattaccat	ttgcagggac	tattggcggt	ttagtagctt	ttacagcatt	gattccagtt	840
ataggtgctt	caattggagc	agctattgga	tttatttttaa	ttatgactca	gtccatgtca	900
caggccatta	tttttatcat	ttttttaatt	attttgcagc	agattgaagg	caatttttatt	960
tatccgaaag	tagttggtgg	atcgattgga	ttaccggcta	tgtgggtatt	aatggcaatt	1020
acaataggcg	cttcttttaa	gggaatagtt	ggtatgatta	ttgcagttcc	tttagcagcg	1080
acactttatc	aagtgattaa	agataatatt	caaaaaagac	aagctattca	aaaaaaacaa	1140
gtttcctaa						1149

<210> SEQ ID NO 380

<211> LENGTH: 382

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 380

Met	Ile	Ile	Lys	Gly	Val	Thr	Met	Lys	Phe	Glu	Lys	Lys	Gln	Val	Phe
1				5					10					15	
Tyr	Leu	Val	Leu	Thr	Phe	Ile	Leu	Cys	Tyr	Gly	Ile	Leu	Ala	Asn	Trp
			20					25					30		
Arg	Asn	Gly	Thr	Ala	Ile	Val	Thr	Thr	Ile	Tyr	Lys	Thr	Ser	Leu	Pro
		35				40					45				
Phe	Phe	Tyr	Gly	Ala	Ala	Gly	Ala	Tyr	Ile	Val	Asn	Ile	Val	Met	Ser
50						55					60				
Ala	Tyr	Glu	Lys	Val	Tyr	Val	Tyr	Ile	Phe	Lys	Asp	Trp	Ser	His	Val
65				70						75				80	
Leu	Lys	Val	Lys	Arg	Gly	Ile	Cys	Leu	Leu	Ala	Tyr	Leu	Thr	Phe	
			85					90					95		
Phe	Ile	Leu	Ile	Thr	Trp	Ile	Ile	Ser	Ile	Val	Ile	Pro	Asp	Leu	Ile
		100						105					110		
Thr	Ser	Ile	Ser	Thr	Leu	Thr	Lys	Phe	Asp	Thr	Ile	Thr	Ile	Gln	Glu
		115					120						125		
Val	Val	Asn	Asn	Leu	Glu	His	Asn	Lys	Leu	Leu	Ala	Arg	Thr	Ile	Gln
		130				135					140				
Tyr	Ile	Gly	Gly	Asp	Gly	Lys	Leu	Thr	Glu	Thr	Ile	Ala	Asn	Tyr	Ser
145				150						155				160	
Gln	Gln	Leu	Leu	Lys	Gln	Phe	Leu	Thr	Val	Leu	Thr	Asn	Ile	Leu	Thr
			165						170				175		
Ser	Val	Thr	Val	Ile	Ala	Ser	Ala	Ile	Ile	Asn	Leu	Phe	Ile	Ser	Phe
		180						185					190		
Val	Phe	Ser	Leu	Tyr	Val	Leu	Ala	Ser	Lys	Glu	Asp	Leu	Cys	Arg	Gln
		195					200					205			
Gly	Asn	Thr	Leu	Val	Asp	Thr	Tyr	Thr	Gly	Lys	Tyr	Ala	Lys	Arg	Ile
	210					215					220				
His	Tyr	Leu	Leu	Glu	Leu	Leu	His	Gln	Arg	Phe	His	Gly	Phe	Phe	Val
225				230						235				240	
Ser	Gln	Thr	Leu	Glu	Ala	Met	Ile	Leu	Gly	Ser	Leu	Thr	Ala	Ser	Gly
			245						250					255	
Met	Phe	Ile	Leu	Arg	Leu	Pro	Phe	Ala	Gly	Thr	Ile	Gly	Val	Leu	Val
		260						265					270		

Ala	Phe	Thr	Ala	Leu	Ile	Pro	Val	Ile	Gly	Ala	Ser	Ile	Gly	Ala	Ala
		275					280					285			
Ile	Gly	Phe	Ile	Leu	Ile	Met	Thr	Gln	Ser	Met	Ser	Gln	Ala	Ile	Ile
	290					295					300				
Phe	Ile	Ile	Phe	Leu	Ile	Ile	Leu	Gln	Gln	Ile	Glu	Gly	Asn	Phe	Ile
305					310					315					320
Tyr	Pro	Lys	Val	Val	Gly	Gly	Ser	Ile	Gly	Leu	Pro	Ala	Met	Trp	Val
			325						330					335	
Leu	Met	Ala	Ile	Thr	Ile	Gly	Ala	Ser	Leu	Lys	Gly	Ile	Val	Gly	Met
		340						345					350		
Ile	Ile	Ala	Val	Pro	Leu	Ala	Ala	Thr	Leu	Tyr	Gln	Val	Ile	Lys	Asp
	355					360					365				
Asn	Ile	Gln	Lys	Arg	Gln	Ala	Ile	Gln	Lys	Lys	Gln	Val	Ser		
	370					375					380				

<210> SEQ ID NO 381

<211> LENGTH: 1074

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 381

atgcgtaa	ac	tttatt	cc	tt	tctagc	agga	gtttt	gggtg	ttatt	gttat	tttaaca	agt	60
ctttcttt	ca	tcttgc	agaa	aaaat	cgggt	tctgg	tagtc	aatcg	gataa	attagt	tatt	120	
tataact	ggg	gagatt	acat	tgatcc	agct	ttgct	caaaa	aattc	accaa	agaaac	gggc	180	
attgaag	tgc	agtatg	aaac	tttcg	attcc	aatga	agcca	tgtac	actaa	aatca	agcag	240	
ggcgga	acca	cttacg	acat	tgctgt	tcct	agtga	ttaca	ccattg	ataa	aatgat	caaa	300	
gaaaac	ctac	tcaata	agct	tgata	agtc	aaatt	agttg	gcatg	gataa	tatcg	ggaaa	360	
gaatttt	tag	ggaaa	agctt	tgaccc	acaa	aacga	ctatt	ctttg	cccta	tttct	ggggg	420	
accgtt	ggga	ttgttt	tataa	tgatca	atta	gttgata	agg	cgcct	atgca	ctggg	aagat	480	
ctgtgg	cgtc	cagaat	tataa	aaatag	tatt	atgctg	attg	atggg	gcgcg	tgaaat	gcta	540	
ggggtt	gggt	taaca	acttt	tggtta	tagt	gtgaat	tcta	aaaat	ctaga	gcagtt	gcag	600	
gcagcc	gaga	gaaaac	tgca	gcagtt	gacg	ccgaat	gtta	aagcc	attgt	agcag	atgag	660	
atgaaa	ggct	acatga	ttca	aggtg	acgct	gctatt	ggaa	ttac	cttttc	tggtg	aagcc	720	
agtga	gatgt	tagata	gtaa	cgaac	acctt	cactac	atcg	tg	cttcaga	aggtt	ctaac	780	
ctttg	gtttg	ataatt	tggt	actac	caaaa	accat	gaaac	acg	aaaaa	aga	agctt	atgct	840
ttttt	gaact	ttatca	atcg	tcctg	aaaaat	gctgc	gcaaa	atg	ctgcata	tattg	gttat	900	
gcgac	accaa	ataaaa	aagc	caagg	cctta	cttcc	agatg	agata	aaaaaa	tgatc	ctgct	960	
ttttat	ccaa	cagatg	acat	tatca	aaaaaa	ttgga	agttt	atgac	aat	ttt	aggtt	caaga	1020
tggtt	ggggg	tttata	atga	tttata	acctc	caattt	aaaaa	tgtat	cgcaa	ataa		1074	

<210> SEQ ID NO 382

<211> LENGTH: 357

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 382

Met	Arg	Lys	Leu	Tyr	Ser	Phe	Leu	Ala	Gly	Val	Leu	Gly	Val	Ile	Val
1			5						10					15	
Ile	Leu	Thr	Ser	Leu	Ser	Phe	Ile	Leu	Gln	Lys	Lys	Ser	Gly	Ser	Gly
		20						25					30		
Ser	Gln	Ser	Asp	Lys	Leu	Val	Ile	Tyr	Asn	Trp	Gly	Asp	Tyr	Ile	Asp
	35					40					45				
Pro	Ala	Leu	Leu	Lys	Lys	Phe	Thr	Lys	Glu	Thr	Gly	Ile	Glu	Val	Gln
	50					55					60				
Tyr	Glu	Thr	Phe	Asp	Ser	Asn	Glu	Ala	Met	Tyr	Thr	Lys	Ile	Lys	Gln
65				70					75					80	
Gly	Gly	Thr	Thr	Tyr	Asp	Ile	Ala	Val	Pro	Ser	Asp	Tyr	Thr	Ile	Asp
				85				90						95	
Lys	Met	Ile	Lys	Glu	Asn	Leu	Leu	Asn	Lys	Leu	Asp	Lys	Ser	Lys	Leu

				100					105					110			
Val	Gly	Met	Asp	Asn	Ile	Gly	Lys	Glu	Phe	Leu	Gly	Lys	Ser	Phe	Asp		
		115						120					125				
Pro	Gln	Asn	Asp	Tyr	Ser	Leu	Pro	Tyr	Phe	Trp	Gly	Thr	Val	Gly	Ile		
		130						135					140				
Val	Tyr	Asn	Asp	Gln	Leu	Val	Asp	Lys	Ala	Pro	Met	His	Trp	Glu	Asp		
145					150					155					160		
Leu	Trp	Arg	Pro	Glu	Tyr	Lys	Asn	Ser	Ile	Met	Leu	Ile	Asp	Gly	Ala		
				165					170						175		
Arg	Glu	Met	Leu	Gly	Val	Gly	Leu	Thr	Thr	Phe	Gly	Tyr	Ser	Val	Asn		
			180					185						190			
Ser	Lys	Asn	Leu	Glu	Gln	Leu	Gln	Ala	Ala	Glu	Arg	Lys	Leu	Gln	Gln		
		195						200					205				
Leu	Thr	Pro	Asn	Val	Lys	Ala	Ile	Val	Ala	Asp	Glu	Met	Lys	Gly	Tyr		
		210				215							220				
Met	Ile	Gln	Gly	Asp	Ala	Ala	Ile	Gly	Ile	Thr	Phe	Ser	Gly	Glu	Ala		
225				230						235					240		
Ser	Glu	Met	Leu	Asp	Ser	Asn	Glu	His	Leu	His	Tyr	Ile	Val	Pro	Ser		
				245					250						255		
Glu	Gly	Ser	Asn	Leu	Trp	Phe	Asp	Asn	Leu	Val	Leu	Pro	Lys	Thr	Met		
			260					265						270			
Lys	His	Glu	Lys	Glu	Ala	Tyr	Ala	Phe	Leu	Asn	Phe	Ile	Asn	Arg	Pro		
		275					280						285				
Glu	Asn	Ala	Ala	Gln	Asn	Ala	Ala	Tyr	Ile	Gly	Tyr	Ala	Thr	Pro	Asn		
		290				295						300					
Lys	Lys	Ala	Lys	Ala	Leu	Leu	Pro	Asp	Glu	Ile	Lys	Asn	Asp	Pro	Ala		
305					310					315					320		
Phe	Tyr	Pro	Thr	Asp	Asp	Ile	Ile	Lys	Lys	Leu	Glu	Val	Tyr	Asp	Asn		
				325					330						335		
Leu	Gly	Ser	Arg	Trp	Leu	Gly	Ile	Tyr	Asn	Asp	Leu	Tyr	Leu	Gln	Phe		
			340					345						350			
Lys	Met	Tyr	Arg	Lys													
				355													

<210> SEQ ID NO 383

<211> LENGTH: 777

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 383

atgaaaaaat	ttgccaatct	ttattttagcg	agtgtctttg	ttttactcta	cattcctatt	60
ttttatttga	ttttctattc	tttcaacaaa	ggtggggata	tgaatggttt	tacaggattt	120
acccttgagc	attaccaaac	catgtttgag	gatagtcgtc	tcattgacaat	cttactgcaa	180
acctttgttc	ttgcttttag	tagcgctcta	ctagcaacga	ttattgggat	ctttggagct	240
atctttatcc	accatgttag	aggtaagtac	caaaatgcc	tgctatcagc	caataatgtc	300
ttgatggtat	caccagatgt	catgattggg	gcttcctttt	taattctttt	tacatcattg	360
aagtttcagc	tgggcatgtc	ttcagtttta	ttaaagtcata	ttgctttttc	gattcctatt	420
gtggttttga	tgggtattgcc	gcgcttgaaa	gagatgaatc	aggacatggg	caacgccgct	480
tatgatttgg	gagctaatta	tttccaaatg	ctcaaagaag	tcattgctgcc	atactttaca	540
ccagggatta	ttgcagggtta	ttttatggcc	tttacctatt	ccttagatga	ttttgcagtg	600
actttctttt	tgactggaaa	tagtgttact	acattatctg	ttgagattta	ttcgcgggct	660
cgtcagggaa	tttccttgga	tatcaatgct	ttgtcaacca	tcgtttttctt	tttctccatc	720
ctcttagtga	tcggttatta	ttatatgtca	caggacaagg	aggaaaaaca	tgcgtaa	777

<210> SEQ ID NO 384

<211> LENGTH: 258

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 384

```

Met Lys Lys Phe Ala Asn Leu Tyr Leu Ala Ser Val Phe Val Leu Leu
1      5      10      15
Tyr Ile Pro Ile Phe Tyr Leu Ile Phe Tyr Ser Phe Asn Lys Gly Gly
20      25      30
Asp Met Asn Gly Phe Thr Gly Phe Thr Leu Glu His Tyr Gln Thr Met
35      40      45
Phe Glu Asp Ser Arg Leu Met Thr Ile Leu Leu Gln Thr Phe Val Leu
50      55      60
Ala Phe Ser Ser Ala Leu Leu Ala Thr Ile Ile Gly Ile Phe Gly Ala
65      70      75      80
Ile Phe Ile His His Val Arg Gly Lys Tyr Gln Asn Ala Met Leu Ser
85      90      95
Ala Asn Asn Val Leu Met Val Ser Pro Asp Val Met Ile Gly Ala Ser
100     105     110
Phe Leu Ile Leu Phe Thr Ser Leu Lys Phe Gln Leu Gly Met Ser Ser
115     120     125
Val Leu Leu Ser His Ile Ala Phe Ser Ile Pro Ile Val Val Leu Met
130     135     140
Val Leu Pro Arg Leu Lys Glu Met Asn Gln Asp Met Val Asn Ala Ala
145     150     155     160
Tyr Asp Leu Gly Ala Asn Tyr Phe Gln Met Leu Lys Glu Val Met Leu
165     170     175
Pro Tyr Phe Thr Pro Gly Ile Ile Ala Gly Tyr Phe Met Ala Phe Thr
180     185     190
Tyr Ser Leu Asp Asp Phe Ala Val Thr Phe Phe Leu Thr Gly Asn Ser
195     200     205
Val Thr Thr Leu Ser Val Glu Ile Tyr Ser Arg Ala Arg Gln Gly Ile
210     215     220
Ser Leu Asp Ile Asn Ala Leu Ser Thr Ile Val Phe Phe Phe Ser Ile
225     230     235     240
Leu Leu Val Ile Gly Tyr Tyr Tyr Met Ser Gln Asp Lys Glu Glu Lys
245     250     255
His Ala

```

<210> SEQ ID NO 385

<211> LENGTH: 816

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 385

```

atgccattga ggaggagcgt aatgaagaaa acctctagtc ttttttcgat tccttacttc      60
ttatggattc tcttttttgt tgtggcacca gtcactctct tgttttacaa gtcctttttt      120
gacatagaag ggcgcgtgac cttagccaat tatgaaacct ttttttagctc ttggacttat      180
ttgaggatga gtgtgaattc tattttatac gctgggatta tcacactcgt cacgctcttg      240
atttcatatc ctacggctct ctttttaacg cgcttaaagc acaagcagtt gtggcttatg      300
ctcattatct tgccaacctg ggtaaaattta ttgctaaagg cctatgcctt tatgggaatc      360
tttgggtcaac aaggagggat taacagcttt ttaaccttta tggggattgg cccgcagcaa      420
atccttttca cagatttctc cttcattttt gtagcctctt acattgagct cccttttatg      480
atgttaccga tttttaacgc tttggatgat attgaccata atgtcatcaa tgccagtcgc      540
gacctaggag ctagtgaatt tcaggccttc tcaaaaagta tttttccctt ttctttaaat      600
ggggttaggg cagggtgttca gtctgtcttt atcccaagtt tgagtctctt tatgttaacc      660
cgtttgattg gtggaaaccg ggtgattaca cttggtacag ccattgaaca acattttttg      720
accacccaaa actggggaat gggatcaacc attggtgtcg tcttgatttt gaccatgggt      780
gctattatgt ggctcacaaa ggagaaaagt aaatga      816

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<210> SEQ ID NO 386

<211> LENGTH: 271

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 386

```
Met Pro Leu Arg Arg Ser Val Met Lys Lys Thr Ser Ser Leu Phe Ser
1      5      10      15
Ile Pro Tyr Phe Leu Trp Ile Leu Phe Phe Val Val Ala Pro Val Thr
20      25      30
Leu Leu Phe Tyr Lys Ser Phe Phe Asp Ile Glu Gly Arg Val Thr Leu
35      40      45
Ala Asn Tyr Glu Thr Phe Phe Ser Ser Trp Thr Tyr Leu Arg Met Ser
50      55      60
Val Asn Ser Ile Leu Tyr Ala Gly Ile Ile Thr Leu Val Thr Leu Leu
65      70      75      80
Ile Ser Tyr Pro Thr Ala Leu Phe Leu Thr Arg Leu Lys His Lys Gln
85      90      95
Leu Trp Leu Met Leu Ile Ile Leu Pro Thr Trp Val Asn Leu Leu Leu
100     105     110
Lys Ala Tyr Ala Phe Met Gly Ile Phe Gly Gln Gln Gly Gly Ile Asn
115     120     125
Ser Phe Leu Thr Phe Met Gly Ile Gly Pro Gln Gln Ile Leu Phe Thr
130     135     140
Asp Phe Ser Phe Ile Phe Val Ala Ser Tyr Ile Glu Leu Pro Phe Met
145     150     155     160
Met Leu Pro Ile Phe Asn Ala Leu Asp Asp Ile Asp His Asn Val Ile
165     170     175
Asn Ala Ser Arg Asp Leu Gly Ala Ser Glu Phe Gln Ala Phe Ser Lys
180     185     190
Val Ile Phe Pro Leu Ser Leu Asn Gly Val Arg Ala Gly Val Gln Ser
195     200     205
Val Phe Ile Pro Ser Leu Ser Leu Phe Met Leu Thr Arg Leu Ile Gly
210     215     220
Gly Asn Arg Val Ile Thr Leu Gly Thr Ala Ile Glu Gln His Phe Leu
225     230     235     240
Thr Thr Gln Asn Trp Gly Met Gly Ser Thr Ile Gly Val Val Leu Ile
245     250     255
Leu Thr Met Val Ala Ile Met Trp Leu Thr Lys Glu Lys Ser Lys
260     265     270
```

<210> SEQ ID NO 387

<211> LENGTH: 963

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 387

```
atgaacaata gacataaacg gcgccaaaaa agaaaagcct tcactctcat taaccttata      60
ctattatttg cctgcattct tggtttgacc ctcattttct atttatatca agggctctaac      120
aaattcgggt tgtcagatgt ctctcgattt gtacctaaaa taagtctttt tcatcacaaa      180
aagacggcaa aaaaagaaac gacaaaactt aagaagactc atttcgattc ctcaaaatct      240
caaaaaaagg ccatttctaa attgacttgg accaagcaag aaacacctgt caagatccca      300
attttaatgt atcatgctat tcatgtaatg tcccctgaag agacggctaa tgctaatttg      360
attgtcaacc cagatctctt tgatcaacaa cttcaaaaaa tgaaagacga gggctactat      420
tttttgagtc ctgaagaggt ctaccgcgct ctttcaaaata atgaattgcc tgctaaaaaa      480
gttgatatggc taacatttga tgacagtatg attgatttct acaatgttgc ttaccaatc      540
ttaaaaaaat atgatgctaa agccaccaat aatgttatta caggactaac cgaaatggga      600
agcgctgcc aatcgactct taagcagatg aaagaaatga aacaagtcgg tatgtctttc      660
caagatcata cagtgaatca tcctgatcta gagcaggcta gtcctgatgt tcaaacaact      720
gaaatgaaag attcaaagga ctatcttgat aagcaattaa accaaaacac tattgccatt      780
gcttatccat ctggtagata taatgacact accttacaaa ttgcagctag acttaactat      840
```

aaattaggtg ttaccactaa cgaaggaata gctagcgcg	ctaattggact tctttctctt	900
aaccggattc gtatcctccc aaacatgagt cctgaaaatc	ttttacaaac aatggaacca	960
taa		963

<210> SEQ ID NO 388
 <211> LENGTH: 320
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 388

Met Asn Asn Arg His Lys Arg Arg Gln Lys Arg Lys Ala Phe Thr Leu	
1 5 10 15	
Ile Asn Leu Ile Leu Leu Phe Ala Cys Ile Leu Gly Leu Thr Leu Ile	
20 25 30	
Phe Tyr Leu Tyr Gln Gly Ser Asn Lys Phe Gly Leu Ser Asp Val Ser	
35 40 45	
Arg Phe Val Pro Lys Ile Ser Leu Phe His His Lys Lys Thr Ala Lys	
50 55 60	
Lys Glu Thr Thr Lys Leu Lys Lys Thr His Phe Asp Ser Ser Lys Ser	
65 70 75 80	
Gln Lys Lys Ala His Ser Lys Leu Thr Trp Thr Lys Gln Glu Thr Pro	
85 90 95	
Val Lys Ile Pro Ile Leu Met Tyr His Ala Ile His Val Met Ser Pro	
100 105 110	
Glu Glu Thr Ala Asn Ala Asn Leu Ile Val Asn Pro Asp Leu Phe Asp	
115 120 125	
Gln Gln Leu Gln Lys Met Lys Asp Glu Gly Tyr Tyr Phe Leu Ser Pro	
130 135 140	
Glu Glu Val Tyr Arg Ala Leu Ser Asn Asn Glu Leu Pro Ala Lys Lys	
145 150 155 160	
Val Val Trp Leu Thr Phe Asp Asp Ser Met Ile Asp Phe Tyr Asn Val	
165 170 175	
Ala Tyr Pro Ile Leu Lys Lys Tyr Asp Ala Lys Ala Thr Asn Asn Val	
180 185 190	
Ile Thr Gly Leu Thr Glu Met Gly Ser Ala Ala Asn Leu Thr Leu Lys	
195 200 205	
Gln Met Lys Glu Met Lys Gln Val Gly Met Ser Phe Gln Asp His Thr	
210 215 220	
Val Asn His Pro Asp Leu Glu Gln Ala Ser Pro Asp Val Gln Thr Thr	
225 230 235 240	
Glu Met Lys Asp Ser Lys Asp Tyr Leu Asp Lys Gln Leu Asn Gln Asn	
245 250 255	
Thr Ile Ala Ile Ala Tyr Pro Ser Gly Arg Tyr Asn Asp Thr Thr Leu	
260 265 270	
Gln Ile Ala Ala Arg Leu Asn Tyr Lys Leu Gly Val Thr Thr Asn Glu	
275 280 285	
Gly Ile Ala Ser Ala Ala Asn Gly Leu Leu Ser Leu Asn Arg Ile Arg	
290 295 300	
Ile Leu Pro Asn Met Ser Pro Glu Asn Leu Leu Gln Thr Met Glu Pro	
305 310 315 320	

<210> SEQ ID NO 389
 <211> LENGTH: 1356
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 389

gtgttattgt tacagggtac ttgctttatg agcttggtta agctactaaa ggtgtgtgcc	60
actatacttc ctccaaaatt tctgagaatt tttgttataa tagtaactat gaaagatata	120

atgataaaaa	ggtgggttat	cctttttttt	atgggtattaa	cttggttcagg	gtttggtaaa	180
acagttctcg	cagctgattt	tcaagtggga	gcagaacatg	cgattgtcgt	agaggcagac	240
tctgggagag	ttctgtatga	gaaagacgct	aagacgccag	atgctattgc	ctctttgacc	300
aaattggtga	cggcttatct	ggttttagat	aagggttaaat	caggccagct	gcaattatca	360
gatcaagtta	atctctcaga	ttatgccttc	gagttaacaa	aagataggtc	tttaagtaat	420
gtaccttttg	acaaaaaaac	ttattcagtt	caagacctgt	tgacagctac	tttggttagca	480
agctcaaata	gcgctgctat	tgcgttagcc	gaaaaagtgg	cgggctcaga	gcttcatttt	540
gtaaatcaaa	tgagagaaca	gctatctcat	tgggggatta	cttctggtaa	aatcctcaac	600
gcttcaggac	tgccgaatga	ggtgctaaa	gaccatcggt	atcctgggtt	tgcggttgaa	660
gaagagaata	tggttgagtgc	tcaggatggt	gccattgtga	cgatgcattt	actggaagat	720
tttcttgaga	tttttagagat	cactaaacaa	acagaagttg	attttgctgg	taattctatt	780
aaaagtttta	atcaactctt	accaggatat	gctaagggta	gagcaggagt	ggatgggcta	840
aagacaggaa	cgacagattt	ggcaggtcac	tgccttggtg	taacttctat	tgaaaaatggt	900
atgaggctga	ttaccgttat	tctaaatgct	gatggatctg	ataaaaacca	aaacacgcgg	960
tttgagcaag	caaatcgctt	gttggaacta	gtggctagaa	cttattgtcg	tcgtaagatt	1020
cttaaaaaag	gaagtcttgt	ctcggagcga	tcgctcccta	ttcaagatgg	ccaagtaaaa	1080
gaactaccga	tatctgttgc	cgaagatgta	accatcattt	tgcaacaggg	tgaacaagtt	1140
cccaaacctt	aacaatttat	gatatcagag	acttctttat	tagcaccgat	tactaaaggt	1200
gaagtgggtg	cttatattgac	gtctccaaga	ataacagatc	agtcagtga	gtattttaag	1260
gaacctaaag	gtattcctct	taaagctagc	caatctctaa	aaaaagcctc	tgacttacag	1320
ctgtggtggc	gagattttct	tgaaaaaaga	cgtaa			1356

<210> SEQ ID NO 390
 <211> LENGTH: 451
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 390

Met	Leu	Leu	Leu	Gln	Gly	Thr	Cys	Phe	Met	Ser	Leu	Phe	Lys	Leu	Leu
1			5					10					15		
Lys	Val	Cys	Ala	Thr	Ile	Leu	Pro	Ser	Lys	Phe	Leu	Arg	Ile	Phe	Val
		20					25					30			
Ile	Ile	Val	Thr	Met	Lys	Asp	Ile	Met	Ile	Lys	Arg	Trp	Val	Ile	Leu
		35				40						45			
Phe	Phe	Met	Val	Leu	Thr	Cys	Ser	Gly	Phe	Gly	Lys	Thr	Val	Leu	Ala
	50					55					60				
Ala	Asp	Phe	Gln	Val	Gly	Ala	Glu	His	Ala	Ile	Val	Val	Glu	Ala	Asp
65				70					75					80	
Ser	Gly	Arg	Val	Leu	Tyr	Glu	Lys	Asp	Ala	Lys	Thr	Pro	Asp	Ala	Ile
			85				90						95		
Ala	Ser	Leu	Thr	Lys	Leu	Val	Thr	Ala	Tyr	Leu	Val	Leu	Asp	Lys	Val
		100					105						110		
Lys	Ser	Gly	Gln	Leu	Gln	Leu	Ser	Asp	Gln	Val	Asn	Leu	Ser	Asp	Tyr
		115				120					125				
Ala	Phe	Glu	Leu	Thr	Lys	Asp	Arg	Ser	Leu	Ser	Asn	Val	Pro	Phe	Asp
	130					135					140				
Lys	Lys	Thr	Tyr	Ser	Val	Gln	Asp	Leu	Leu	Thr	Ala	Thr	Leu	Val	Ala
145				150					155					160	
Ser	Ser	Asn	Ser	Ala	Ala	Ile	Ala	Leu	Ala	Glu	Lys	Val	Ala	Gly	Ser
			165				170						175		
Glu	Leu	His	Phe	Val	Asn	Gln	Met	Arg	Glu	Gln	Leu	Ser	His	Trp	Gly
		180				185						190			
Ile	Thr	Ser	Gly	Lys	Ile	Leu	Asn	Ala	Ser	Gly	Leu	Pro	Asn	Glu	Val
	195					200						205			
Leu	Lys	Asp	His	Arg	Tyr	Pro	Gly	Ser	Ala	Leu	Glu	Glu	Glu	Asn	Met
	210				215						220				
Leu	Ser	Ala	Gln	Asp	Val	Ala	Ile	Val	Thr	Met	His	Leu	Leu	Glu	Asp
225					230					235					240

Phe	Pro	Glu	Ile	Leu	Glu	Ile	Thr	Lys	Gln	Thr	Glu	Val	Asp	Phe	Ala	
				245					250					255		
Gly	Asn	Ser	Ile	Lys	Ser	Phe	Asn	Gln	Leu	Leu	Pro	Gly	Met	Ala	Lys	
			260					265					270			
Gly	Arg	Ala	Gly	Val	Asp	Gly	Leu	Lys	Thr	Gly	Thr	Thr	Asp	Leu	Ala	
		275					280					285				
Gly	His	Cys	Leu	Val	Val	Thr	Ser	Ile	Glu	Asn	Gly	Met	Arg	Leu	Ile	
	290					295					300					
Thr	Val	Ile	Leu	Asn	Ala	Asp	Gly	Ser	Asp	Lys	Asn	Gln	Asn	Thr	Arg	
305					310					315					320	
Phe	Glu	Gln	Ala	Asn	Arg	Leu	Leu	Asp	Tyr	Val	Ala	Arg	Thr	Tyr	Cys	
				325					330					335		
Arg	Arg	Lys	Ile	Leu	Lys	Lys	Gly	Ser	Leu	Val	Ser	Glu	Arg	Ser	Leu	
		340						345					350			
Pro	Ile	Gln	Asp	Gly	Gln	Val	Lys	Glu	Leu	Pro	Ile	Ser	Val	Ala	Glu	
		355					360					365				
Asp	Val	Thr	Ile	Ile	Leu	Gln	Gln	Gly	Glu	Gln	Val	Pro	Lys	Pro	Lys	
	370					375					380					
Gln	Phe	Met	Ile	Ser	Glu	Thr	Ser	Leu	Leu	Ala	Pro	Ile	Thr	Lys	Gly	
385					390					395					400	
Glu	Val	Val	Ala	Tyr	Leu	Thr	Ser	Pro	Arg	Ile	Thr	Asp	Gln	Ser	Val	
				405					410				415			
Arg	Tyr	Leu	Lys	Glu	Pro	Lys	Arg	Ile	Pro	Leu	Lys	Ala	Ser	Gln	Ser	
		420						425				430				
Leu	Lys	Lys	Ala	Ser	Asp	Leu	Gln	Leu	Trp	Trp	Arg	Asp	Phe	Leu	Glu	
		435					440					445				
Lys	Arg	Arg														
	450															

<210> SEQ ID NO 391

<211> LENGTH: 747

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 391

ttgttttgct	tactatacac	taaacgctca	gcaatatata	gaatgggagt	aactaatatg	60
ttgaaaatac	aaaatctaaa	aaaatcttat	ggtaagagaa	ccatattgaa	taatgtcaat	120
atgaatatcc	ctaaggga	agtgtatgct	ttaatcggtc	caaatgggtc	tggaaaatca	180
actattatga	aaattttgac	aggcttagtt	agtaagacaa	gtggttctat	tatttttgaa	240
ggtagagaat	ggtcacgtcg	ggatctgcga	aaaaatcgga	gtattattga	agaaccacca	300
ctttataaaa	atttgagtgc	ttacgataat	atgaaggtag	ttacaacaat	gcttggtgtt	360
tcagaaagca	ctatacttcc	attattaaat	aaagttggtc	taggaaatat	tgacaagaga	420
ccagtaaaac	aattttctct	tggaatgaag	caacggttag	gtatagctat	ctctttaata	480
aattcaccta	aactacttat	attagacgaa	cctactaatg	gcttggaacc	aattggaatt	540
caagaattaa	gggaaattat	agagtcattt	aaatcagaag	gaatgacaat	tatgatttca	600
agccatatac	tgtcagaagt	tgaacatcta	gctgatttta	ttggatttat	ctatgaagga	660
aagattattc	tggaaaaaga	atatgacggc	tctgagaatc	ttgaagagtt	attcaataat	720
caaattttat	ttgaaaagag	gaggtag				747

<210> SEQ ID NO 392

<211> LENGTH: 248

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 392

Met	Phe	Cys	Leu	Leu	Tyr	Thr	Lys	Arg	Ser	Ala	Ile	Tyr	Arg	Met	Gly
1			5				10					15			
Val	Thr	Asn	Met	Leu	Lys	Ile	Gln	Asn	Leu	Lys	Lys	Ser	Tyr	Gly	Lys
		20					25					30			

Arg	Thr	Ile	Leu	Asn	Asn	Val	Asn	Met	Asn	Ile	Pro	Lys	Gly	Lys	Val
	35						40					45			
Tyr	Ala	Leu	Ile	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Ile	Met	Lys
	50					55					60				
Ile	Leu	Thr	Gly	Leu	Val	Ser	Lys	Thr	Ser	Gly	Ser	Ile	Ile	Phe	Glu
65					70					75					80
Gly	Arg	Glu	Trp	Ser	Arg	Arg	Asp	Leu	Arg	Lys	Ile	Gly	Ser	Ile	Ile
				85					90					95	
Glu	Glu	Pro	Pro	Leu	Tyr	Lys	Asn	Leu	Ser	Ala	Tyr	Asp	Asn	Met	Lys
		100						105					110		
Val	Val	Thr	Met	Leu	Gly	Val	Ser	Glu	Ser	Thr	Ile	Leu	Pro	Leu	
	115					120					125				
Leu	Asn	Lys	Val	Gly	Leu	Gly	Asn	Ile	Asp	Lys	Arg	Pro	Val	Lys	Gln
	130					135					140				
Phe	Ser	Leu	Gly	Met	Lys	Gln	Arg	Leu	Gly	Ile	Ala	Ile	Ser	Leu	Ile
145					150					155					160
Asn	Ser	Pro	Lys	Leu	Leu	Ile	Leu	Asp	Glu	Pro	Thr	Asn	Gly	Leu	Asp
			165						170					175	
Pro	Ile	Gly	Ile	Gln	Glu	Leu	Arg	Glu	Ile	Ile	Glu	Ser	Phe	Lys	Ser
		180						185					190		
Glu	Gly	Met	Thr	Ile	Met	Ile	Ser	Ser	His	Ile	Leu	Ser	Glu	Val	Glu
	195						200				205				
His	Leu	Ala	Asp	Phe	Ile	Gly	Phe	Ile	Tyr	Glu	Gly	Lys	Ile	Ile	Leu
	210					215					220				
Glu	Lys	Glu	Tyr	Asp	Gly	Ser	Glu	Asn	Leu	Glu	Glu	Leu	Phe	Asn	Asn
225					230					235					240
Gln	Ile	Leu	Phe	Glu	Lys	Arg	Arg								
				245											

<210> SEQ ID NO 393

<211> LENGTH: 1362

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 393

ttggttataa	atgggatgtt	taaaaaatat	tcaataaaaa	atcgtgtttg	gcgcgccgtc	60
gttgaaattg	tctttggagt	ttgtatcact	gttttaaatga	ttgcgataat	atcgctttct	120
ttttcaaagt	taaatatagt	gacatctcat	aatgtgggag	aagaatttta	tattaaagat	180
aaacagtcaa	tcaaacagtt	gaacaattat	atgaagacat	tgggattaga	ttatgttggt	240
tttgatagaa	aaacagataa	agctatggaa	ggaaaaatatt	tatctaaaga	attttcttta	300
tttaacgaag	ttgcagaaga	aaaaaataat	ctgactttta	attctgtaca	ttatgattta	360
tatactaata	tcaattataa	tattgttata	agatataatg	agataccgga	gttctctaac	420
cattacctta	gaaatgtttc	atataacatg	ttgacatttt	atattctggg	aataggaacg	480
agtatcagca	ttgtagtgtc	tttaacacgg	tttgtaaaaag	aaatttcttt	gaatttcaag	540
gaaatcaaga	agttagcaaa	taaaatgggg	atagaagtcc	tttctgaaaa	tgaaaattat	600
tctaaaataa	tcgagtttga	tgatatactt	agaactttac	atattaaagg	tgataatttg	660
aaaagtttga	ttgagcgaga	aatatttgaa	aagcaagatc	tatcctttca	aattgcagca	720
ctttcgcgat	atattaaaaac	acctttaacg	gttttaaaaag	gaaatcttga	gttattagaa	780
ttgactactt	taaataaaaa	tcaggaaggt	tatattgtat	ctatgaacaa	tagtatttct	840
gtttttgaag	gctattttcaa	ttctttaata	tcttatacac	gcatgctttc	agaggataga	900
tcagtgaaac	taatttttagt	tgaggagcta	ttaagtga	tacattttga	agtcgatgac	960
ttattgaata	tcaataatat	tgaattttct	atttgaata	gacttattat	cacttctttt	1020
tatggagatg	aggaaaatct	gataagagct	ctttctaacc	ttttagttaa	tgcaataaga	1080
tttatgcccg	tattagataa	aaaaatcgaa	gttatactgt	ctgagtcagg	agagcaaatt	1140
cattttgaaa	tatggaataa	tggtgagcgt	ttcagtgata	gtacactgaa	aaagggagat	1200
aaattatttt	acacggaaga	ttatagcaga	ggtaacaaac	attatggaat	cggtttggca	1260
tttgttaaaag	gcgttgctat	caaacacggt	gggaatcttc	aattgaataa	tccagctaga	1320
ggaggtgcta	gcgccataat	ctcgataaaa	aagaaaattt	aa		1362

<210> SEQ ID NO 394
 <211> LENGTH: 453
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 394

Met	Val	Ile	Asn	Gly	Met	Phe	Lys	Lys	Tyr	Ser	Ile	Lys	Asn	Arg	Val
1			5						10					15	
Trp	Arg	Ala	Val	Val	Glu	Ile	Val	Phe	Gly	Val	Cys	Ile	Thr	Val	Leu
			20					25					30		
Met	Ile	Ala	Ile	Ile	Ser	Leu	Ser	Phe	Ser	Lys	Leu	Asn	Ile	Val	Thr
		35					40					45			
Ser	His	Asn	Val	Gly	Glu	Glu	Phe	Tyr	Ile	Lys	Asp	Lys	Gln	Ser	Ile
	50					55					60				
Lys	Gln	Leu	Asn	Asn	Tyr	Met	Lys	Thr	Leu	Gly	Leu	Asp	Tyr	Val	Val
65					70					75					80
Phe	Asp	Arg	Lys	Thr	Asp	Lys	Ala	Met	Glu	Gly	Lys	Tyr	Leu	Ser	Lys
				85						90					95
Glu	Phe	Ser	Leu	Phe	Asn	Glu	Val	Ala	Glu	Glu	Lys	Asn	Asn	Leu	Thr
			100					105					110		
Phe	Asn	Ser	Val	His	Tyr	Asp	Leu	Tyr	Thr	Asn	Ile	Asn	Tyr	Asn	Ile
		115					120					125			
Val	Ile	Arg	Tyr	Asn	Glu	Ile	Pro	Glu	Phe	Ser	Asn	His	Tyr	Leu	Arg
	130					135					140				
Asn	Val	Ser	Tyr	Asn	Met	Leu	Thr	Phe	Tyr	Ile	Leu	Gly	Ile	Gly	Thr
145				150						155					160
Ser	Ile	Ser	Ile	Val	Val	Ala	Leu	Thr	Arg	Phe	Val	Lys	Glu	Ile	Ser
				165					170						175
Leu	Asn	Phe	Lys	Glu	Ile	Lys	Lys	Leu	Ala	Asn	Lys	Met	Gly	Ile	Glu
		180					185						190		
Val	Leu	Ser	Glu	Asn	Glu	Asn	Tyr	Ser	Lys	Ile	Ile	Glu	Phe	Asp	Asp
		195					200					205			
Ile	Leu	Arg	Thr	Leu	His	Ile	Lys	Gly	Asp	Asn	Leu	Lys	Ser	Leu	Ile
	210					215					220				
Glu	Arg	Glu	Ile	Leu	Glu	Lys	Gln	Asp	Leu	Ser	Phe	Gln	Ile	Ala	Ala
225				230						235					240
Leu	Ser	His	Asp	Ile	Lys	Thr	Pro	Leu	Thr	Val	Leu	Lys	Gly	Asn	Leu
				245					250					255	
Glu	Leu	Leu	Glu	Leu	Thr	Thr	Leu	Asn	Lys	Asn	Gln	Glu	Gly	Tyr	Ile
			260				265					270			
Val	Ser	Met	Asn	Asn	Ser	Ile	Ser	Val	Phe	Glu	Gly	Tyr	Phe	Asn	Ser
		275				280						285			
Leu	Ile	Ser	Tyr	Thr	Arg	Met	Leu	Ser	Glu	Asp	Arg	Ser	Val	Lys	Leu
	290					295					300				
Ile	Leu	Val	Glu	Glu	Leu	Leu	Ser	Glu	Leu	His	Phe	Glu	Val	Asp	Asp
305					310					315					320
Leu	Leu	Asn	Ile	Asn	Asn	Ile	Glu	Phe	Ser	Ile	Cys	Asn	Arg	Leu	Ile
				325					330					335	
Ile	Thr	Ser	Phe	Tyr	Gly	Asp	Glu	Glu	Asn	Leu	Ile	Arg	Ala	Leu	Ser
			340					345					350		
Asn	Leu	Leu	Val	Asn	Ala	Ile	Arg	Phe	Met	Pro	Val	Leu	Asp	Lys	Lys
		355					360					365			
Ile	Glu	Val	Ile	Leu	Ser	Glu	Ser	Gly	Glu	Gln	Ile	His	Phe	Glu	Ile
	370					375					380				
Trp	Asn	Asn	Gly	Glu	Arg	Phe	Ser	Asp	Ser	Thr	Leu	Lys	Lys	Gly	Asp
385					390					395					400
Lys	Leu	Phe	Tyr	Thr	Glu	Asp	Tyr	Ser	Arg	Gly	Asn	Lys	His	Tyr	Gly

				405					410					415			
Ile	Gly	Leu	Ala	Phe	Val	Lys	Gly	Val	Ala	Ile	Lys	His	Gly	Gly	Asn		
			420					425					430				
Leu	Gln	Leu	Asn	Asn	Pro	Ala	Arg	Gly	Gly	Ala	Ser	Ala	Ile	Ile	Ser		
		435					440					445					
Ile	Lys	Lys	Lys	Ile													
	450																

<210> SEQ ID NO 395

<211> LENGTH: 687

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 395

atgtataaga	ttttagccat	agatgatgat	aaagaaattc	tgaagcttat	gaagactgct	60
ttggagattg	aaaattatca	tggtataacc	tgtaagaga	tagaattacc	aatagttttt	120
gatgatttta	aaggatatga	tttgatctta	ttggatatca	tgatgcctaa	tataagtggg	180
actgagtttt	gttataaaat	tcgggaagaa	gttcattctc	caattatttt	tgtttagcgt	240
ttagatggcg	ataatgaaat	tgtccaagct	ttaaataatag	ggggagacga	ttttattgtg	300
aaaccattta	gcttaaaaca	attcgtagct	aaagttaact	ctcatttgaa	gagagaagag	360
agagcaaaga	taaagaatga	ggctgaggag	agagtgaagc	gtagttttcc	acctatagaa	420
atctatctag	aggaacgtat	gttatatatt	gataaacagc	cgttattcct	gacttataga	480
gagtacgaaa	ttttagaatt	actgtcacgt	catccgtata	aagttttcac	aaaagaagag	540
atatatgaac	aagtatatag	cgatgaagct	tcagcattgt	ttcattctat	ttcagaatat	600
atctatcaga	ttagaatgaa	attttcaagt	tttggaatta	atccaataaa	aactattcgc	660
gggattgggt	ataaatggga	tggtttaa				687

<210> SEQ ID NO 396

<211> LENGTH: 228

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 396

Met	Tyr	Lys	Ile	Leu	Ala	Ile	Asp	Asp	Asp	Lys	Glu	Ile	Leu	Lys	Leu
1				5					10					15	
Met	Lys	Thr	Ala	Leu	Glu	Ile	Glu	Asn	Tyr	His	Val	Ile	Thr	Cys	Gln
			20					25					30		
Glu	Ile	Glu	Leu	Pro	Ile	Val	Phe	Asp	Asp	Phe	Lys	Gly	Tyr	Asp	Leu
		35					40					45			
Ile	Leu	Leu	Asp	Ile	Met	Met	Pro	Asn	Ile	Ser	Gly	Thr	Glu	Phe	Cys
	50				55					60					
Tyr	Lys	Ile	Arg	Glu	Glu	Val	His	Ser	Pro	Ile	Ile	Phe	Val	Ser	Ala
65				70					75					80	
Leu	Asp	Gly	Asp	Asn	Glu	Ile	Val	Gln	Ala	Leu	Asn	Ile	Gly	Gly	Asp
			85					90					95		
Asp	Phe	Ile	Val	Lys	Pro	Phe	Ser	Leu	Lys	Gln	Phe	Val	Ala	Lys	Val
			100					105					110		
Asn	Ser	His	Leu	Lys	Arg	Glu	Glu	Arg	Ala	Lys	Ile	Lys	Asn	Glu	Ala
		115				120						125			
Glu	Glu	Arg	Val	Lys	Arg	Ser	Phe	Pro	Pro	Ile	Glu	Ile	Tyr	Leu	Glu
	130					135					140				
Glu	Arg	Met	Leu	Tyr	Ile	Asp	Lys	Gln	Pro	Leu	Phe	Leu	Thr	Tyr	Arg
145				150					155					160	
Glu	Tyr	Glu	Ile	Leu	Glu	Leu	Leu	Ser	Arg	His	Pro	Tyr	Lys	Val	Phe
			165					170					175		
Thr	Lys	Glu	Glu	Ile	Tyr	Glu	Gln	Val	Tyr	Ser	Asp	Glu	Ala	Ser	Ala
			180					185					190		
Leu	Phe	His	Ser	Ile	Ser	Glu	Tyr	Ile	Tyr	Gln	Ile	Arg	Met	Lys	Phe
		195				200						205			

Ser Ser Phe Gly Ile Asn Pro Ile Lys Thr Ile Arg Gly Ile Gly Tyr
 210 215 220
 Lys Trp Asp Val
 225

<210> SEQ ID NO 397
 <211> LENGTH: 399
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 397
 ttgctatctg cttcttattt aagagtgatt gttgctccag cttcttcaag tttagctttg 60
 atttcttcag cttctgcagc agcaacgcct tctttaacgt tagcaggtgc tccatcaaca 120
 agaccttttag cttctttaag accaagacct gtgatttcac gaacagcttt gataacgcca 180
 acttttttgt cgccagcaga tgtcaattca acgtcgaatg aatcttttagc agcttcttca 240
 gcaccaccag cagctgcagc agctacagga gcagctgcag ttacaccaaa ttcttcttcg 300
 atagctttta caagatcggt aagctcaagg attgaagctt ctttaatttc agcaataatg 360
 ttttcaatgt tcaatgccat tgtgatttcc tccaaataa 399

<210> SEQ ID NO 398
 <211> LENGTH: 132
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 398
 Met Leu Ser Ala Ser Tyr Leu Arg Val Ile Val Ala Pro Ala Ser Ser
 1 5 10 15
 Ser Leu Ala Leu Ile Ser Ser Ala Ser Ala Ala Thr Pro Ser Leu
 20 25 30
 Thr Leu Ala Gly Ala Pro Ser Thr Arg Pro Leu Ala Ser Leu Arg Pro
 35 40 45
 Arg Pro Val Ile Ser Arg Thr Ala Leu Ile Thr Pro Thr Phe Leu Ser
 50 55 60
 Pro Ala Asp Val Asn Ser Thr Ser Asn Glu Ser Leu Ala Ala Ser Ser
 65 70 75 80
 Ala Pro Pro Ala Ala Ala Ala Thr Gly Ala Ala Ala Val Thr Pro
 85 90 95
 Asn Ser Ser Ser Ile Ala Phe Thr Arg Ser Leu Ser Ser Arg Ile Glu
 100 105 110
 Ala Ser Leu Ile Ser Ala Ile Met Phe Ser Met Phe Asn Ala Ile Val
 115 120 125
 Ile Ser Ser Lys
 130

<210> SEQ ID NO 399
 <211> LENGTH: 1650
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 399
 atgcgaggtg aacaggtgga agaacatttt aaaaaacaat tacaagatga tatttctaga 60
 catttttcgt accaatcggt aatgttatca ttgttgctaa ttggtctttt tattattttt 120
 tcattagcgc cacaacaatt aggcctctat cgtgatatca atgccactgc aaccctgtat 180
 caccgtttga ttagcaaaaca agaagccttg ctggatgact tagggaaaaa tagcttacta 240
 ccttttttaa ataaaaacct cagcactgct gatttaagca agcactattt tcatttgcgc 300
 catagcagcc aaacgtcacc agaactttta ctattttcac ctagtcaaga ccttttattt 360
 gctagtaacc cacatttagg aaatgttttt agtaaactctg tttatattca agaagtcttg 420
 agagcaactc atttctccaaa aaccttggtt aaagatgcta tggatagtga agatgggtcac 480
 tacttgatga tcattatgcc aatgatagat caaaaccaac taaagggata tgctttttta 540
 gtgatgagtg gcaaagattt tcttcatcct acaaaaaacat tgacgtcaga gttgggtcatt 600

gctgataagc	tggacaatac	gtttacgttt	tccaatcgtg	agtttatagc	atctagtcta	660
gataagatca	atagccagta	tttacaccat	tattttgttt	ttcaagataa	tcgagccttt	720
atcacaagaa	agggtgcctt	acaaggaggt	ctttggcttt	acatgtatag	gcccttgatt	780
ccaatgggat	cgggtgatgtt	attttcactt	atttcacag	ctgttatctt	tgtgattttg	840
caacgtaaat	caagtgggtt	agctaaccga	attgcagcta	aaaattcaag	agcaatcaat	900
caaatgggta	gagatatgag	tgcgatctct	cggcaagaaa	aaagacgtat	tgaccttgag	960
agtcaagatg	aatttcaata	tttatctgat	caaatcaatc	aaatggtaga	gcgattgcaa	1020
cagttacatg	ataaaacgtt	agattttggaa	actcaaaaaat	tattattttga	aaaacggatg	1080
ttagaagctc	aattcaatcc	gcatttcctc	tacaatacgc	tagaaaccat	tttgattacg	1140
agccattatg	attctgccct	aacagaaaaa	attgttatcc	aattgacaaa	attgttgcg	1200
tatagtctca	cggattctag	caaacctgtc	ttgctcaaaag	atgatttaag	tgcatcgag	1260
tcttattttag	tgattaatca	ggtgcggttt	gaagaattgc	aatatagcat	taacctatcc	1320
ccagaccttg	atagtcttga	agtgccataa	ttgttcttgt	tacctttgat	agaaaaatgcc	1380
atcaaatatg	gcttgaaaaga	acgacacgat	gtcaagatta	acattgcttg	ttattatcaa	1440
gatgaccaca	ttattttttc	tgtgagagat	aatggttcgg	gaattgatgc	tcatcaccaa	1500
aaagtgattc	gagagcaatt	ggaagctgga	gagtcacacc	atgggttaat	taactcttat	1560
cgtcggctta	agtatcattt	ttcagaagta	tccttggttt	ttgatcaagg	tgataaacag	1620
tttaatgtta	gttaccatgt	taaggagtag				1650

<210> SEQ ID NO 400

<211> LENGTH: 549

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 400

Met	Arg	Gly	Glu	Gln	Val	Glu	Glu	His	Phe	Lys	Lys	Gln	Leu	Gln	Asp
1			5						10					15	
Asp	Ile	Ser	Arg	His	Phe	Ser	Tyr	Gln	Ser	Leu	Met	Leu	Ser	Leu	Leu
			20					25					30		
Leu	Ile	Gly	Leu	Phe	Ile	Ile	Phe	Ser	Leu	Ala	Pro	Gln	Gln	Leu	Gly
		35					40					45			
Leu	Tyr	Arg	Asp	Ile	Asn	Ala	Thr	Ala	Thr	Arg	Tyr	His	Arg	Leu	Ile
	50				55						60				
Ser	Lys	Gln	Glu	Ala	Leu	Leu	Asp	Asp	Leu	Gly	Lys	Asn	Ser	Leu	Leu
65					70					75				80	
Pro	Phe	Leu	Asn	Lys	Asn	Leu	Ser	Thr	Ala	Asp	Leu	Ser	Lys	His	Tyr
			85						90					95	
Phe	His	Leu	Arg	His	Ser	Ser	Gln	Thr	Ser	Pro	Glu	Leu	Leu	Leu	Phe
			100						105					110	
Ser	Pro	Ser	Gln	Asp	Leu	Leu	Phe	Ala	Ser	Asn	Pro	His	Leu	Gly	Asn
			115					120					125		
Val	Phe	Ser	Lys	Ser	Val	Tyr	Ile	Gln	Glu	Val	Leu	Arg	Ala	Thr	His
	130					135					140				
Ser	Pro	Lys	Thr	Leu	Phe	Lys	Asp	Ala	Met	Asp	Ser	Glu	Asp	Gly	His
145					150					155					160
Tyr	Leu	Met	Ile	Ile	Met	Pro	Met	Ile	Asp	Gln	Asn	Gln	Leu	Lys	Gly
			165						170					175	
Tyr	Ala	Phe	Leu	Val	Met	Ser	Gly	Lys	Asp	Phe	Leu	His	Pro	Thr	Lys
			180						185					190	
Thr	Leu	Thr	Ser	Glu	Leu	Val	Ile	Ala	Asp	Lys	Leu	Asp	Asn	Thr	Phe
		195						200						205	
Thr	Phe	Ser	Asn	Arg	Glu	Phe	Ile	Ala	Ser	Ser	Leu	Asp	Lys	Ile	Asn
	210					215						220			
Ser	Gln	Tyr	Leu	His	His	Tyr	Phe	Val	Phe	Gln	Asp	Asn	Arg	Ala	Phe
225					230					235					240
Ile	Thr	Arg	Lys	Val	Ala	Leu	Gln	Gly	Gly	Leu	Trp	Leu	Tyr	Met	Tyr
			245						250					255	
Arg	Pro	Leu	Ile	Pro	Met	Val	Ser	Val	Met	Leu	Phe	Ser	Leu	Ile	Ser

	260		265		270										
Ser	Ala	Val	Ile	Phe	Val	Ile	Leu	Gln	Arg	Lys	Ser	Ser	Gly	Leu	Ala
	275		280		285										
Asn	Arg	Ile	Ala	Ala	Lys	Asn	Ser	Arg	Ala	Ile	Asn	Gln	Met	Val	Arg
	290		295		300										
Asp	Met	Ser	Ala	Ile	Ser	Arg	Gln	Glu	Lys	Arg	Arg	Ile	Asp	Leu	Glu
305			310		315				320						
Ser	Gln	Asp	Glu	Phe	Gln	Tyr	Leu	Ser	Asp	Gln	Ile	Asn	Gln	Met	Val
	325		330		335										
Glu	Arg	Leu	Gln	Gln	Leu	His	Asp	Lys	Thr	Leu	Asp	Leu	Glu	Thr	Gln
	340		345		350										
Lys	Leu	Leu	Phe	Glu	Lys	Arg	Met	Leu	Glu	Ala	Gln	Phe	Asn	Pro	His
	355		360		365										
Phe	Leu	Tyr	Asn	Thr	Leu	Glu	Thr	Ile	Leu	Ile	Thr	Ser	His	Tyr	Asp
370			375		380										
Ser	Ala	Leu	Thr	Glu	Lys	Ile	Val	Ile	Gln	Leu	Thr	Lys	Leu	Leu	Arg
385			390		395				400						
Tyr	Ser	Leu	Thr	Asp	Ser	Ser	Lys	Pro	Val	Leu	Leu	Lys	Asp	Asp	Leu
	405		410		415										
Ser	Val	Ile	Glu	Ser	Tyr	Leu	Val	Ile	Asn	Gln	Val	Arg	Phe	Glu	Glu
	420		425		430										
Leu	Gln	Tyr	Ser	Ile	Asn	Leu	Ser	Pro	Asp	Leu	Asp	Ser	Leu	Glu	Val
	435		440		445										
Pro	Lys	Leu	Phe	Leu	Leu	Pro	Leu	Ile	Glu	Asn	Ala	Ile	Lys	Tyr	Gly
450			455		460										
Leu	Lys	Glu	Arg	His	Asp	Val	Lys	Ile	Asn	Ile	Ala	Cys	Tyr	Tyr	Gln
465			470		475				480						
Asp	Asp	His	Ile	Ile	Phe	Ser	Val	Arg	Asp	Asn	Gly	Ser	Gly	Ile	Asp
	485		490		495										
Ala	His	His	Gln	Lys	Val	Ile	Arg	Glu	Gln	Leu	Glu	Ala	Gly	Glu	Ser
	500		505		510										
His	His	Gly	Leu	Ile	Asn	Ser	Tyr	Arg	Arg	Leu	Lys	Tyr	His	Phe	Ser
	515		520		525										
Glu	Val	Ser	Leu	Val	Phe	Asp	Gln	Gly	Asp	Lys	Gln	Phe	Asn	Val	Ser
530			535		540										
Tyr	His	Val	Lys	Glu											
545															

<210> SEQ ID NO 401

<211> LENGTH: 1020

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 401

atgtcaactc	acttaagaaa	acttccaggg	ctgttacttt	gcttattggt	agctcttcca	60
gcttggtggt	tagggcgctt	atttcccatt	attggagcac	ctgtttttgc	tattctttta	120
ggaatggtgt	tagccttggt	ttatgaacat	cgtgacaaga	ctaaagaggg	aattagtttt	180
acatccaagt	atattttaca	aacagcagtg	gttttgcttg	gttttggtt	aaacctaacc	240
caagttatgg	cagtgggcat	gcagtcttta	ccgattatca	tttcaactat	tgcgacagct	300
cttttggtag	cttatggctt	acagaaatgg	ctgcgcttag	atgtcaatac	agccaccttg	360
gtaggtgtag	gatcttccat	ttgtgggggg	tctgctggtg	cagcgacagc	tcctgtcatt	420
aaggcaaagg	atgacgaggt	tgctaaggca	atttcagtca	tttttctctt	taatatgtta	480
gcagctttgc	tatttccaag	tttaggacaa	ttactaggct	tatctaata	aggttttgct	540
atttttgccg	ggacagctgt	taacgacact	tcttccgtga	ctgcaacggc	cacggcctgg	600
gatgcccttc	accattccaa	tacactagat	ggagcaacca	ttgttaaatt	gactcgcacc	660
ttggctattc	tcccaattac	tttaggttta	tccctttacc	gagcgaaaaa	agagcacgac	720
atcgttacag	aagaaaactt	tagccttagg	aagtcattcc	ctcgtttcat	cctcttcttt	780
ttattagctt	ctctcatcac	aacattgatg	accagtttgg	gagtttctgc	cgatagtttc	840


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cattacctaa aaaccttatc aaaattcttt atcgtgatgg ctatggcagc gattgggtta 900
aacacaaacc tggttaaact gattaagacg ggcggtcagg ctatcctttt aggagctatt 960
tgctgggtag ctatcaccct tgtcagttta gccatgcaat taagtttggg catttggttaa 1020

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<210> SEQ ID NO 402

<211> LENGTH: 339

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 402

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Met Ser Thr His Leu Arg Lys Leu Pro Gly Leu Leu Leu Cys Leu Leu
1      5      10      15
Leu Ala Leu Pro Ala Trp Cys Leu Gly Arg Leu Phe Pro Ile Ile Gly
20     25     30
Ala Pro Val Phe Ala Ile Leu Leu Gly Met Leu Leu Ala Leu Phe Tyr
35     40     45
Glu His Arg Asp Lys Thr Lys Glu Gly Ile Ser Phe Thr Ser Lys Tyr
50     55     60
Ile Leu Gln Thr Ala Val Val Leu Leu Gly Phe Gly Leu Asn Leu Thr
65     70     75     80
Gln Val Met Ala Val Gly Met Gln Ser Leu Pro Ile Ile Ile Ser Thr
85     90     95
Ile Ala Thr Ala Leu Leu Val Ala Tyr Gly Leu Gln Lys Trp Leu Arg
100    105    110
Leu Asp Val Asn Thr Ala Thr Leu Val Gly Val Gly Ser Ser Ile Cys
115    120    125
Gly Gly Ser Ala Val Ala Ala Thr Ala Pro Val Ile Lys Ala Lys Asp
130    135    140
Asp Glu Val Ala Lys Ala Ile Ser Val Ile Phe Leu Phe Asn Met Leu
145    150    155    160
Ala Ala Leu Leu Phe Pro Ser Leu Gly Gln Leu Leu Gly Leu Ser Asn
165    170    175
Glu Gly Phe Ala Ile Phe Ala Gly Thr Ala Val Asn Asp Thr Ser Ser
180    185    190
Val Thr Ala Thr Ala Thr Ala Trp Asp Ala Leu His His Ser Asn Thr
195    200    205
Leu Asp Gly Ala Thr Ile Val Lys Leu Thr Arg Thr Leu Ala Ile Leu
210    215    220
Pro Ile Thr Leu Gly Leu Ser Leu Tyr Arg Ala Lys Lys Glu His Asp
225    230    235    240
Ile Val Thr Glu Glu Asn Phe Ser Leu Arg Lys Ser Phe Pro Arg Phe
245    250    255
Ile Leu Phe Phe Leu Leu Ala Ser Leu Ile Thr Thr Leu Met Thr Ser
260    265    270
Leu Gly Val Ser Ala Asp Ser Phe His Tyr Leu Lys Thr Leu Ser Lys
275    280    285
Phe Phe Ile Val Met Ala Met Ala Ala Ile Gly Leu Asn Thr Asn Leu
290    295    300
Val Lys Leu Ile Lys Thr Gly Gly Gln Ala Ile Leu Leu Gly Ala Ile
305    310    315    320
Cys Trp Val Ala Ile Thr Leu Val Ser Leu Ala Met Gln Leu Ser Leu
325    330    335
Gly Ile Trp

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<210> SEQ ID NO 403

<211> LENGTH: 645

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

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<400> SEQUENCE: 403
gtggagggttg tgatggtaga aaacactaaa ttactatgta gctggggtatg gttatttagcg      60
ttagctatttc tcataacgat ctattcaacg tggctgtggt atcctcttga ggtggaccat      120
ctaaagtttag aacaagttgt ttttatgagc aaggatgcta tcttgcataa ctataacgga      180
ctactcaatt acctcaccaa tccttttgtg acaaggttgg aatttgctaa ttttcaactca      240
tcggcagacg gactcaagca ttttgcagat gtgaagtggc tttttcacct aactcaagtc      300
gtttttcttg gccttcttta cccaaccctt aagactttca cacaaagggtt aaaaacccaaa      360
cgtttctggc tccttcaaaa acctttaata ctagcagctt tgtttcctct tatgattgggt      420
ctaattggcta gtttcattgg gtttgaacat ttttttactc tttttcatca ggtgcttttt      480
gtaggagata gcagctggct ctttgatccc ttgaaagatt ctgtgatttg gatccttcca      540
gaagtctttt tcttgcactg tttccttttc tttatgatag tttacgaaat catcctgtgg      600
agcttagtag gtttagcaag atggcagcgc ctaaagttag aatga                        645

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<210> SEQ ID NO 404
<211> LENGTH: 214
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 404

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Met Glu Val Val Met Val Glu Asn Thr Lys Leu Leu Cys Ser Trp Val
1          5          10          15
Trp Leu Leu Ala Leu Ala Ile Leu Ile Thr Ile Tyr Ser Thr Trp Leu
20          25          30
Trp Tyr Pro Leu Glu Val Asp His Leu Lys Leu Glu Gln Val Val Phe
35          40          45
Met Ser Lys Asp Ala Ile Leu His Asn Tyr Asn Gly Leu Leu Asn Tyr
50          55          60
Leu Thr Asn Pro Phe Val Thr Arg Leu Glu Phe Ala Asn Phe His Ser
65          70          75          80
Ser Ala Asp Gly Leu Lys His Phe Ala Asp Val Lys Trp Leu Phe His
85          90          95
Leu Thr Gln Val Val Phe Leu Gly Leu Leu Tyr Pro Thr Leu Lys Thr
100         105         110
Phe Thr Gln Arg Leu Lys Thr Lys Arg Phe Trp Leu Leu Gln Lys Pro
115         120         125
Leu Ile Leu Ala Ala Leu Phe Pro Leu Met Ile Gly Leu Met Ala Ser
130         135         140
Phe Ile Gly Phe Glu His Phe Phe Thr Leu Phe His Gln Val Leu Phe
145         150         155         160
Val Gly Asp Ser Ser Trp Leu Phe Asp Pro Leu Lys Asp Ser Val Ile
165         170         175
Trp Ile Leu Pro Glu Val Phe Phe Leu His Cys Phe Leu Phe Phe Met
180         185         190
Ile Val Tyr Glu Ile Ile Leu Trp Ser Leu Val Gly Leu Ala Arg Trp
195         200         205
Gln Arg Leu Asn Val Glu
210

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<210> SEQ ID NO 405
<211> LENGTH: 957
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 405

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atgaaacgat ttttaaatag tcgtccttgg ttaggaatgg tatcagtctt ttttgcgatt      60
ctcctttttt taactgcagc atcgagcaat cataataact ctaactcgca aatttatagt      120
ccgattgaaa cctatacgca tagccttaaa gatgtaccaa ttgatatgaa gtatgatagt      180
gacaaatatt ttatcagtgg gtattcttat ggtgcggaag tttatctaac ctccactaat      240
cgtatcaaat tagattctga agtgaacaat gatacacgta attttaagat tgtggcggat      300

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ctaacacata	gtcatccagg	tacagtaagt	gtcaacctaa	gagtagaaaa	ccttccttct	360
ggggtgacag	ctaccgtatc	tccagataaa	atatcagtca	caattggcaa	aaaagaatct	420
aagggtatttc	ctggttagagg	aagcgttgat	gctaaacaaa	ttgcaaatgg	ttatgaaatt	480
agcaaaattg	aaacgggggt	taataagggt	gaagtgacca	gtgatgaatc	taccattgct	540
ttaattgatc	acgttggtggc	aaagttacct	gatgatcaag	tgtagatag	gaattatagt	600
agtcgagtga	ccttacaagc	tgtctcagct	gatggaacta	ttttagcaag	tgcaattgat	660
cctgcaaaaa	caaatttatc	agttgctgta	aaaaaaataa	cgaaatcagt	cccgattaga	720
gttgaggcag	tggggatgat	ggatgatagc	ttatcagata	ttcaatacaa	attgtcaaaa	780
caaacagctg	ttatctcagg	tagtcgagag	gtccttagaag	atattgatga	aattattgca	840
gaagttaaca	tttctgatgt	cactaaaaat	actagtaaga	ccgtgagttt	gtccttctagt	900
caggtgtcaa	ttgagccgtc	agtagtgacc	gttcagttga	caaccaccaa	aaaataa	957

<210> SEQ ID NO 406

<211> LENGTH: 318

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 406

Met	Lys	Arg	Phe	Leu	Asn	Ser	Arg	Pro	Trp	Leu	Gly	Met	Val	Ser	Val
1				5					10					15	
Phe	Phe	Ala	Ile	Leu	Leu	Phe	Leu	Thr	Ala	Ala	Ser	Ser	Asn	His	Asn
			20					25					30		
Asn	Ser	Asn	Ser	Gln	Ile	Tyr	Ser	Pro	Ile	Glu	Thr	Tyr	Thr	His	Ser
		35				40					45				
Leu	Lys	Asp	Val	Pro	Ile	Asp	Met	Lys	Tyr	Asp	Ser	Asp	Lys	Tyr	Phe
	50					55				60					
Ile	Ser	Gly	Tyr	Ser	Tyr	Gly	Ala	Glu	Val	Tyr	Leu	Thr	Ser	Thr	Asn
65					70					75				80	
Arg	Ile	Lys	Leu	Asp	Ser	Glu	Val	Asn	Asn	Asp	Thr	Arg	Asn	Phe	Lys
			85					90					95		
Ile	Val	Ala	Asp	Leu	Thr	His	Ser	His	Pro	Gly	Thr	Val	Ser	Val	Asn
			100					105					110		
Leu	Arg	Val	Glu	Asn	Leu	Pro	Ser	Gly	Val	Thr	Ala	Thr	Val	Ser	Pro
	115					120					125				
Asp	Lys	Ile	Ser	Val	Thr	Ile	Gly	Lys	Lys	Glu	Ser	Lys	Val	Phe	Pro
	130					135				140					
Val	Arg	Gly	Ser	Val	Asp	Ala	Lys	Gln	Ile	Ala	Asn	Gly	Tyr	Glu	Ile
145					150					155				160	
Ser	Lys	Ile	Glu	Thr	Gly	Val	Asn	Lys	Val	Glu	Val	Thr	Ser	Asp	Glu
			165					170					175		
Ser	Thr	Ile	Ala	Leu	Ile	Asp	His	Val	Val	Ala	Lys	Leu	Pro	Asp	Asp
			180					185					190		
Gln	Val	Leu	Asp	Arg	Asn	Tyr	Ser	Ser	Arg	Val	Thr	Leu	Gln	Ala	Val
		195				200						205			
Ser	Ala	Asp	Gly	Thr	Ile	Leu	Ala	Ser	Ala	Ile	Asp	Pro	Ala	Lys	Thr
	210					215					220				
Asn	Leu	Ser	Val	Ala	Val	Lys	Lys	Ile	Thr	Lys	Ser	Val	Pro	Ile	Arg
225					230					235				240	
Val	Glu	Ala	Val	Gly	Met	Met	Asp	Asp	Ser	Leu	Ser	Asp	Ile	Gln	Tyr
			245					250					255		
Lys	Leu	Ser	Lys	Gln	Thr	Ala	Val	Ile	Ser	Gly	Ser	Arg	Glu	Val	Leu
		260						265					270		
Glu	Asp	Ile	Asp	Glu	Ile	Ile	Ala	Glu	Val	Asn	Ile	Ser	Asp	Val	Thr
	275					280					285				
Lys	Asn	Thr	Ser	Lys	Thr	Val	Ser	Leu	Ser	Ser	Ser	Gln	Val	Ser	Ile
	290					295					300				
Glu	Pro	Ser	Val	Val	Thr	Val	Gln	Leu	Thr	Thr	Thr	Lys	Lys		
305					310					315					

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<210> SEQ ID NO 407
<211> LENGTH: 2487
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 407
gtggtatatt tttacttagt aaatcaattt actttttatta tctcattttt atattggagg      60
aatttatcag tgaatactta tttttgcaca caccataaac aattactact ttattcaaac      120
ctattcctta gctttgctat gatgggccaa ggaactgcc a tttatgccga tacactgact      180
tcaaattcag aacctaataa tacttacttt caaacgcaaa cgctcactac tacagatagc      240
gaaaaaaagg tagtacagcc acaacaaaaa gactactata ctgaattgtt agaccaatgg      300
aacagtatta tcgcaggcaa cgatgcttat gataaaacca atcctgacat ggtcactttt      360
cataataaag ctgaaaagga tgctcaaaac attattaaaa gctatcaagg gcctgaccac      420
gaaaaatgaa cttacctttg ggaacatgca aaggattatt ccgcttctgc taatatcacg      480
aaaacttacc gcaatattga aaaaatagca aaacagatca ctaatcctga atcatgctat      540
tatcaagata gtaaagctat tgctattgta aaagacggta tggccttcat gtatgaacac      600
gcttataatc tagatcgtga aaatcatcaa acaactggaa aagaaaacaa agaaaaattgg      660
tggttttatg aaattggaac tcctcgtgct attaataata ccttatcctt gatgtatcct      720
tattttactc aagaagaaat tcttaaatac acagctccaa tcgaaaaatt tgtgcctgac      780
cctactcggt ttagggttcg cgctgccaat ttttcacctt ttgaagccaa tagcggaat      840
ttaattgata tggggcgtgt taaactcatt tccggtatct ttcgtaaaga tgatctcgaa      900
attagtgata caatcaaagc aattgagaaa gttttcacgc tagttgatga aggaaatgg      960
ttttaccaag acggttcttt aattgatcac gtggttacta acgctcaaag tccactttat     1020
aaaaaaggca ttgcttacac tggagcttac ggtaatgtgc ttatagatgg cttatcgcaa     1080
ttaattccta ttattcaaaa aacaaagtct cctataaaaag cggataaaat ggctactatc     1140
tatcattgga ttaaccattc tttttccct atcatcgctt gtggagaaat gatggatatg     1200
actcgagggc gttctatcag tcgttttaat gcccaatctc atgttgctgg cattgaagca     1260
cttcgtgcta ttttacgtat tgctgacatg tctgaagagc ctcaccgttt ggcacttaaa     1320
acacgtataa aaacactcgt cacacaaggg aatgcttttt acaatgtcta tgataatttg     1380
aaaacctatc acgatatcaa acttatgaaa gaactactaa gtgatacttc tgttccagtc     1440
caaaaacttg atagttacgt agctagtttc aatagtatgg ataaattggc actatataat     1500
aataaacacg attttgcttt tggcctatca atgttttcga atcgaactca aaattatgaa     1560
gctatgaata atgaaaatct tcatggctgg tttacttctg atggaatgtt ttacctatac     1620
aataacgatt taggacacta cagtgaaaac tattgggcaa cggtaaatcc ctaccgctta     1680
cctggaacca cagaaactga gcaaaaacca ctagagggaa ctctgagaa tattaanaacg     1740
aactatcaac aagttggcat gactgggtct tctgatgacg cttttgttgc aagtaaaaaa     1800
cttaataaca caagtgtctt agctgctatg accttcacta attggaataa aagcctcacc     1860
ctcaataaag ggtggtttat cttaggaaac aaaataatct ttgttggtag caatatcaaa     1920
aaccaatcat ctcacaaggc gtatacaact attgaacaac gaaaagaaaa tcaaaaagta     1980
ccttactggt cttatgttaa caatcaacc gttgacttga ataatacagct agttgatttt     2040
acaaacacta aaagtatttt cttgaaagt gatgatcccg ctcaaaaatat tggttactac     2100
ttcttcaagc caacaacact tagcataagt aaggcacttc aaacagggaa atggcaaaac     2160
ataaaagctg atgacaaatc accagaagcc atcaaagaag tttcaaatac ctttatcact     2220
atcatgcaaa accatactca agatggcgat cgttatgcct atatgatgct tccaaatatg     2280
actcgtcaag aatttgaaac ctatattagc aagcttgata tcgacttatt agaaaacaat     2340
gacaaactgg ccgctgtcta cgatcatgat agtcaacaga tgcacgtcat tcaatatgga     2400
aaaaaagcaa cgatgttttc aaatcataat ctttctcatc aaggctttta tagttttcct     2460
catcctgtca ggcaaatca acaataa
2487

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<210> SEQ ID NO 408
<211> LENGTH: 828
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 408
Met Val Tyr Phe Tyr Leu Val Asn Gln Phe Thr Phe Ile Ile Ser Phe
1           5           10           15
Leu Tyr Trp Arg Asn Leu Ser Val Asn Thr Tyr Phe Cys Thr His His

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			20					25					30			
Lys	Gln	Leu	Leu	Leu	Tyr	Ser	Asn	Leu	Phe	Leu	Ser	Phe	Ala	Met	Met	
		35					40					45				
Gly	Gln	Gly	Thr	Ala	Ile	Tyr	Ala	Asp	Thr	Leu	Thr	Ser	Asn	Ser	Glu	
	50					55					60					
Pro	Asn	Asn	Thr	Tyr	Phe	Gln	Thr	Gln	Thr	Leu	Thr	Thr	Thr	Asp	Ser	
65					70					75					80	
Glu	Lys	Lys	Val	Val	Gln	Pro	Gln	Gln	Lys	Asp	Tyr	Tyr	Thr	Glu	Leu	
			85						90					95		
Leu	Asp	Gln	Trp	Asn	Ser	Ile	Ile	Ala	Gly	Asn	Asp	Ala	Tyr	Asp	Lys	
		100						105					110			
Thr	Asn	Pro	Asp	Met	Val	Thr	Phe	His	Asn	Lys	Ala	Glu	Lys	Asp	Ala	
		115					120					125				
Gln	Asn	Ile	Ile	Lys	Ser	Tyr	Gln	Gly	Pro	Asp	His	Glu	Asn	Arg	Thr	
	130					135					140					
Tyr	Leu	Trp	Glu	His	Ala	Lys	Asp	Tyr	Ser	Ala	Ser	Ala	Asn	Ile	Thr	
145					150					155					160	
Lys	Thr	Tyr	Arg	Asn	Ile	Glu	Lys	Ile	Ala	Lys	Gln	Ile	Thr	Asn	Pro	
			165						170					175		
Glu	Ser	Cys	Tyr	Tyr	Gln	Asp	Ser	Lys	Ala	Ile	Ala	Ile	Val	Lys	Asp	
		180				185							190			
Gly	Met	Ala	Phe	Met	Tyr	Glu	His	Ala	Tyr	Asn	Leu	Asp	Arg	Glu	Asn	
	195					200						205				
His	Gln	Thr	Thr	Gly	Lys	Glu	Asn	Lys	Glu	Asn	Trp	Trp	Val	Tyr	Glu	
	210					215						220				
Ile	Gly	Thr	Pro	Arg	Ala	Ile	Asn	Asn	Thr	Leu	Ser	Leu	Met	Tyr	Pro	
225					230					235					240	
Tyr	Phe	Thr	Gln	Glu	Glu	Ile	Leu	Lys	Tyr	Thr	Ala	Pro	Ile	Glu	Lys	
			245						250					255		
Phe	Val	Pro	Asp	Pro	Thr	Arg	Phe	Arg	Val	Arg	Ala	Ala	Asn	Phe	Ser	
		260						265					270			
Pro	Phe	Glu	Ala	Asn	Ser	Gly	Asn	Leu	Ile	Asp	Met	Gly	Arg	Val	Lys	
	275					280						285				
Leu	Ile	Ser	Gly	Ile	Leu	Arg	Lys	Asp	Asp	Leu	Glu	Ile	Ser	Asp	Thr	
	290					295					300					
Ile	Lys	Ala	Ile	Glu	Lys	Val	Phe	Thr	Leu	Val	Asp	Glu	Gly	Asn	Gly	
305					310					315					320	
Phe	Tyr	Gln	Asp	Gly	Ser	Leu	Ile	Asp	His	Val	Val	Thr	Asn	Ala	Gln	
			325						330					335		
Ser	Pro	Leu	Tyr	Lys	Lys	Gly	Ile	Ala	Tyr	Thr	Gly	Ala	Tyr	Gly	Asn	
		340						345					350			
Val	Leu	Ile	Asp	Gly	Leu	Ser	Gln	Leu	Ile	Pro	Ile	Ile	Gln	Lys	Thr	
	355					360						365				
Lys	Ser	Pro	Ile	Lys	Ala	Asp	Lys	Met	Ala	Thr	Ile	Tyr	His	Trp	Ile	
	370					375						380				
Asn	His	Ser	Phe	Phe	Pro	Ile	Ile	Val	Arg	Gly	Glu	Met	Met	Asp	Met	
385					390					395					400	
Thr	Arg	Gly	Arg	Ser	Ile	Ser	Arg	Phe	Asn	Ala	Gln	Ser	His	Val	Ala	
			405					410						415		
Gly	Ile	Glu	Ala	Leu	Arg	Ala	Ile	Leu	Arg	Ile	Ala	Asp	Met	Ser	Glu	
		420						425				430				
Glu	Pro	His	Arg	Leu	Ala	Leu	Lys	Thr	Arg	Ile	Lys	Thr	Leu	Val	Thr	
		435					440					445				
Gln	Gly	Asn	Ala	Phe	Tyr	Asn	Val	Tyr	Asp	Asn	Leu	Lys	Thr	Tyr	His	
	450					455					460					
Asp	Ile	Lys	Leu	Met	Lys	Glu	Leu	Leu	Ser	Asp	Thr	Ser	Val	Pro	Val	
465					470					475					480	

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<210> SEQ ID NO 409
<211> LENGTH: 1512
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 409
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<210> SEQ ID NO 409
<211> LENGTH: 1512
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 409
```

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caagaactaa cagttaaaaag cttgcaacag catttttcaag gtttggggcg agacaccgca      480
aaagagttgg ccgagcttct gaccacagac aaattaaaaac ggttccgtga gttttttgct      540
agacctactc aggcaaactct gaccacagct tctttttgcgc ctgttctttt ctcagatagt      600
catgcgacgt ttgagacttt gtctgacatg cttgaccact tttatcaaga caaggctgag      660
cgtgaccgta tcaatcagca agccagtgat ttgatccacc gtgtgcaaac tgaactggac      720
aaaaatcgca acaagctaag taagcaagaa gctgagctgc tagccactga aaatgctgag      780
ttgttccgtc aaaaaggaga attattgacc acctacctca gtctggtccc aaacaaccaa      840
gactctgtga ttttagacaa ttattataca ggggaaaaaaa ttgagattgc cttagacaag      900
gctctgacac caaatcaaaa tgctcaacgt tatttttaaaa aataccaaaaa gctaaaagaa      960
gctgtcaaac acttatctgg attgattgcc gataccaagc aaagtattac ttactttgag     1020
agcgtagact acaatttatc tcaagcaagt atcgacgaca tcgaagatat tcgcgaagaa     1080
ttatatcagg ctggcctttt gaaaagtcgc caaagagaca aacgccataa acgtaaaaaag     1140
cctgagcagt acctggcttc agatggaaca accattctca tgggtgggacg caataacttg     1200
caaatgaag aactcacctt taaaatggct aaaaaaggag aactctgggt ccatgctaag     1260
gatatccctg gaagtcatgt catcatcaaa gacaatcttg acccaagtga cgaggttaaa     1320
actgatgctg ccgaactagc tgcttattat tcgaaaagcta gggtatcaaaa tctcgttcag     1380
gtcgaatatga ttgaagctaa aaaattacac aaacctagtg gcgccaagcc aggatttgtg     1440
acttatactg gtcaaaaaaac tttacggggtt actcctgacc aagccaaaat tctctctatg     1500
aaattatcct ga                                           1512

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<210> SEQ ID NO 410

<211> LENGTH: 503

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 410

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Met Leu Leu Ser Ala His Pro Val Phe Gly Arg Val Gln Ile Thr Gln
1          5          10          15
Ala Asp Phe Gln Asn Pro Gln Val Pro Asn Thr Phe Thr Met Ile Met
20        25        30
Arg Lys Tyr Leu Gln Gly Ala Val Ile Glu Gln Leu Glu Gln Ile Asp
35        40        45
Asn Asp Arg Ile Ile Glu Ile Lys Val Ser Asn Lys Asn Glu Ile Gly
50        55        60
Asp Ala Ile Gln Ala Thr Leu Ile Ile Glu Ile Met Gly Lys His Ser
65        70        75        80
Asn Ile Ile Leu Val Asp Arg Ala Glu Asn Lys Ile Ile Glu Ser Ile
85        90        95
Lys His Val Gly Phe Ser Gln Asn Ser Tyr Arg Thr Ile Leu Pro Gly
100       105       110
Ser Thr Tyr Ile Glu Pro Pro Lys Thr Ala Ala Val Asn Pro Phe Thr
115       120       125
Ile Thr Asp Val Pro Leu Phe Glu Ile Leu Gln Thr Gln Glu Leu Thr
130       135       140
Val Lys Ser Leu Gln Gln His Phe Gln Gly Leu Gly Arg Asp Thr Ala
145       150       155       160
Lys Glu Leu Ala Glu Leu Leu Thr Thr Asp Lys Leu Lys Arg Phe Arg
165       170       175
Glu Phe Phe Ala Arg Pro Thr Gln Ala Asn Leu Thr Thr Ala Ser Phe
180       185       190
Ala Pro Val Leu Phe Ser Asp Ser His Ala Thr Phe Glu Thr Leu Ser
195       200       205
Asp Met Leu Asp His Phe Tyr Gln Asp Lys Ala Glu Arg Asp Arg Ile
210       215       220
Asn Gln Gln Ala Ser Asp Leu Ile His Arg Val Gln Thr Glu Leu Asp
225       230       235       240
Lys Asn Arg Asn Lys Leu Ser Lys Gln Glu Ala Glu Leu Leu Ala Thr
245       250       255

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Glu	Asn	Ala	Glu	Leu	Phe	Arg	Gln	Lys	Gly	Glu	Leu	Leu	Thr	Thr	Tyr			
			260					265					270					
Leu	Ser	Leu	Val	Pro	Asn	Asn	Gln	Asp	Ser	Val	Ile	Leu	Asp	Asn	Tyr			
			275				280					285						
Tyr	Thr	Gly	Glu	Lys	Ile	Glu	Ile	Ala	Leu	Asp	Lys	Ala	Leu	Thr	Pro			
			290			295					300							
Asn	Gln	Asn	Ala	Gln	Arg	Tyr	Phe	Lys	Lys	Tyr	Gln	Lys	Leu	Lys	Glu			
305					310					315					320			
Ala	Val	Lys	His	Leu	Ser	Gly	Leu	Ile	Ala	Asp	Thr	Lys	Gln	Ser	Ile			
			325						330					335				
Thr	Tyr	Phe	Glu	Ser	Val	Asp	Tyr	Asn	Leu	Ser	Gln	Ala	Ser	Ile	Asp			
			340					345					350					
Asp	Ile	Glu	Asp	Ile	Arg	Glu	Glu	Leu	Tyr	Gln	Ala	Gly	Phe	Leu	Lys			
		355				360						365						
Ser	Arg	Gln	Arg	Asp	Lys	Arg	His	Lys	Arg	Lys	Lys	Pro	Glu	Gln	Tyr			
	370				375						380							
Leu	Ala	Ser	Asp	Gly	Thr	Thr	Ile	Leu	Met	Val	Gly	Arg	Asn	Asn	Leu			
385				390					395						400			
Gln	Asn	Glu	Glu	Leu	Thr	Phe	Lys	Met	Ala	Lys	Lys	Gly	Glu	Leu	Trp			
			405					410					415					
Phe	His	Ala	Lys	Asp	Ile	Pro	Gly	Ser	His	Val	Ile	Ile	Lys	Asp	Asn			
			420				425					430						
Leu	Asp	Pro	Ser	Asp	Glu	Val	Lys	Thr	Asp	Ala	Ala	Glu	Leu	Ala	Ala			
		435				440					445							
Tyr	Tyr	Ser	Lys	Ala	Arg	Leu	Ser	Asn	Leu	Val	Gln	Val	Asp	Met	Ile			
	450				455						460							
Glu	Ala	Lys	Lys	Leu	His	Lys	Pro	Ser	Gly	Ala	Lys	Pro	Gly	Phe	Val			
465				470					475					480				
Thr	Tyr	Thr	Gly	Gln	Lys	Thr	Leu	Arg	Val	Thr	Pro	Asp	Gln	Ala	Lys			
			485					490					495					
Ile	Leu	Ser	Met	Lys	Leu	Ser												
			500															

<210> SEQ ID NO 411

<211> LENGTH: 1182

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 411

atgcccttaa	tacctgaaaa	gtctagaaca	gatagcttat	tttacaaatg	gtttttaaat	60
aatcaagcta	ccatggcttt	agtaataaca	cttttagcct	ttttaacgat	ttttgttttt	120
actaaaatct	cttttttatt	tatgccagtg	atttcttttt	ttgcggtcac	catgttgccc	180
ttgggtatttt	cgaccattct	gtattatctg	accaaaccct	tagttgacct	tattaatcac	240
ttggggccga	atcgtagcac	ctctattttt	attgtttttg	gtttgattac	cttacttttt	300
gtctggggcga	tttcaggctt	tggtcccatg	gtacagaccc	aacttaccag	ttttattgag	360
gatctgcccc	aatacgtggg	caaggccaat	gaagaagcca	ataaacttct	tgaaaatgaa	420
tggttagtca	gctataagcc	ccaactccaa	gacatgctta	cccatacaag	tcaaaaggct	480
ttggattacg	cgaaaagttt	ttcaaaaaat	gctattgact	gggctggtaa	ttttgctggt	540
gccattgctc	ggattaccgt	ggctattatt	atttcgcctt	ttattctctt	ttatttttta	600
cgagacagta	gccacatgaa	aaatggcctt	gtgaatgtct	tacctctcaa	attacgggtg	660
cctatgggtc	gagtcctggg	agatattaac	aagcaattat	caggctatgt	gcaagggcag	720
gttacgggtg	caattgttgt	cggctttatg	ttttctatca	tgtttagcct	tgtagggactg	780
aaatatgccca	tcacttttgg	gattattgct	ggctttctta	acatgatacc	ttacttagga	840
agtttccttg	ccatgatacc	tggtgtgatt	atggctatgg	tacaaggccc	atttatgttg	900
gttaagggtc	ttgttatctt	tatgattgag	caaaccatcg	aagggcggtt	tgtagcaccg	960
cttgttttgg	gaaataagct	gagcattcat	cctattacca	ttatgttctt	gttattgact	1020
gcaggctcta	tgtttggtgt	ctgggggtgt	ttccttgcca	tcccaatcta	cgcttctgtc	1080
aaagttgtga	ttaaagaatt	atttgactgg	tacaaaaaag	ttagcggttt	gtatgacgaa	1140

1182

<400> SEQUENCE: 412

Met 1	Pro	Leu	Ile	Pro 5	Glu	Lys	Ser	Arg	Thr 10	Asp	Ser	Leu	Phe	Tyr 15	Lys
Trp	Phe	Leu	Asn 20	Asn	Gln	Ala	Thr	Met 25	Ala	Leu	Val	Ile	Thr 30	Leu	Leu
Ala	Phe	Leu	Thr	Ile	Phe	Val	Phe	Thr	Lys	Ile	Ser	Phe	Leu	Phe	Met
Pro	Val	Ile	Ser	Phe	Phe	Ala	Val	Ile	Met	Leu	Pro	Leu	Val	Ile	Ser
Thr 65	Ile	Leu	Tyr	Tyr	Leu 70	Thr	Lys	Pro	Leu	Val 75	Asp	Leu	Ile	Asn 80	His
Leu	Gly	Pro	Asn 85	Arg	Thr	Thr	Ser	Ile	Phe 90	Ile	Val	Phe	Gly	Leu 95	Ile
Thr	Leu	Leu	Phe 100	Val	Trp	Ala	Ile	Ser	Gly 105	Phe	Val	Pro	Met 110	Val	Gln
Thr	Gln	Leu	Thr	Ser	Phe	Ile	Glu	Asp	Leu	Pro	Lys	Tyr	Val	Gly	Lys
Val	Asn 130	Glu	Glu	Ala	Asn	Lys	Leu	Leu	Glu	Asn	Glu	Trp	Leu	Val	Ser
Tyr 145	Lys	Pro	Gln	Leu	Gln	Asp	Met	Leu	Thr	His 155	Thr	Ser	Gln	Lys	Ala 160
Leu	Asp	Tyr	Ala	Gln	Ser	Phe	Ser	Lys	Asn 170	Ala	Ile	Asp	Trp	Ala 175	Gly
Asn	Phe	Ala	Gly 180	Ala	Ile	Ala	Arg	Ile	Thr 185	Val	Ala	Ile	Ile 190	Ile	Ser
Pro	Phe	Ile	Leu	Phe	Tyr	Phe	Leu	Arg	Asp	Ser	Ser	His	Met	Lys	Asn
Gly	Leu	Val	Asn 210	Val	Leu	Pro	Leu	Lys	Leu	Arg	Val	Pro	Met	Val	Arg
Val	Leu	Gly	Asp	Ile	Asn 230	Lys	Gln	Leu	Ser	Gly 235	Tyr	Val	Gln	Gly	Gln
Val	Thr	Val	Ala	Ile	Val	Val	Gly	Phe	Met	Phe	Ser	Ile	Met	Phe	Ser
Leu	Val	Gly	Leu 260	Lys	Tyr	Ala	Ile	Thr 265	Phe	Gly	Ile	Ile	Ala 270	Gly	Phe
Leu	Asn	Met	Ile	Pro	Tyr	Leu	Gly	Ser	Phe	Leu	Ala	Met	Ile	Pro	Val
Val	Ile	Met	Ala	Met	Val	Gln	Gly	Pro	Phe	Met	Leu	Val	Lys	Val	Leu
Val	Ile	Phe	Met	Ile	Glu	Gln	Thr	Ile	Glu	Gly 315	Arg	Phe	Val	Ala	Pro
Leu	Val	Leu	Gly	Asn 325	Lys	Leu	Ser	Ile	His 330	Pro	Ile	Thr	Ile	Met	Phe
Leu	Leu	Leu	Thr	Ala	Gly	Ser	Met	Phe	Gly	Val	Trp	Gly	Val	Phe	Leu
Val	Ile	Pro	Ile	Tyr	Ala	Ser	Val	Lys	Val	Val	Ile	Lys	Glu	Leu	Phe
Asp	Trp	Tyr	Lys	Lys	Val	Ser	Gly	Leu	Tyr	Asp	Glu	Val	Leu	Val	Val
Ile 385	Glu	Glu	Val	Lys	Asp	His	Val	Lys							

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<210> SEQ ID NO 413
<211> LENGTH: 711
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 413
    atgagatata attgtcgcta ctcacatatt gataagaaaa tctacagcat gattatatgt      60
    ttgtcatttc ttttatattc caatgttggt caagcaaatt cttataatac aaccaataga      120
    cataatctag aatcgcttta taagcatgat tctaacttga ttgaagccga tagtataaaa      180
    aattctccag atattgtaac aagccatatg ttgaaatata gtgtcaagga taaaaatttg      240
    tcagtttttt ttgagaaaga ttggatatca caggaattca aagataaaga agtagatatt      300
    tatgtcttat ctgcacaaga ggtttgtgaa tgtccaggga aaaggatatga agcgtttggt      360
    ggaattacat taactaattc agaaaaaaaa gaaattaaag ttctgtgtaa cgtgtgggat      420
    aaaagtaaac aacagccgcc tatgtttatt acagtcaata aaccgaaagt aaccgctcag      480
    gaagtggata taaaagttag aaagttattg attaagaaat acgatatcta taataaccgg      540
    gaacaaaaat actctaaagg aactgttacc ttagatttaa attcaggtaa agatattggt      600
    tttgatttgg attattttgg caatggagac tttaatagca tgctaaaaat atattccaat      660
    aacgagagaa tagactcaac tcaatttcat gtagatgtgt caatcagcta a              711

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<210> SEQ ID NO 414
<211> LENGTH: 236
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 414
    Met Arg Tyr Asn Cys Arg Tyr Ser His Ile Asp Lys Lys Ile Tyr Ser
    1          5          10          15
    Met Ile Ile Cys Leu Ser Phe Leu Leu Tyr Ser Asn Val Val Gln Ala
    20          25          30
    Asn Ser Tyr Asn Thr Thr Asn Arg His Asn Leu Glu Ser Leu Tyr Lys
    35          40          45
    His Asp Ser Asn Leu Ile Glu Ala Asp Ser Ile Lys Asn Ser Pro Asp
    50          55          60
    Ile Val Thr Ser His Met Leu Lys Tyr Ser Val Lys Asp Lys Asn Leu
    65          70          75          80
    Ser Val Phe Phe Glu Lys Asp Trp Ile Ser Gln Glu Phe Lys Asp Lys
    85          90          95
    Glu Val Asp Ile Tyr Ala Leu Ser Ala Gln Glu Val Cys Glu Cys Pro
    100         105         110
    Gly Lys Arg Tyr Glu Ala Phe Gly Gly Ile Thr Leu Thr Asn Ser Glu
    115         120         125
    Lys Lys Glu Ile Lys Val Pro Val Asn Val Trp Asp Lys Ser Lys Gln
    130         135         140
    Gln Pro Pro Met Phe Ile Thr Val Asn Lys Pro Lys Val Thr Ala Gln
    145         150         155         160
    Glu Val Asp Ile Lys Val Arg Lys Leu Leu Ile Lys Lys Tyr Asp Ile
    165         170         175
    Tyr Asn Asn Arg Glu Gln Lys Tyr Ser Lys Gly Thr Val Thr Leu Asp
    180         185         190
    Leu Asn Ser Gly Lys Asp Ile Val Phe Asp Leu Tyr Tyr Phe Gly Asn
    195         200         205
    Gly Asp Phe Asn Ser Met Leu Lys Ile Tyr Ser Asn Asn Glu Arg Ile
    210         215         220
    Asp Ser Thr Gln Phe His Val Asp Val Ser Ile Ser
    225         230         235

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<210> SEQ ID NO 415
<211> LENGTH: 780

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```

<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 415
gtgagaaaaa ttgtaaatgt taatttttaa aagtttttaa cttcatcttt tctattgtgg      60
gtatttatat cagctataat tccaacgtgt tacgcgtatg agatgagtag tgtgggagtt      120
attaatttaa ggaatttata ctctacatat gatccaacag aagtaaaagg aaaaataaat      180
gaagggtccgc cattttcagg tagtttggtc tacaaaaata ttccttatgg caatagtctg      240
attgaattaa aagtagaact taatagcgta gaaaaagcta attttttttc tggtaaaagg      300
gtggatatat ttactttgga gtattctcct ccctgtaact ctaatatata aaagaattca      360
tatggaggta ttactttaag cgacggtaat agaattgata aaaaaaatat acctgttaat      420
attttcatag acggcggttca acaaaaaatat agctatacag atataagtac agtgagtact      480
gataagaaag aggttacgat tcaggaactt gatgtgaaat caagatatta tcttcaaaaa      540
cattttaata tatacggatt cggatgatgt aaagattttg gccgctcctc tagatttcaa      600
tctggccttg aggaaggaaa tattattttt catttgaata gtggagagag aatttcttat      660
aatctttttg atacaggaca tggtgacaga gagagtatgc taaaaaaata cagtgataat      720
aagaccgcctt attctgatca acttcatatt gatataact tagttaaatt taataaataa      780

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<210> SEQ ID NO 416
<211> LENGTH: 259
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 416
Met Arg Lys Ile Val Asn Val Asn Phe Lys Lys Phe Leu Thr Ser Ser
1          5          10          15
Phe Leu Leu Trp Val Phe Ile Ser Ala Ile Ile Pro Thr Cys Tyr Ala
20          25          30
Tyr Glu Met Ser Ser Val Gly Val Ile Asn Leu Arg Asn Leu Tyr Ser
35          40          45
Thr Tyr Asp Pro Thr Glu Val Lys Gly Lys Ile Asn Glu Gly Pro Pro
50          55          60
Phe Ser Gly Ser Leu Phe Tyr Lys Asn Ile Pro Tyr Gly Asn Ser Ser
65          70          75          80
Ile Glu Leu Lys Val Glu Leu Asn Ser Val Glu Lys Ala Asn Phe Phe
85          90          95
Ser Gly Lys Arg Val Asp Ile Phe Thr Leu Glu Tyr Ser Pro Pro Cys
100         105         110
Asn Ser Asn Ile Lys Lys Asn Ser Tyr Gly Gly Ile Thr Leu Ser Asp
115         120         125
Gly Asn Arg Ile Asp Lys Lys Asn Ile Pro Val Asn Ile Phe Ile Asp
130         135         140
Gly Val Gln Gln Lys Tyr Ser Tyr Thr Asp Ile Ser Thr Val Ser Thr
145         150         155         160
Asp Lys Lys Glu Val Thr Ile Gln Glu Leu Asp Val Lys Ser Arg Tyr
165         170         175
Tyr Leu Gln Lys His Phe Asn Ile Tyr Gly Phe Gly Asp Val Lys Asp
180         185         190
Phe Gly Arg Ser Ser Arg Phe Gln Ser Gly Phe Glu Glu Gly Asn Ile
195         200         205
Ile Phe His Leu Asn Ser Gly Glu Arg Ile Ser Tyr Asn Leu Phe Asp
210         215         220
Thr Gly His Gly Asp Arg Glu Ser Met Leu Lys Lys Tyr Ser Asp Asn
225         230         235         240
Lys Thr Ala Tyr Ser Asp Gln Leu His Ile Asp Ile Tyr Leu Val Lys
245         250         255
Phe Asn Lys

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<210> SEQ ID NO 417

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<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 417
    ttgataaaat tagcgtctaa accaacaata ctgctagctt tgagattaat cacattgatt      60
    ttgtttgcat cgattgtccc accgataatc tggtcggctc ttagcttgat aaactcccct      120
    aacttagccc caaaagctcc attaaccgtc gtattgccat caagagcgat gtttttacca      180
    gctatttgca caccgcggga attcaagtta atcgctgaga taatatcgct gccagacatt      240
    ttactttgcg ggattttgtc tttaatcgca agcatgatac tgtcgccaga ttgccgcaag      300
    agggaactgta tttttcctaa gggtcacagac tga                                  333

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<210> SEQ ID NO 418
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 418
    Met Ile Lys Leu Ala Ser Lys Pro Thr Ile Leu Leu Ala Leu Arg Leu
    1           5           10           15
    Ile Thr Leu Ile Leu Phe Ala Ser Ile Val Pro Pro Ile Ile Trp Ser
           20           25           30
    Ala Leu Ser Leu Ile Asn Ser Pro Asn Leu Ala Pro Lys Ala Pro Leu
           35           40           45
    Thr Val Val Leu Pro Ser Arg Ala Met Phe Leu Pro Ala Ile Cys Thr
           50           55           60
    Pro Arg Glu Phe Lys Leu Ile Ala Glu Ile Ile Ser Leu Pro Asp Ile
    65           70           75           80
    Leu Leu Cys Gly Ile Leu Ser Leu Ile Ala Ser Met Ile Leu Ser Pro
           85           90           95
    Asp Cys Arg Lys Arg Asp Cys Ile Phe Pro Lys Val Thr Asp
           100           105           110

```

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<210> SEQ ID NO 419
<211> LENGTH: 270
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 419
    gtgaataaac gaatcaagaa aaaacataaa ttggaaacag cagttgtgtt gcttatcgca      60
    gaaaatgcta tgcaggctga agctattaag aatcaaaaaca gacaaattgc agagctgaga      120
    tcgattatac aacaaaacgc ccaagcaata aatagagagt ttgcagcagt taaaggtgtg      180
    tgtcttgata atcaagcagc tattacaaac attgcagttg atattaacta cgtcaagaaa      240
    aactacaaac ggaagtgggg gaagaaatag                                  270

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<210> SEQ ID NO 420
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 420
    Met Asn Lys Arg Ile Lys Lys Lys His Lys Leu Glu Thr Ala Val Val
    1           5           10           15
    Leu Leu Ile Ala Glu Asn Ala Met Gln Ala Glu Ala Ile Lys Asn Gln
           20           25           30
    Asn Arg Gln Ile Ala Glu Leu Arg Ser Ile Ile Gln Gln Asn Ala Gln
           35           40           45
    Ala Ile Asn Arg Glu Phe Ala Ala Val Lys Gly Val Cys Leu Asp Asn
           50           55           60
    Gln Ala Ala Ile Thr Asn Ile Ala Val Asp Ile Asn Tyr Val Lys Lys
    65           70           75           80

```

Asn Tyr Lys Arg Lys Trp Gly Lys Lys
85

<210> SEQ ID NO 421

<211> LENGTH: 870

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 421

```
atgaaaggta ttattcttgc aggaggttca gggacacgct tgtatccact gaccctgtgcc      60
gcatctaaac agttgatgcc catttatgac aaaccaatga tttattaccc attgtcaacc      120
ttgatgttgg cagggattaa agatgtttta atcatttcaa ctccccaaga tcttcctcgt      180
ttcgaagaat tgctaggaga cgggtcagaa tttggcatta gcttatccta taaggaacaa      240
ccaagcccag atggttttagc acaagctttc attattggag aggagtttat cggtgatgac      300
cgtgttgctc ttatttttagg agataatatt taccacggtg atggcctcac taaaatgctt      360
caaaaggcag ctgccaaaga aaaaggagcc accgtttttg gttatcaagt gaaagaccct      420
gagcgctttg gagtggttga atttgatgag aacatgaatg ctatctctat cgaagaaaaa      480
ccagaagtgc ctaagtctca ctttgcagtg actggacttt atttctatga caatgacgtg      540
gtagagattg ctaaaaacat taaaccaagc gcgcgtggtg agttggaaaat tacagacgtc      600
aacaaggctt acttggaaac tggtgacctc tccgttgaat tgatggggcg tggtttttgc      660
tggttagaca ctggaacgca tgaaagtcta cttgaagcgg ctcaatatat tgaaactgtt      720
caacgcttgc aaaacgctca agtggcaaat ctggaagaaa ttgcctatcg catgggctat      780
atcagtaaag aagatgtcca taaattggcg caatctttaa agaaaaacga atacgggcaa      840
tacttgcttc gtttgattgg agaagcttaa                                     870
```

<210> SEQ ID NO 422

<211> LENGTH: 289

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 422

```
Met Lys Gly Ile Ile Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro
1          5          10          15
Leu Thr Arg Ala Ala Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro
20        25        30
Met Ile Tyr Tyr Pro Leu Ser Thr Leu Met Leu Ala Gly Ile Lys Asp
35        40        45
Val Leu Ile Ile Ser Thr Pro Gln Asp Leu Pro Arg Phe Glu Glu Leu
50        55        60
Leu Gly Asp Gly Ser Glu Phe Gly Ile Ser Leu Ser Tyr Lys Glu Gln
65        70        75        80
Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe
85        90        95
Ile Gly Asp Asp Arg Val Ala Leu Ile Leu Gly Asp Asn Ile Tyr His
100       105       110
Gly Asn Gly Leu Thr Lys Met Leu Gln Lys Ala Ala Ala Lys Glu Lys
115       120       125
Gly Ala Thr Val Phe Gly Tyr Gln Val Lys Asp Pro Glu Arg Phe Gly
130       135       140
Val Val Glu Phe Asp Glu Asn Met Asn Ala Ile Ser Ile Glu Glu Lys
145       150       155       160
Pro Glu Val Pro Lys Ser His Phe Ala Val Thr Gly Leu Tyr Phe Tyr
165       170       175
Asp Asn Asp Val Val Glu Ile Ala Lys Asn Ile Lys Pro Ser Ala Arg
180       185       190
Gly Glu Leu Glu Ile Thr Asp Val Asn Lys Ala Tyr Leu Glu Arg Gly
195       200       205
Asp Leu Ser Val Glu Leu Met Gly Arg Gly Phe Ala Trp Leu Asp Thr
210       215       220
```

Gly	Thr	His	Glu	Ser	Leu	Leu	Glu	Ala	Ala	Gln	Tyr	Ile	Glu	Thr	Val
225					230					235					240
Gln	Arg	Leu	Gln	Asn	Ala	Gln	Val	Ala	Asn	Leu	Glu	Glu	Ile	Ala	Tyr
			245						250					255	
Arg	Met	Gly	Tyr	Ile	Ser	Lys	Glu	Asp	Val	His	Lys	Leu	Ala	Gln	Ser
		260						265					270		
Leu	Lys	Lys	Asn	Glu	Tyr	Gly	Gln	Tyr	Leu	Leu	Arg	Leu	Ile	Gly	Glu
		275					280					285			
Ala															

<210> SEQ ID NO 423
 <211> LENGTH: 900
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 423

atgacaaaaa	taaaaaatag	tgtgattg	ggtccgacag	cggttgga	aacagcactt	60
gggattagtt	tagccaaggc	ttttaatgga	gaaattat	caggagatag	ccagcaagtt	120
tatcgacagt	tggatattgg	aacagccaag	gccactcaag	aagagcaaga	agcagcgg	180
catcacttaa	ttgatattcg	tgagggtgacg	gagtccttatt	cggcctacga	ttttgttcaa	240
gatgctcaaa	aatctatttc	agatattg	agtcgtggga	aattaccaat	tattgtaggt	300
ggaactgg	tttacttaca	aagtttactc	gaagggtatc	atctaggagg	tcaagttgat	360
caagaggcgg	taaaagccta	tcggaatgag	ttggagcaat	tggacgatca	cgactt	420
gaacgcttgc	aagtcaataa	cattaccatt	gagcaggtga	atcgcagacg	ggcgatccga	480
gcccttgaat	tggctcagtt	tgctgatgaa	ttagagaatg	ccgagacggc	ttatgagccg	540
cttattatcg	gcttgaatga	tgaccgccaa	gtcatctatg	accgtatcaa	tcagcgcgtg	600
aatcgatga	ttgaaaacgg	cttattggaa	gaagcaaaat	ggttatatga	gcattacc	660
actgttcagg	ctagtcgtgg	cataggttat	aaggaattat	tcccctat	tgtaggtgaa	720
atgactttgg	cagaagctag	tgatcaatta	aaacaaaaca	cgagacgttt	tgccaagcga	780
cagctaactt	ggttccgcaa	tcgaatggct	gtttagcttca	ctgccataac	ggctcctgat	840
taccacag	tagtacatga	tagggtcagg	gattttcttg	gtcagaaaaga	gaagtcatga	900

<210> SEQ ID NO 424
 <211> LENGTH: 299
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 424

Met	Thr	Lys	Ile	Lys	Ile	Val	Val	Ile	Val	Gly	Pro	Thr	Ala	Val	Gly
1				5					10					15	
Lys	Thr	Ala	Leu	Gly	Ile	Ser	Leu	Ala	Lys	Ala	Phe	Asn	Gly	Glu	Ile
			20					25					30		
Ile	Ser	Gly	Asp	Ser	Gln	Gln	Val	Tyr	Arg	Gln	Leu	Asp	Ile	Gly	Thr
		35				40					45				
Ala	Lys	Ala	Thr	Gln	Glu	Glu	Gln	Glu	Ala	Ala	Val	His	His	Leu	Ile
	50				55					60					
Asp	Ile	Arg	Glu	Val	Thr	Glu	Ser	Tyr	Ser	Ala	Tyr	Asp	Phe	Val	Gln
65				70					75					80	
Asp	Ala	Gln	Lys	Ser	Ile	Ser	Asp	Ile	Val	Ser	Arg	Gly	Lys	Leu	Pro
			85					90					95		
Ile	Ile	Val	Gly	Gly	Thr	Gly	Leu	Tyr	Leu	Gln	Ser	Leu	Leu	Glu	Gly
		100					105						110		
Tyr	His	Leu	Gly	Gly	Gln	Val	Asp	Gln	Glu	Ala	Val	Lys	Ala	Tyr	Arg
		115				120						125			
Asn	Glu	Leu	Glu	Gln	Leu	Asp	His	Asp	Leu	Tyr	Glu	Arg	Leu	Gln	
	130				135					140					
Val	Asn	Asn	Ile	Thr	Ile	Glu	Gln	Val	Asn	Arg	Arg	Arg	Ala	Ile	Arg
145				150					155					160	
Ala	Leu	Glu	Leu	Ala	Gln	Phe	Ala	Asp	Glu	Leu	Glu	Asn	Ala	Glu	Thr

				165					170					175			
Ala	Tyr	Glu	Pro	Leu	Ile	Ile	Gly	Leu	Asn	Asp	Asp	Arg	Gln	Val	Ile		
			180					185					190				
Tyr	Asp	Arg	Ile	Asn	Gln	Arg	Val	Asn	Arg	Met	Ile	Glu	Asn	Gly	Leu		
		195					200					205					
Leu	Glu	Glu	Ala	Lys	Trp	Leu	Tyr	Glu	His	Tyr	Pro	Thr	Val	Gln	Ala		
	210					215					220						
Ser	Arg	Gly	Ile	Gly	Tyr	Lys	Glu	Leu	Phe	Pro	Tyr	Phe	Val	Gly	Glu		
225				230						235				240			
Met	Thr	Leu	Ala	Glu	Ala	Ser	Asp	Gln	Leu	Lys	Gln	Asn	Thr	Arg	Arg		
			245					250					255				
Phe	Ala	Lys	Arg	Gln	Leu	Thr	Trp	Phe	Arg	Asn	Arg	Met	Ala	Val	Ser		
	260							265					270				
Phe	Thr	Ala	Ile	Thr	Ala	Pro	Asp	Tyr	Pro	Gln	Val	Val	His	Asp	Arg		
	275					280						285					
Val	Arg	Asp	Phe	Leu	Gly	Gln	Lys	Glu	Lys	Ser							
	290					295											

<210> SEQ ID NO 425

<211> LENGTH: 723

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 425

ttgcaaaata	atttgcta	at	ttttccgaa	ttctttttcca	gatc	tagttc	tcca	atctat	60
gaatatgtta	taataaggat	tatg	aaatta	ctacttttta	ttaccattgc	ctatttactt			120
ggttctattc	caactggact	atgg	attgga	cagtactttt	accacatcaa	cttacgagag			180
catggatcag	gaaatactgg	aacc	acaaat	actttttc	ggga	tttttaggtgt	caaggcagga		240
acagctacct	tagctattga	tatg	tttaaa	gggacacttt	caatattgtt	accaattatt			300
tttggtatga	cttcaatttc	atcc	attgct	atcggctttt	tcgcagtttt	agggcatact			360
tttcttattt	ttgccaactt	taaagg	tgggt	aaggccgtag	caacaagtgc	tgggtgtattg			420
ctaggctttg	ctccgttata	tctctttttt	ttagcatcta	tctttgtttt	agttctctat				480
ttatttagta	tgatatcttt	agctagtgtg	gtttcagcta	tcgttggtgt	gttatctgtt				540
ttaacatttc	ctgccattca	ttttctttta	ccaaattatg	actacttttt	aacttttatt				600
gtgatattac	ttgcgttcac	tattattata	agacacaaag	ataacattag	tcgtatcaaa				660
catcactactg	aaaatcta	accttg	ggggg	ctaaatttaa	gcaaacaagt	gcctaaaaaa			720
taa									723

<210> SEQ ID NO 426

<211> LENGTH: 240

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 426

Met	Gln	Asn	Asn	Leu	Leu	Ile	Phe	Ser	Glu	Phe	Phe	Ser	Arg	Ser	Ser
1			5					10					15		
Ser	Pro	Ile	Tyr	Glu	Tyr	Val	Ile	Ile	Arg	Ile	Met	Lys	Leu	Leu	Leu
		20					25				30				
Phe	Ile	Thr	Ile	Ala	Tyr	Leu	Leu	Gly	Ser	Ile	Pro	Thr	Gly	Leu	Trp
	35					40				45					
Ile	Gly	Gln	Tyr	Phe	Tyr	His	Ile	Asn	Leu	Arg	Glu	His	Gly	Ser	Gly
	50				55			60							
Asn	Thr	Gly	Thr	Thr	Asn	Thr	Phe	Arg	Ile	Leu	Gly	Val	Lys	Ala	Gly
65				70				75					80		
Thr	Ala	Thr	Leu	Ala	Ile	Asp	Met	Phe	Lys	Gly	Thr	Leu	Ser	Ile	Leu
			85				90					95			
Leu	Pro	Ile	Ile	Phe	Gly	Met	Thr	Ser	Ile	Ser	Ser	Ile	Ala	Ile	Gly
	100						105					110			
Phe	Phe	Ala	Val	Leu	Gly	His	Thr	Phe	Pro	Ile	Phe	Ala	Asn	Phe	Lys

		115				120				125							
Gly	Gly	Lys	Ala	Val	Ala	Thr	Ser	Ala	Gly	Val	Leu	Leu	Gly	Phe	Ala		
	130					135					140						
Pro	Leu	Tyr	Leu	Phe	Phe	Leu	Ala	Ser	Ile	Phe	Val	Leu	Val	Leu	Tyr		
145					150					155					160		
Leu	Phe	Ser	Met	Ile	Ser	Leu	Ala	Ser	Val	Val	Ser	Ala	Ile	Val	Gly		
			165						170					175			
Val	Leu	Ser	Val	Leu	Thr	Phe	Pro	Ala	Ile	His	Phe	Leu	Leu	Pro	Asn		
		180				185							190				
Tyr	Asp	Tyr	Phe	Leu	Thr	Phe	Ile	Val	Ile	Leu	Leu	Ala	Phe	Ile	Ile		
	195					200						205					
Ile	Ile	Arg	His	Lys	Asp	Asn	Ile	Ser	Arg	Ile	Lys	His	His	Thr	Glu		
	210					215					220						
Asn	Leu	Ile	Pro	Trp	Gly	Leu	Asn	Leu	Ser	Lys	Gln	Val	Pro	Lys	Lys		
225					230					235					240		

<210> SEQ ID NO 427

<211> LENGTH: 651

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 427

atgattaata	tcccattaat	gaaagatagt	ttaggatttg	tggtatcggg	attaccttat	60
acccttggtg	tttcggtgct	cagttttttt	acgggtctgt	ttttagggtt	aggcctagcc	120
cttctgggaa	ggtcacgtca	gccgttgatt	cattatcttg	ttagagcgta	catctctatt	180
atgcgagggtg	tgccgatgat	cgtggtgctc	tttggtcttt	atttcgggtt	gccttattat	240
ggtttagaat	tgccagcttt	actttgctg	tatcttggtt	tttctatggt	tagcgctgcc	300
tatatttctg	aagtttttctg	ctcttctata	gaagctattg	acaagggaca	atgggaagca	360
gctaaggctt	tagggttgcc	atatgctctt	atgggtaaga	aaattattct	tcctcaagcc	420
tttcgaattg	cagtttcctcc	tttaggaaat	gtcattattg	atatgggttaa	aagttcgtcg	480
ctagctgcca	tgattaccgt	accagatatt	tttcaaaatg	ccaaaattat	tggcggtaga	540
gagtgggatt	acatgtccat	gtatatttta	gtagccttta	tctattggct	tattgctttt	600
ttgttagaac	gttaccaaga	attccttagaa	aataagctag	cacttggtta	a	651

<210> SEQ ID NO 428

<211> LENGTH: 216

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 428

Met	Ile	Asn	Ile	Pro	Leu	Met	Lys	Asp	Ser	Leu	Gly	Phe	Val	Leu	Ser
1			5					10						15	
Gly	Leu	Pro	Tyr	Thr	Leu	Gly	Ile	Ser	Leu	Leu	Ser	Phe	Phe	Thr	Gly
		20					25						30		
Leu	Phe	Leu	Gly	Leu	Gly	Leu	Ala	Leu	Leu	Gly	Arg	Ser	Arg	Gln	Pro
		35				40					45				
Leu	Ile	His	Tyr	Leu	Val	Arg	Ala	Tyr	Ile	Ser	Ile	Met	Arg	Gly	Val
	50					55				60					
Pro	Met	Ile	Val	Val	Leu	Phe	Val	Leu	Tyr	Phe	Gly	Leu	Pro	Tyr	Tyr
65					70				75					80	
Gly	Leu	Glu	Leu	Pro	Ala	Leu	Leu	Cys	Ala	Tyr	Leu	Gly	Phe	Ser	Met
			85					90					95		
Val	Ser	Ala	Ala	Tyr	Ile	Ser	Glu	Val	Phe	Arg	Ser	Ser	Ile	Glu	Ala
		100					105						110		
Ile	Asp	Lys	Gly	Gln	Trp	Glu	Ala	Lys	Ala	Leu	Gly	Leu	Pro	Tyr	
	115					120					125				
Ala	Leu	Met	Val	Lys	Lys	Ile	Ile	Leu	Pro	Gln	Ala	Phe	Arg	Ile	Ala
	130					135					140				
Val	Pro	Pro	Leu	Gly	Asn	Val	Ile	Ile	Asp	Met	Val	Lys	Ser	Ser	Ser

145		150		155		160									
Leu	Ala	Ala	Met	Ile	Thr	Val	Pro	Asp	Ile	Phe	Gln	Asn	Ala	Lys	Ile
		165							170					175	
Ile	Gly	Gly	Arg	Glu	Trp	Asp	Tyr	Met	Ser	Met	Tyr	Ile	Leu	Val	Ala
		180						185					190		
Phe	Ile	Tyr	Trp	Leu	Ile	Ala	Phe	Leu	Leu	Glu	Arg	Tyr	Gln	Glu	Phe
		195					200					205			
Leu	Glu	Asn	Lys	Leu	Ala	Leu	Val								
	210					215									

<210> SEQ ID NO 429
 <211> LENGTH: 1260
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 429

ttgtttatta	gaaaaaatagg	agggtgacatg	tttaatcgta	tccgcattcg	ttttatcatg	60
attgcttcta	ttgccatttt	tattattttta	agttcaattg	ttggtattat	taacacggca	120
cgctgttacc	aaagtcaaca	agaaattaac	cgtatttttac	atttaatttc	ctcaaataaaa	180
ggtaaattac	ctggcactac	ggaaaagctct	aaacgacttg	gaacgaaact	gtctgaagat	240
agcctaagcc	agtttcggta	ttatagtgtc	atttttaaatg	ctaattggaca	tctactttct	300
tctaatactg	ctaataatttc	agcttttagat	agagaagaag	cccaatattt	tgctagactt	360
tttgctaagt	ctggggaaga	aaaaggcagt	taccgtcacc	aagatagtgt	ttattcgtac	420
ttgattactc	agctgccaaa	tgaagaaaaa	ctggttgtaa	ttttagatac	taccttttat	480
tttcgtagtg	taggagattt	attagctggt	tcagtgatgt	tggcctttgg	aggatttatc	540
ttttttgttg	ttttagttag	tcttttttcc	ggtatggtca	tcaaaccctt	tgtccaaaat	600
tatgagaagc	agcgtcgctt	tattactaat	gcaggccacg	agttaaaaaac	accactagcc	660
attatctcag	ccaataatga	attggtcgaa	ttaatgactg	gagaatcaga	atggaccaag	720
agtacaagtg	atcagggtgaa	gcgattgaca	ggcttgatta	atcaaatagat	tactttggct	780
cgtttgagg	aacagccaga	tgtggtatta	catatggtag	acttttcagc	tattgctcaa	840
gatgcagctg	aagatttttaa	gagtctgggt	ttgaaaagatg	gtaaaacgttt	tgatttgacg	900
attcaaccga	atattatgat	taaagcggag	gaaaagtcac	tgtttgaaact	tgtgacaatt	960
ttagttgata	atgccaataa	atattgtgat	cctaaaggct	tggtcaagggt	atctttaacc	1020
actattggaa	gaagacgaaa	acgagcgaaa	ttagaagttt	ctaataccta	tttggaagga	1080
aaatccattg	attacagccg	cttcttttgaa	cgcttttatc	gcgaagacga	atcccataat	1140
agcaaagaaa	aagggttatgg	aattggttta	tctatggcag	aaagtatggg	taagttattt	1200
aaaggaacga	taactgtaaa	ttataaaaaac	gatgctattg	tttttacagt	ggtgatttga	1260

<210> SEQ ID NO 430
 <211> LENGTH: 419
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 430

Met	Phe	Ile	Arg	Lys	Ile	Gly	Gly	Asp	Met	Phe	Asn	Arg	Ile	Arg	Ile
1				5					10					15	
Arg	Phe	Ile	Met	Ile	Ala	Ser	Ile	Ala	Ile	Phe	Ile	Ile	Leu	Ser	Ser
			20					25					30		
Ile	Val	Gly	Ile	Ile	Asn	Thr	Ala	Arg	Cys	Tyr	Gln	Ser	Gln	Gln	Glu
		35					40					45			
Ile	Asn	Arg	Ile	Leu	His	Leu	Ile	Ser	Ser	Asn	Lys	Gly	Lys	Leu	Pro
	50					55				60					
Gly	Thr	Thr	Glu	Ser	Ser	Lys	Arg	Leu	Gly	Thr	Lys	Leu	Ser	Glu	Asp
65				70					75					80	
Ser	Leu	Ser	Gln	Phe	Arg	Tyr	Tyr	Ser	Val	Ile	Phe	Asn	Ala	Asn	Gly
			85					90						95	
His	Leu	Leu	Ser	Ser	Asn	Thr	Ala	Asn	Ile	Ser	Ala	Leu	Asp	Arg	Glu
			100					105					110		
Glu	Ala	Gln	Tyr	Phe	Ala	Arg	Leu	Phe	Ala	Lys	Ser	Gly	Glu	Glu	Lys

		115					120					125					
Gly	Ser	Tyr	Arg	His	Gln	Asp	Ser	Val	Tyr	Ser	Tyr	Leu	Ile	Thr	Gln		
	130					135					140						
Leu	Pro	Asn	Glu	Glu	Lys	Leu	Val	Val	Ile	Leu	Asp	Thr	Thr	Phe	Tyr		
145					150					155					160		
Phe	Arg	Ser	Val	Gly	Asp	Leu	Leu	Ala	Val	Ser	Val	Met	Leu	Ala	Phe		
				165					170					175			
Gly	Gly	Phe	Ile	Phe	Phe	Val	Val	Leu	Val	Ser	Leu	Phe	Ser	Gly	Met		
		180						185				190					
Val	Ile	Lys	Pro	Phe	Val	Gln	Asn	Tyr	Glu	Lys	Gln	Arg	Arg	Phe	Ile		
	195					200					205						
Thr	Asn	Ala	Gly	His	Glu	Leu	Lys	Thr	Pro	Leu	Ala	Ile	Ile	Ser	Ala		
210					215					220							
Asn	Asn	Glu	Leu	Val	Glu	Leu	Met	Thr	Gly	Glu	Ser	Glu	Trp	Thr	Lys		
225					230				235						240		
Ser	Thr	Ser	Asp	Gln	Val	Lys	Arg	Leu	Thr	Gly	Leu	Ile	Asn	Gln	Met		
			245					250						255			
Ile	Thr	Leu	Ala	Arg	Leu	Glu	Glu	Gln	Pro	Asp	Val	Val	Leu	His	Met		
		260						265					270				
Val	Asp	Phe	Ser	Ala	Ile	Ala	Gln	Asp	Ala	Ala	Glu	Asp	Phe	Lys	Ser		
	275					280					285						
Leu	Val	Leu	Lys	Asp	Gly	Lys	Arg	Phe	Asp	Leu	Thr	Ile	Gln	Pro	Asn		
290					295					300							
Ile	Met	Ile	Lys	Ala	Glu	Glu	Lys	Ser	Leu	Phe	Glu	Leu	Val	Thr	Ile		
305				310					315					320			
Leu	Val	Asp	Asn	Ala	Asn	Lys	Tyr	Cys	Asp	Pro	Lys	Gly	Leu	Val	Lys		
			325					330					335				
Val	Ser	Leu	Thr	Thr	Ile	Gly	Arg	Arg	Arg	Lys	Arg	Ala	Lys	Leu	Glu		
		340				345						350					
Val	Ser	Asn	Thr	Tyr	Leu	Glu	Gly	Lys	Ser	Ile	Asp	Tyr	Ser	Arg	Phe		
	355					360					365						
Phe	Glu	Arg	Phe	Tyr	Arg	Glu	Asp	Glu	Ser	His	Asn	Ser	Lys	Glu	Lys		
370					375						380						
Gly	Tyr	Gly	Ile	Gly	Leu	Ser	Met	Ala	Glu	Ser	Met	Val	Lys	Leu	Phe		
385				390					395					400			
Lys	Gly	Thr	Ile	Thr	Val	Asn	Tyr	Lys	Asn	Asp	Ala	Ile	Val	Phe	Thr		
			405					410						415			
Val	Val	Ile															

<210> SEQ ID NO 431

<211> LENGTH: 1020

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 431

atgagaaaaa	gatgctattc	aacttcagct	gcagtattgg	cagcagtgac	tttatttgtt	60
ctatcggtag	atcgtggtgt	tatagcagat	agtttttctg	ctaatcaaga	gattagatat	120
tcggaagtaa	caccttatca	cgttacttcc	gttttgacca	aaggagttac	tcctccagca	180
aacttcaactc	aaggtgaaga	tgttttttcac	gctccttatg	ttgctaacca	aggatgggat	240
gatattacca	aaacattcaa	tggaaaagac	gatcttcttt	gcggggctgc	cacagcaggg	300
aatatgcttc	actggtggtt	cgatcaaaac	aaagaccaa	ttaaacgtta	tttggaagag	360
catccagaaa	agcaaaaaat	aaacttcaat	ggcgaacaga	tgtttgacgt	aaaagaagct	420
atcgacacta	aaaaccacca	gctagatagt	aaattatttg	aatattttta	agaaaaagct	480
ttcccttata	tatctactaa	acacctagga	gttttccctg	atcatgtaat	tgatatgttc	540
attaacggct	accgccttag	tctaactaac	cacggtccaa	cgccagtaaa	agaaggtagt	600
aaagatcccc	gaggtggtat	ttttgacgcc	gtatttacia	gaggtgatca	aagtaagcta	660
ttgacaagtc	gtcatgattt	taaagaaaaa	aatctcaaag	aatcagtgta	tctcattaag	720
aaagagttaa	ccgaaggcaa	ggctctaggc	ctatcacaca	cctacgctaa	cgtacgcatac	780

aaccatgtta	taaacctgtg	gggagctgac	tttgattcta	acgggaacct	taaagctatt	840
tatgtaacag	actctgatag	taatgcatct	attggtatga	agaaatactt	tgttggtggt	900
aattccgctg	gaaaagtagc	tatttctgct	aaagaaataa	aagaagataa	tattggtgct	960
caagtactag	ggttatttac	actttcaaca	gggcaagata	gttggaatca	gaccaattaa	1020

<210> SEQ ID NO 432

<211> LENGTH: 339

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 432

Met	Arg	Lys	Arg	Cys	Tyr	Ser	Thr	Ser	Ala	Ala	Val	Leu	Ala	Ala	Val
1				5					10					15	
Thr	Leu	Phe	Val	Leu	Ser	Val	Asp	Arg	Gly	Val	Ile	Ala	Asp	Ser	Phe
			20					25					30		
Ser	Ala	Asn	Gln	Glu	Ile	Arg	Tyr	Ser	Glu	Val	Thr	Pro	Tyr	His	Val
		35					40					45			
Thr	Ser	Val	Trp	Thr	Lys	Gly	Val	Thr	Pro	Pro	Ala	Asn	Phe	Thr	Gln
	50					55					60				
Gly	Glu	Asp	Val	Phe	His	Ala	Pro	Tyr	Val	Ala	Asn	Gln	Gly	Trp	Tyr
65					70					75					80
Asp	Ile	Thr	Lys	Thr	Phe	Asn	Gly	Lys	Asp	Asp	Leu	Leu	Cys	Gly	Ala
				85					90					95	
Ala	Thr	Ala	Gly	Asn	Met	Leu	His	Trp	Trp	Phe	Asp	Gln	Asn	Lys	Asp
			100					105					110		
Gln	Ile	Lys	Arg	Tyr	Leu	Glu	Glu	His	Pro	Glu	Lys	Gln	Lys	Ile	Asn
		115					120					125			
Phe	Asn	Gly	Glu	Gln	Met	Phe	Asp	Val	Lys	Glu	Ala	Ile	Asp	Thr	Lys
	130					135					140				
Asn	His	Gln	Leu	Asp	Ser	Lys	Leu	Phe	Glu	Tyr	Phe	Lys	Glu	Lys	Ala
145					150					155					160
Phe	Pro	Tyr	Leu	Ser	Thr	Lys	His	Leu	Gly	Val	Phe	Pro	Asp	His	Val
				165					170					175	
Ile	Asp	Met	Phe	Ile	Asn	Gly	Tyr	Arg	Leu	Ser	Leu	Thr	Asn	His	Gly
			180					185					190		
Pro	Thr	Pro	Val	Lys	Glu	Gly	Ser	Lys	Asp	Pro	Arg	Gly	Gly	Ile	Phe
		195					200						205		
Asp	Ala	Val	Phe	Thr	Arg	Gly	Asp	Gln	Ser	Lys	Leu	Leu	Thr	Ser	Arg
	210					215					220				
His	Asp	Phe	Lys	Glu	Lys	Asn	Leu	Lys	Glu	Ile	Ser	Asp	Leu	Ile	Lys
225					230					235					240
Lys	Glu	Leu	Thr	Glu	Gly	Lys	Ala	Leu	Gly	Leu	Ser	His	Thr	Tyr	Ala
				245					250					255	
Asn	Val	Arg	Ile	Asn	His	Val	Ile	Asn	Leu	Trp	Gly	Ala	Asp	Phe	Asp
			260					265					270		
Ser	Asn	Gly	Asn	Leu	Lys	Ala	Ile	Tyr	Val	Thr	Asp	Ser	Asp	Ser	Asn
	275						280					285			
Ala	Ser	Ile	Gly	Met	Lys	Lys	Tyr	Phe	Val	Gly	Val	Asn	Ser	Ala	Gly
	290					295					300				
Lys	Val	Ala	Ile	Ser	Ala	Lys	Glu	Ile	Lys	Glu	Asp	Asn	Ile	Gly	Ala
305					310					315					320
Gln	Val	Leu	Gly	Leu	Phe	Thr	Leu	Ser	Thr	Gly	Gln	Asp	Ser	Trp	Asn
				325					330					335	
Gln	Thr	Asn													

<210> SEQ ID NO 433

<211> LENGTH: 600

<212> TYPE: DNA

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<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 433
ttgaagggtga aaaaaaggag aagaagggct aaatcatcag taaatcgact tgtcttaggg      60
ttagtattac ttaatctgat tgtagtatg tggacactaa aattgggaaa ccagcgatta      120
gctccgtatg cggatcacga aactctgaca tttgtcagga agattagtca tgctgctcaa      180
tcagtcgctc aaaagaaaca gttatatagt tcggtgatga tggctcaggc catttttagaa      240
tccaataatg gtaagtcaca actaagtcaa aaaccttatt ataatttttt cgggattaag      300
gggagctata aagaacggtc agtcattttt ccaactttag aagacgatgg acaagggaat      360
ctttatcaaa ttgatgctgc ttttcgttcc tatgggagcc tgacagcttg ttttttagat      420
tacgcaagag ttttgaatga tccactttat gacaaaaccc acaaaaagt ttggtctcat      480
tatcaagatg ctactgcaac cttaacaggc acttacgcc a ctgatacaac ttaccatacc      540
aaattaaatg aattgattga atggtatcaa ctactaatt ttgatggtct aatgaaatag      600

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<210> SEQ ID NO 434
<211> LENGTH: 199
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 434
Met Lys Val Lys Lys Arg Arg Arg Arg Ala Lys Ser Ser Val Asn Arg
1          5          10          15
Leu Val Leu Gly Leu Val Leu Leu Asn Leu Ile Val Ser Met Trp Thr
20          25          30
Leu Lys Leu Gly Asn Gln Arg Leu Ala Pro Tyr Ala Asp His Glu Thr
35          40          45
Leu Thr Phe Val Arg Lys Ile Ser His Ala Ala Gln Ser Val Ala Gln
50          55          60
Lys Lys Gln Leu Tyr Ser Ser Val Met Met Ala Gln Ala Ile Leu Glu
65          70          75          80
Ser Asn Asn Gly Lys Ser Gln Leu Ser Gln Lys Pro Tyr Tyr Asn Phe
85          90          95
Phe Gly Ile Lys Gly Ser Tyr Lys Glu Arg Ser Val Ile Phe Pro Thr
100         105         110
Leu Glu Asp Asp Gly Gln Gly Asn Leu Tyr Gln Ile Asp Ala Ala Phe
115         120         125
Arg Ser Tyr Gly Ser Leu Thr Ala Cys Phe Leu Asp Tyr Ala Arg Val
130         135         140
Leu Asn Asp Pro Leu Tyr Asp Lys Thr His Lys Lys Phe Trp Ser His
145         150         155         160
Tyr Gln Asp Ala Thr Ala Thr Leu Thr Gly Thr Tyr Ala Thr Asp Thr
165         170         175
Thr Tyr His Thr Lys Leu Asn Glu Leu Ile Glu Trp Tyr Gln Leu Thr
180         185         190
Asn Phe Asp Gly Leu Met Lys
195

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<210> SEQ ID NO 435
<211> LENGTH: 1947
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 435
atgaaaattc aagattttatt gagaaaagat attatgattc tcgattttaca ggctattttct      60
aaagaagttg ccattgacga gatgattact aaattagttg aaaaagatat tgtacatgat      120
tttgatgtct ttaaaaagag tatcatgaca cgtgaagaac aaacatcaac agggcttgggt      180
gatgggattg ccatgcctca ttctaaaaat attgtagtag ataaaccagc ggtcttgttt      240
gcgaaatcaa ataaaggtgt ggattacaag gcttttagatg gtcaaccaac ggatctcttc      300
tttatgattg ctgcgcctca aggagcaaat gatactcact tggctgcact agcagaatta      360
tcacaatacc ttttgaaaga cggcttttgct gataaacttc gtgctgcagc gacaccagaa      420

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gcagtcattg ctgtttttga tgaagcgta acagctaaag aagaagtggg tgctccaaca 480
agtgggtcaag actttatcgt tgctgtttaca gcttgtccga caggaattgc tcacacttat 540
atggcagaag aggcctttgaa aaaacaagct gcagaaatgg gagtagctat taaagttgaa 600
acaaacgggtg cttctgggtg ggctaatacgt ttaaccgctg aagatattca gagagctaaa 660
ggaggttattg ttgcagctga taaagcgggt gaaatggacc gttttgatgg taaacaattc 720
attgctcgcc ctggtgcaga tggatatcaag aaaagtcagg aattgatttc tttgatttta 780
aacaatgaag gaaacactta tcatgctaaa aatggaaaat ctgaaacagc agtatcaact 840
gagaaaacaa gtttaggcgg tgcttttctat aaacacttga tgggcgggtg ctcaaaaatg 900
ttgccatttg ttattgggtg cgggattatg attgctctag catttttatt ggataacatg 960
cttgggtgtgc caaatgatca gcttgggaag cttggatcct atcatgaaat agcagctatt 1020
tttatgaaca ttggtggagc agccttttcc ttcattgttac cagtactagc aggttatatc 1080
gcttatttcta ttgctgaaaa accgggccta gtagctgggt ttgtggcagg tgccattgcc 1140
tcaaatgggtc ttgcttttgg taaggtacca tttgcagcag gaggagaagt gagcttgggc 1200
ttaacggggcg tgccatcagg ttctcttggg gcgcttgggt gtggtttcct tgccgggtgg 1260
gttattcttg cccttcgtaa attgttggca ggcctaccac gttctctaga aggggttaaa 1320
tctatcctcc ttaccatt acttggcgtc cttgtcactg gtttcttgat gctttttgtc 1380
aatattccaa tggcagctat taacacagcc cttaatgatt tcttacaagg tctttcagga 1440
agctctgctg tccttatggg acttcttgtt ggtggaatga tggctgttga catgggtggg 1500
cctgttaata aggcagctta tgtttttggg acaggaactt tagcagctac tgtggcaaat 1560
ggtggttcgg tcgttatggc cgctgttatg gcaggttgta tgggtacctc tcttgctgtt 1620
ttttagacca ctctcttgtt taaagataaa ttaccaaaag aagaacgtga atcaggcttg 1680
acaaatattg ttatgggact ttcattcatc accgaaggag caattccgtt tgggtgcagc 1740
gacccagcac gtgcgattcc tagctttatc gcaggttctg ccttgacagg agctcttgtt 1800
ggtttggctg gtattaaatt aatggcgcca catgggtggt tcttcgtaat cgctttaaca 1860
agcaatccaa tcttatatct tgtctttgtt gtgattggtg cccttgatc aggtatctta 1920
tttggcgctc ttcgcaaaaa agcctaa 1947

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<210> SEQ ID NO 436

<211> LENGTH: 648

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 436

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Met Lys Ile Gln Asp Leu Leu Arg Lys Asp Ile Met Ile Leu Asp Leu
1           5           10           15
Gln Ala Ile Ser Lys Glu Val Ala Ile Asp Glu Met Ile Thr Lys Leu
20          25          30
Val Glu Lys Asp Ile Val His Asp Phe Asp Val Phe Lys Lys Ser Ile
35          40          45
Met Thr Arg Glu Glu Gln Thr Ser Thr Gly Leu Gly Asp Gly Ile Ala
50          55          60
Met Pro His Ser Lys Asn Ile Val Val Asp Lys Pro Ala Val Leu Phe
65          70          75          80
Ala Lys Ser Asn Lys Gly Val Asp Tyr Lys Ala Leu Asp Gly Gln Pro
85          90          95
Thr Asp Leu Phe Phe Met Ile Ala Ala Pro Gln Gly Ala Asn Asp Thr
100         105         110
His Leu Ala Ala Leu Ala Glu Leu Ser Gln Tyr Leu Leu Lys Asp Gly
115         120         125
Phe Ala Asp Lys Leu Arg Ala Ala Ala Thr Pro Glu Ala Val Ile Ala
130         135         140
Val Phe Asp Glu Ala Ser Thr Ala Lys Glu Glu Val Val Ala Pro Thr
145         150         155         160
Ser Gly Gln Asp Phe Ile Val Ala Val Thr Ala Cys Pro Thr Gly Ile
165         170         175
Ala His Thr Tyr Met Ala Glu Glu Ala Leu Lys Lys Gln Ala Ala Glu
180         185         190
Met Gly Val Ala Ile Lys Val Glu Thr Asn Gly Ala Ser Gly Val Ala

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		195					200				205				
Asn	Arg	Leu	Thr	Ala	Glu	Asp	Ile	Gln	Arg	Ala	Lys	Gly	Val	Ile	Val
	210					215					220				
Ala	Ala	Asp	Lys	Ala	Val	Glu	Met	Asp	Arg	Phe	Asp	Gly	Lys	Gln	Phe
225					230					235					240
Ile	Ala	Arg	Pro	Val	Ala	Asp	Gly	Ile	Lys	Lys	Ser	Gln	Glu	Leu	Ile
				245					250					255	
Ser	Leu	Ile	Leu	Asn	Asn	Glu	Gly	Asn	Thr	Tyr	His	Ala	Lys	Asn	Gly
			260					265					270		
Lys	Ser	Glu	Thr	Ala	Val	Ser	Thr	Glu	Lys	Thr	Ser	Leu	Gly	Gly	Ala
		275					280					285			
Phe	Tyr	Lys	His	Leu	Met	Gly	Gly	Val	Ser	Gln	Met	Leu	Pro	Phe	Val
	290					295					300				
Ile	Gly	Gly	Gly	Ile	Met	Ile	Ala	Leu	Ala	Phe	Leu	Leu	Asp	Asn	Met
305					310					315					320
Leu	Gly	Val	Pro	Asn	Asp	Gln	Leu	Gly	Ser	Leu	Gly	Ser	Tyr	His	Glu
				325					330					335	
Ile	Ala	Ala	Ile	Phe	Met	Asn	Ile	Gly	Gly	Ala	Ala	Phe	Ser	Phe	Met
			340					345					350		
Leu	Pro	Val	Leu	Ala	Gly	Tyr	Ile	Ala	Tyr	Ser	Ile	Ala	Glu	Lys	Pro
		355					360					365			
Gly	Leu	Val	Ala	Gly	Phe	Val	Ala	Gly	Ala	Ile	Ala	Ser	Asn	Gly	Leu
	370					375					380				
Ala	Phe	Gly	Lys	Val	Pro	Phe	Ala	Ala	Gly	Gly	Glu	Val	Ser	Leu	Gly
385					390					395					400
Leu	Thr	Gly	Val	Pro	Ser	Gly	Phe	Leu	Gly	Ala	Leu	Val	Gly	Gly	Phe
				405					410					415	
Leu	Ala	Gly	Gly	Val	Ile	Leu	Ala	Leu	Arg	Lys	Leu	Leu	Ala	Gly	Leu
			420					425					430		
Pro	Arg	Ser	Leu	Glu	Gly	Val	Lys	Ser	Ile	Leu	Leu	Tyr	Pro	Leu	Leu
		435					440					445			
Gly	Val	Leu	Val	Thr	Gly	Phe	Leu	Met	Leu	Phe	Val	Asn	Ile	Pro	Met
	450					455					460				
Ala	Ala	Ile	Asn	Thr	Ala	Leu	Asn	Asp	Phe	Leu	Gln	Gly	Leu	Ser	Gly
465					470					475					480
Ser	Ser	Ala	Val	Leu	Met	Gly	Leu	Leu	Val	Gly	Gly	Met	Met	Ala	Val
				485					490					495	
Asp	Met	Gly	Gly	Pro	Val	Asn	Lys	Ala	Ala	Tyr	Val	Phe	Gly	Thr	Gly
			500					505					510		
Thr	Leu	Ala	Ala	Thr	Val	Ala	Asn	Gly	Gly	Ser	Val	Val	Met	Ala	Ala
		515					520					525			
Val	Met	Ala	Gly	Gly	Met	Val	Pro	Pro	Leu	Ala	Val	Phe	Val	Ala	Thr
	530					535					540				
Leu	Leu	Phe	Lys	Asp	Lys	Phe	Thr	Lys	Glu	Glu	Arg	Glu	Ser	Gly	Leu

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<210> SEQ ID NO 437
<211> LENGTH: 1059
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 437
atgacaacaa cagataaaga gacatttagt tcttttatga ataaggtctt ggctggtaca      60
gcgattgcta tcgttgtggc actcattcca aatgctatatt tagcgacttt cttaaaaccg      120
cttttgccaa atatggcagc tgctgaattt ttacacattg tgcaagtctt ccaattcttc      180
acgccgatta tggctggttt cttgattggg caacaattta agtttaatcc tatgcaacag      240
ttggctgttg gtggagctgc ttatatcggc tctggagcct gggcttatac agaagtcatt      300
caaaaagggtg tggcgacagg aacattccaa cttagaggta ttggggactt aatcaatatg      360
atgattacag ctagccttgc ggtttttagc gtgaaatatt ttgggaataa atttggctct      420
ttaaccatta tcttgttacc tatcactata ggaactggcg taggttatat tggttggaaa      480
tttttgcctt atgtgtctta cgtgacaacc ctgatcggac aagggattaa ttcttttaca      540
accttacaac ctattttaat gtctatttta attgcagttg ctttctcgct tatcattgtt      600
agtccgattt caactgttgc aatcggttta gctattgggc ttaatggaat ggctgcggga      660
gcagcttcta tgggaattgc atcgacagca gcagtccttag tgtggcgac gcttaaagtt      720
aataaatctg gtgtaccaat tgctatcgca cttggggcta tgaaaatgat gatgccaaac      780
ttcttgaaac atcctatcat ggctattccg atggtgttca ctgcagcaat tagctcatta      840
acagtaccat tgtttaatct tgttgaaca ccagcttcat ctggttttgg cttagtgtgt      900
gcagtaggtc cgattgcttc tttagcaggt ggtagctcaa tacttattat tacccttgc      960
tggatcattg ttccgtttgc ggttgctttt gcggcgcata aggtttctaa agatattcta     1020
aaactgtata aagaagacat tttcgtcttt gaaggctaa      1059

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<210> SEQ ID NO 438
<211> LENGTH: 352
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 438
Met Thr Thr Thr Asp Lys Glu Thr Phe Ser Ser Phe Met Asn Lys Val
1      5      10      15
Leu Ala Gly Thr Ala Ile Ala Ile Val Val Ala Leu Ile Pro Asn Ala
20     25     30
Ile Leu Ala Thr Phe Leu Lys Pro Leu Leu Pro Asn Met Ala Ala Ala
35     40     45
Glu Phe Leu His Ile Val Gln Val Phe Gln Phe Phe Thr Pro Ile Met
50     55     60
Ala Gly Phe Leu Ile Gly Gln Gln Phe Lys Phe Asn Pro Met Gln Gln
65     70     75     80
Leu Ala Val Gly Gly Ala Ala Tyr Ile Gly Ser Gly Ala Trp Ala Tyr
85     90     95
Thr Glu Val Ile Gln Lys Gly Val Ala Thr Gly Thr Phe Gln Leu Arg
100    105    110
Gly Ile Gly Asp Leu Ile Asn Met Met Ile Thr Ala Ser Leu Ala Val
115    120    125
Leu Ala Val Lys Tyr Phe Gly Asn Lys Phe Gly Ser Leu Thr Ile Ile
130    135    140
Leu Leu Pro Ile Thr Ile Gly Thr Gly Val Gly Tyr Ile Gly Trp Lys
145    150    155    160
Phe Leu Pro Tyr Val Ser Tyr Val Thr Thr Leu Ile Gly Gln Gly Ile
165    170    175
Asn Ser Phe Thr Thr Leu Gln Pro Ile Leu Met Ser Ile Leu Ile Ala
180    185    190
Val Ala Phe Ser Leu Ile Ile Val Ser Pro Ile Ser Thr Val Ala Ile
195    200    205
Gly Leu Ala Ile Gly Leu Asn Gly Met Ala Ala Gly Ala Ala Ser Met

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210	215	220
Gly Ile Ala Ser Thr	Ala Ala Val Leu Val	Trp Ala Thr Leu Lys Val
225	230	235
Asn Lys Ser Gly Val	Pro Ile Ala Ile Ala	Leu Gly Ala Met Lys Met
245	250	255
Met Met Pro Asn Phe	Leu Lys His Pro	Ile Met Ala Ile Pro Met Val
260	265	270
Phe Thr Ala Ala Ile	Ser Ser Leu Thr	Val Pro Leu Phe Asn Leu Val
275	280	285
Gly Thr Pro Ala Ser	Ser Gly Phe Gly	Leu Val Gly Ala Val Gly Pro
290	295	300
Ile Ala Ser Leu Ala	Gly Gly Ser Ser	Ile Leu Ile Ile Ile Leu Ala
305	310	315
Trp Ile Ile Val Pro	Phe Ala Val Ala	Phe Ala His Lys Val Ser
325	330	335
Lys Asp Ile Leu Lys	Leu Tyr Lys Glu	Asp Ile Phe Val Phe Glu Gly
340	345	350

<210> SEQ ID NO 439
 <211> LENGTH: 876
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 439

atgccagcaa gtaaaaaagt caccattatt tttatattaa atcttagttt ttccctcatt	60
gaatttattt ttgggacatt attcttttctg ggtgctattt tagcagatgc tgtccacgat	120
tttggagatg ccattgctat tggatatctca gctatcttag aaagaaaggc tgtaaaaaaa	180
gagagtccaa attttttact aggctataag cgatttagcc ttttaggagc gctaacgaca	240
aatctaatac ttattagcgg gtcattatta gtaatgattg aaacgatacc aaaattatgg	300
catcctacta ttgttaatta tgacggtatg ttcgttttag ctatttttgc aattataatc	360
aatggatttg ctagcttcat cattcactct aaccagacaa aaaatgaaga aatattaagc	420
cttcactttt tagaagatat ccttgggtgg ttagccatta tcatactgtc actgatctta	480
aaatggaaac cttggtacat tcttgatcct ttattatcaa ttgccattgc ttcttttata	540
ttatctaaag ctcttccaaa gttagtagca actgctaaca ttttttttaga tgggtgttcct	600
gattctatag actattgcac tttgcaccat gaactcagcc aacttcctca tatagtgtct	660
gttaatcagc ttaatgtttg gtcgatggat ggtattgatc atagagcaac tatacattgc	720
tgcttgagag aatctaccac tgaaaaacat tgcaaaaaat ctattagact gatttgtcaa	780
aggtacaata taaactcagt cactgtggaa atcgatactt cttaaacga acaccaacat	840
cactgttctt ctctttctag tattgaagtc aactaa	876

<210> SEQ ID NO 440
 <211> LENGTH: 291
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 440

Met Pro Ala Ser Lys Lys Val Thr Ile Ile Phe Ile Leu Asn Leu Ser	1	5	10	15
Phe Ser Leu Ile Glu Phe Ile Phe Gly Thr Leu Phe Phe Ser Gly Ala	20	25	30	
Ile Leu Ala Asp Ala Val His Asp Phe Gly Asp Ala Ile Ala Ile Gly	35	40	45	
Ile Ser Ala Ile Leu Glu Arg Lys Ala Val Lys Lys Glu Ser Pro Asn	50	55	60	
Phe Ser Leu Gly Tyr Lys Arg Phe Ser Leu Leu Gly Ala Leu Thr Thr	65	70	75	80
Asn Leu Ile Leu Ile Ser Gly Ser Leu Leu Val Met Ile Glu Thr Ile	85	90	95	
Pro Lys Leu Trp His Pro Thr Ile Val Asn Tyr Asp Gly Met Phe Val				

			100					105				110					
Leu	Ala	Ile	Phe	Ala	Ile	Ile	Ile	Asn	Gly	Phe	Ala	Ser	Phe	Ile	Ile		
		115					120					125					
His	Ser	Asn	Gln	Thr	Lys	Asn	Glu	Glu	Ile	Leu	Ser	Leu	His	Phe	Leu		
		130				135					140						
Glu	Asp	Ile	Leu	Gly	Trp	Leu	Ala	Ile	Ile	Ile	Leu	Ser	Leu	Ile	Leu		
145				150				155			160						
Lys	Trp	Lys	Pro	Trp	Tyr	Ile	Leu	Asp	Pro	Leu	Leu	Ser	Ile	Ala	Ile		
			165					170			175						
Ala	Ser	Phe	Ile	Leu	Ser	Lys	Ala	Leu	Pro	Lys	Leu	Val	Ala	Thr	Ala		
		180					185				190						
Asn	Ile	Phe	Leu	Asp	Gly	Val	Pro	Asp	Ser	Ile	Asp	Tyr	Cys	Thr	Leu		
		195				200					205						
His	His	Glu	Leu	Ser	Gln	Leu	Pro	His	Ile	Val	Ser	Val	Asn	Gln	Leu		
210				215				220									
Asn	Val	Trp	Ser	Met	Asp	Gly	Ile	Asp	His	Arg	Ala	Thr	Ile	His	Cys		
225				230				235			240						
Cys	Leu	Arg	Glu	Ser	Thr	Thr	Glu	Lys	His	Cys	Lys	Lys	Ser	Ile	Arg		
			245				250				255						
Leu	Ile	Cys	Gln	Arg	Tyr	Asn	Ile	Asn	Ser	Val	Thr	Val	Glu	Ile	Asp		
		260				265					270						
Thr	Ser	Leu	Asn	Glu	His	Gln	His	His	Cys	Ser	Ser	Leu	Ser	Ser	Ile		
		275				280					285						
Glu	Val	Asn															
		290															

<210> SEQ ID NO 441

<211> LENGTH: 1260

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 441

gtgaaagatg	tcatttatga	tgtggaagaa	gtgccaaagg	caggtatggt	agttggtttg	60
tcctttcagc	acttatttgc	tatgttttgt	gcgactgttc	tggttcccat	tctagttgga	120
attgacccat	cagttgcttt	gttatctagt	ggttaggaa	cccttgccca	cttatcagtg	180
accaaattta	aaattccagc	ctacatgggc	tcaagttttg	cttatatagc	agctatgcag	240
ttactgatga	agacaaatgg	tattggtgct	gtagctcaag	gggctatgac	aggaggtctc	300
gtttacctga	ttgtagcttt	gattgttaaa	gctattggca	atgattggat	tgataacatc	360
ttaccaccga	ttgtgggttg	tccgattgtt	atggtcattg	gtctaagcct	agcttctaca	420
gctgttaatg	atgtcatgct	aaaaaatggg	aactataatc	tgacttatct	tgttattggg	480
ttagtcacct	tattatcagt	tatttttttc	aatatttatg	gtaagggaa	tgttgctatt	540
gtaccgcttt	tattagggct	attagtttgt	tatgtttag	cccttttagt	gggtgttctc	600
accggtcaag	aaattgttga	ttttaccaat	gtggctcagg	ccaaatgggt	tagtatccca	660
tcagtggaaa	ttcctttctt	aacctacggg	gttaaattct	acccaagtgc	cattttaact	720
atggcaccca	ttgcctttgt	tacaatgaca	gaacattttg	gacacattat	ggctctaaat	780
agtttgacaa	aaagagatta	tttcaaggat	ccaggacttg	aaaagacttt	aactgggtgat	840
ggttttgcgc	aaatcattgc	cggcttctta	ggggcacctc	cggtcacttc	ttatggtgaa	900
aacatcggtg	taatggcttt	gaataaaaata	ttctcggtct	atgttattgc	agggtccgca	960
gtgattgccg	ctctcctcag	ttttatcggg	aaggatcag	ccttaattca	atctattcca	1020
acaccagtta	ttggagggtat	atcagttgcc	ttgtttggtg	tgatagcttc	tagcggtttg	1080
aaaatcttga	ttgaatccaa	agttgatatg	gataataaga	aaaacttatt	gattgctagt	1140
gttatttttg	tctctgggat	tggaggattg	atgcttcaag	taaatggtct	tcaaatttca	1200
ggtgtcgctt	tctcaacact	ccttggcatc	atcttatatc	aggtacttcc	tgaaaaaatag	1260

<210> SEQ ID NO 442

<211> LENGTH: 419

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 442

Met	Lys	Asp	Val	Ile	Tyr	Asp	Val	Glu	Glu	Val	Pro	Lys	Ala	Gly	Met
1				5				10						15	
Leu	Val	Gly	Leu	Ser	Phe	Gln	His	Leu	Phe	Ala	Met	Phe	Gly	Ala	Thr
			20					25					30		
Val	Leu	Val	Pro	Ile	Leu	Val	Gly	Ile	Asp	Pro	Ser	Val	Ala	Leu	Leu
			35				40					45			
Ser	Ser	Gly	Leu	Gly	Thr	Leu	Ala	His	Leu	Ser	Val	Thr	Lys	Phe	Lys
	50					55					60				
Ile	Pro	Ala	Tyr	Met	Gly	Ser	Ser	Phe	Ala	Tyr	Ile	Ala	Ala	Met	Gln
65					70					75					80
Leu	Leu	Met	Lys	Thr	Asn	Gly	Ile	Gly	Ala	Val	Ala	Gln	Gly	Ala	Met
				85				90					95		
Thr	Gly	Gly	Leu	Val	Tyr	Leu	Ile	Val	Ala	Leu	Ile	Val	Lys	Ala	Ile
			100					105					110		
Gly	Asn	Asp	Trp	Ile	Asp	Asn	Ile	Leu	Pro	Pro	Ile	Val	Val	Gly	Pro
	115						120					125			
Ile	Val	Met	Val	Ile	Gly	Leu	Ser	Leu	Ala	Ser	Thr	Ala	Val	Asn	Asp
	130					135					140				
Val	Met	Leu	Lys	Asn	Gly	Asn	Tyr	Asn	Leu	Thr	Tyr	Leu	Val	Ile	Gly
145					150					155					160
Leu	Val	Thr	Leu	Leu	Ser	Val	Ile	Phe	Phe	Asn	Ile	Tyr	Gly	Lys	Gly
				165				170					175		
Ile	Val	Ala	Ile	Val	Pro	Leu	Leu	Leu	Gly	Leu	Leu	Val	Gly	Tyr	Val
			180					185					190		
Val	Ala	Leu	Leu	Val	Gly	Val	Leu	Thr	Gly	Gln	Glu	Ile	Val	Asp	Phe
	195						200					205			
Thr	Asn	Val	Ala	Gln	Ala	Lys	Trp	Phe	Ser	Ile	Pro	Ser	Val	Glu	Ile
	210					215					220				
Pro	Phe	Leu	Thr	Tyr	Gly	Val	Lys	Phe	Tyr	Pro	Ser	Ala	Ile	Leu	Thr
225					230					235					240
Met	Ala	Pro	Ile	Ala	Phe	Val	Thr	Met	Thr	Glu	His	Phe	Gly	His	Ile
				245					250				255		
Met	Val	Leu	Asn	Ser	Leu	Thr	Lys	Arg	Asp	Tyr	Phe	Lys	Asp	Pro	Gly
			260					265					270		
Leu	Glu	Lys	Thr	Leu	Thr	Gly	Asp	Gly	Phe	Ala	Gln	Ile	Ile	Ala	Gly
		275				280						285			
Phe	Leu	Gly	Ala	Pro	Pro	Val	Thr	Ser	Tyr	Gly	Glu	Asn	Ile	Gly	Val
	290					295					300				
Met	Ala	Leu	Asn	Lys	Ile	Phe	Ser	Val	Tyr	Val	Ile	Ala	Gly	Ala	Ala
305					310					315					320
Val	Ile	Ala	Ala	Leu	Leu	Ser	Phe	Ile	Gly	Lys	Val	Ser	Ala	Leu	Ile
				325					330				335		
Gln	Ser	Ile	Pro	Thr	Pro	Val	Ile	Gly	Gly	Ile	Ser	Val	Ala	Leu	Phe
			340					345					350		
Gly	Val	Ile	Ala	Ser	Ser	Gly	Leu	Lys	Ile	Leu	Ile	Glu	Ser	Lys	Val
		355				360						365			
Asp	Met	Asp	Asn	Lys	Lys	Asn	Leu	Leu	Ile	Ala	Ser	Val	Ile	Leu	Val
	370					375					380				
Ser	Gly	Ile	Gly	Gly	Leu	Met	Leu	Gln	Val	Asn	Gly	Leu	Gln	Ile	Ser
385					390					395					400
Gly	Val	Ala	Phe	Ser	Thr	Leu	Leu	Gly	Ile	Ile	Leu	Tyr	Gln	Val	Leu
				405					410					415	
Pro	Glu	Lys													

<210> SEQ ID NO 443

<211> LENGTH: 459

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<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 443
atgaaaaaac gattgtttgt gcttagcttg atcctccttg tagctttgga tcaacttagt    60
aaattttgga ttgtttctca tatagcgctt ggagaagtga aaccctttat cccaggtatc    120
gtcagcttga cttacttgca aaacaatggg gctgcctttt ccatattgca ggaccagcaa    180
tggttctttg ttgtcataac ggttttagtt atcggttatg ctatttatta ccttgctact    240
catccccatt taaatatctg gaaacaatta gctctcttgc ttattatttc tgggtggaatc    300
gggaatttta ttgatcgctt gcgtttagct tacgtgattg atatgattca tttagacttt    360
gtggattttg ccatttttaa tgtggcagat tcatacctta ccgttggtgt catattatta    420
ttgatatggt tatggaaaga agaggattat ggaaattaa    459

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<210> SEQ ID NO 444
<211> LENGTH: 152
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 444
Met Lys Lys Arg Leu Phe Val Leu Ser Leu Ile Leu Leu Val Ala Leu
 1             5             10            15
Asp Gln Leu Ser Lys Phe Trp Ile Val Ser His Ile Ala Leu Gly Glu
      20            25            30
Val Lys Pro Phe Ile Pro Gly Ile Val Ser Leu Thr Tyr Leu Gln Asn
      35            40            45
Asn Gly Ala Ala Phe Ser Ile Leu Gln Asp Gln Gln Trp Phe Phe Val
      50            55            60
Val Ile Thr Val Leu Val Ile Gly Tyr Ala Ile Tyr Tyr Leu Ala Thr
      65            70            75            80
His Pro His Leu Asn Ile Trp Lys Gln Leu Ala Leu Leu Leu Ile Ile
      85            90            95
Ser Gly Gly Ile Gly Asn Phe Ile Asp Arg Leu Arg Leu Ala Tyr Val
      100           105           110
Ile Asp Met Ile His Leu Asp Phe Val Asp Phe Ala Ile Phe Asn Val
      115           120           125
Ala Asp Ser Tyr Leu Thr Val Gly Val Ile Leu Leu Leu Ile Cys Leu
      130           135           140
Trp Lys Glu Glu Asp Tyr Gly Asn
145           150

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<210> SEQ ID NO 445
<211> LENGTH: 1287
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 445
atgattaatc cttcaaaaaca aaaccaaacg attttttttat ggaatatggt aggaagttaa    60
tcaacagctg taatatcagt tatattactt atggtggtta ctaggttact aacttcggct    120
gattcagata tttacgcctt tgcctattct tttgctaata tgatggtagt tgttggaact    180
tttcagggtc gtaattatca agcaacagat attaatgaaa aatattcctt tagtcagtac    240
ttagtggtgaa gactgatgac ttgtttatta atgttagcca taacagtaat ttatttaacg    300
ttaactaaga cagatagcta caagagtaca attgtctttc tagtctgttt ctatagatcg    360
acagatgctt tttcggattht atatcaggga atgttccaac aacatgaacg gctggatatt    420
gcaggtaaat cgctagccta cagaaatact cttattttta tgggtgtacac agcaataata    480
ttatattcca aaaatcttac tttagcatta gtagctgtct gtatagtttt attagttttt    540
ataatgtatt atgacattgg tcattcgaaa aaatttcaaa agttgatggt tagtgaatta    600
ttaagtaata tttcattttc aaacagttta aagttattaa aagaaaagtt tccacttttt    660
ctaaacgggt ttttgattat ctatatattt actcaaccaa aatacgctat tgaactaatg    720
acgactttag gtgaagttgc tttgggctct caaacaattt ttaatatatt atttatgccca    780
gcctttgtta tgaatttgct aattttattt tttagacctc atattacaca gatggctatt    840

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gctttaatca gaggtcaaat aaaagagttt aataagatac aagttcaatt gtttgcttat      900
ttaggagttt ttctactgat agcgtagttt ggaagtgggt tggttggtat tcccttttta      960
tcaatactat atggtactaa ccttacggat tattgggtag attttatggt gattatgcta    1020
ggaggctcga ttggtagttt tgcgacagtt atcgataata tcttaaccgc tatgagaaaa    1080
cagcaacttc ttcttattcc atatacagga ggatttttga tttcgttatt aattaccaat    1140
ctttttgtta tgaaatatca tatttttagga gctgctttga gctttttaat aacaatgttg    1200
gtttggtttg gattatccat tatgatttat ctatttatta tgaatagatt taagaaggga    1260
agagttaatg caacaatcta tgactaa                                     1287

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<210> SEQ ID NO 446
 <211> LENGTH: 428
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 446

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Met Ile Asn Pro Ser Lys Gln Asn Gln Thr Ile Phe Leu Trp Asn Met
1           5           10           15
Leu Gly Ser Leu Ser Thr Ala Val Ile Ser Val Ile Leu Leu Met Val
          20           25           30
Val Thr Arg Leu Leu Thr Ser Ala Asp Ser Asp Ile Tyr Ala Phe Ala
          35           40           45
Tyr Ser Phe Ala Asn Met Met Val Val Val Gly Leu Phe Gln Val Arg
          50           55           60
Asn Tyr Gln Ala Thr Asp Ile Asn Glu Lys Tyr Ser Phe Ser Gln Tyr
          65           70           75           80
Leu Val Ala Arg Leu Met Thr Cys Leu Leu Met Leu Ala Ile Thr Val
          85           90           95
Ile Tyr Leu Thr Leu Thr Lys Thr Asp Ser Tyr Lys Ser Thr Ile Val
          100          105          110
Phe Leu Val Cys Phe Tyr Arg Ser Thr Asp Ala Phe Ser Asp Leu Tyr
          115          120          125
Gln Gly Met Phe Gln Gln His Glu Arg Leu Asp Ile Ala Gly Lys Ser
          130          135          140
Leu Ala Tyr Arg Asn Thr Leu Ile Phe Met Val Tyr Thr Ala Ile Ile
          145          150          155          160
Leu Tyr Ser Lys Asn Leu Thr Leu Ala Leu Val Ala Val Cys Ile Val
          165          170          175
Ser Leu Val Phe Ile Met Tyr Tyr Asp Ile Gly His Ser Lys Lys Phe
          180          185          190
Gln Lys Leu Met Phe Ser Glu Leu Leu Ser Asn Ile Ser Phe Gln Asn
          195          200          205
Ser Leu Lys Leu Leu Lys Glu Ser Phe Pro Leu Phe Leu Asn Gly Phe
          210          215          220
Leu Ile Ile Tyr Ile Tyr Thr Gln Pro Lys Tyr Ala Ile Glu Leu Met
          225          230          235          240
Thr Thr Leu Gly Glu Val Ala Leu Gly Ser Gln Thr Ile Phe Asn Ile
          245          250          255
Leu Phe Met Pro Ala Phe Val Met Asn Leu Leu Ile Leu Phe Phe Arg
          260          265          270
Pro His Ile Thr Gln Met Ala Ile Ala Leu Ile Arg Gly Gln Ile Lys
          275          280          285
Glu Phe Asn Lys Ile Gln Val Gln Leu Phe Ala Tyr Leu Gly Val Phe
          290          295          300
Ser Leu Ile Ala Leu Val Gly Ser Gly Leu Phe Gly Ile Pro Phe Leu
          305          310          315          320
Ser Ile Leu Tyr Gly Thr Asn Leu Thr Asp Tyr Trp Val Asp Phe Met
          325          330          335
Leu Ile Met Leu Gly Gly Ser Ile Gly Ser Phe Ala Thr Val Ile Asp

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				340					345					350			
Asn	Ile	Leu	Thr	Ala	Met	Arg	Lys	Gln	Gln	Leu	Leu	Leu	Ile	Pro	Tyr		
		355					360					365					
Thr	Gly	Gly	Phe	Leu	Ile	Ser	Leu	Leu	Ile	Thr	Asn	Leu	Phe	Val	Met		
	370					375					380						
Lys	Tyr	His	Ile	Leu	Gly	Ala	Ala	Leu	Ser	Phe	Leu	Ile	Thr	Met	Leu		
385					390					395					400		
Val	Trp	Leu	Gly	Leu	Ser	Ile	Met	Ile	Tyr	Leu	Phe	Ile	Met	Asn	Arg		
			405						410					415			
Phe	Lys	Lys	Gly	Arg	Val	Asn	Ala	Thr	Ile	Tyr	Asp						
			420					425									

<210> SEQ ID NO 447
 <211> LENGTH: 696
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 447

gtgaaaaagt	taatcattat	tctgtcttac	aatgaaagca	gtaatatgt	caatactata	60
cgtactattg	aatcagatgc	cccggatttt	gactatatca	ttattgatga	ttgctcaacg	120
gataatacgt	tagcaatatg	tcaaaaacag	gggttcaatg	ttatttcttt	gcccatatac	180
ctgggaattg	gcggtgcggt	gcaaaactggc	tatcgttatg	cacaaagatg	tggatatgac	240
gttgcagttc	aagtagatgg	agatggtcag	cacaatccat	gctatttgga	aaaaatgggt	300
gaggtattag	ttcaatcttc	agtaaatatg	gtaattggat	cacgatttat	cacaaaagaa	360
gggtttcagt	catcatttgc	tcgacgtatc	ggcataaagt	attttacttg	gcttattgcg	420
ctactaacag	gaaaaaaaaat	aacagatgca	acgtcaggtc	taaggttaat	tgaccgttca	480
ttgattgaac	gttttgctaa	tcattatcca	gatgattatc	ctgaacctga	aacagttggt	540
gatgtattgg	ttagtcattt	taaagtgaag	gaaattcctg	ttgtaatgaa	tgagcgacaa	600
ggcgggtgtg	catctatctc	gttgacgaaa	tcggtctatt	atatgattaa	agtgacttta	660
gctatttttag	ttgtagaatt	gaaaggaaat	cgttaa			696

<210> SEQ ID NO 448
 <211> LENGTH: 231
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 448

Met	Lys	Lys	Leu	Ile	Ile	Ile	Pro	Ala	Tyr	Asn	Glu	Ser	Ser	Asn	Ile
1			5						10					15	
Val	Asn	Thr	Ile	Arg	Thr	Ile	Glu	Ser	Asp	Ala	Pro	Asp	Phe	Asp	Tyr
		20					25					30			
Ile	Ile	Ile	Asp	Asp	Cys	Ser	Thr	Asp	Asn	Thr	Leu	Ala	Ile	Cys	Gln
	35					40					45				
Lys	Gln	Gly	Phe	Asn	Val	Ile	Ser	Leu	Pro	Ile	Asn	Leu	Gly	Ile	Gly
	50					55				60					
Gly	Ala	Val	Gln	Thr	Gly	Tyr	Arg	Tyr	Ala	Gln	Arg	Cys	Gly	Tyr	Asp
65					70				75					80	
Val	Ala	Val	Gln	Val	Asp	Gly	Asp	Gly	Gln	His	Asn	Pro	Cys	Tyr	Leu
			85					90						95	
Glu	Lys	Met	Val	Glu	Val	Leu	Val	Gln	Ser	Ser	Val	Asn	Met	Val	Ile
		100						105					110		
Gly	Ser	Arg	Phe	Ile	Thr	Lys	Glu	Gly	Phe	Gln	Ser	Ser	Phe	Ala	Arg
	115					120						125			
Arg	Ile	Gly	Ile	Lys	Tyr	Phe	Thr	Trp	Leu	Ile	Ala	Leu	Leu	Thr	Gly
	130					135					140				
Lys	Lys	Ile	Thr	Asp	Ala	Thr	Ser	Gly	Leu	Arg	Leu	Ile	Asp	Arg	Ser
145					150				155					160	
Leu	Ile	Glu	Arg	Phe	Ala	Asn	His	Tyr	Pro	Asp	Asp	Tyr	Pro	Glu	Pro
			165					170						175	

Glu Thr Val Val Asp Val Leu Val Ser His Phe Lys Val Lys Glu Ile	
	180 185 190
Pro Val Val Met Asn Glu Arg Gln Gly Gly Val Ser Ser Ile Ser Leu	
	195 200 205
Thr Lys Ser Val Tyr Tyr Met Ile Lys Val Thr Leu Ala Ile Leu Val	
	210 215 220
Val Arg Leu Lys Gly Asn Arg	
	225 230

<210> SEQ ID NO 449

<211> LENGTH: 2475

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 449

atgattaaag	acacattttt	aaaaaccaat	tggttaaata	ttagtcacca	tattatcctt	60
cttgttttgc	gtttttat	cagtttttac	agtttggcga	aagaactagt	aagctccacg	120
gcacaaccgg	taaactatta	tgctcattta	ctaaatgttt	cttttgtggg	atatattata	180
tcaactgattg	gattatctta	ttatttgagt	cgccaagtta	gtcgacagtt	gtttttgaaa	240
actagtttta	ttgtgatata	ttatctaatt	gtcagctatt	gggtacaaat	aacacagcac	300
ctgaatgata	aacggtttga	tatctgggtca	ttaactaaaa	atcaatttta	tcaatttcaa	360
gctctacctt	ctttactcat	tatttttagtg	atggccactt	taataaaaaat	attggcagca	420
tattttgcaa	tagaaaaaga	tagatttgagg	ctattaggct	atcaaggtaa	tactttttct	480
gtagctctga	ttttagcagt	tgtgccaatt	aatgacatac	atctgttaaa	actaataagt	540
tctcgatttt	ctgaattagt	aacagcaggt	aatagccaaa	ttgcaactgt	aaaaataagt	600
ggactgttga	tagttttact	tgctcatatt	gcaacaatca	tatacgtggg	tttaaatgct	660
ctaaaacacc	ttaagtcaaa	taaaccttca	ttttcagtag	cagctactac	tagtttggtt	720
ttagcattag	tttttaacta	tacgttccag	tatggagtaa	aagggtgatga	agcattgcta	780
ggatattatg	ttttccctgg	agctactctt	tttcagatag	tagctattac	actagttgct	840
cttttagcat	acgtgataac	gaatagatat	tggccaacta	ccttcttttt	gcttattctg	900
ggaacaatta	tttctgttgt	taatgattta	aaagaatcaa	tgagaagcga	gccgttatta	960
gtaactgatt	ttgtttgggt	acaagaatta	ggtttagtga	caagctttgt	taaaaaatcg	1020
gtgattgtga	aaatgggtgt	aggacttgct	atttgtattg	tggtagcttg	gtatctacat	1080
ggccgagttt	tagcagggaa	attatttatg	agccctgtca	aacgggcaag	tgctgtatta	1140
ggtttattta	ttgtatcttg	tagtatgtta	ataccatttt	cttatgaaaa	agaaggtaaa	1200
atattatctg	gtcttccgat	tatttcgggt	ttaaataatg	ataatgacat	aaactggtta	1260
ggtttttcaa	caaatgctag	gtacaaatct	ttagcatatg	tttggacaag	acagggtgacc	1320
aagaaaaata	tggaaaaacc	gacaaaattat	agccaagaaa	caatagcgag	tatcgctcag	1380
aagtacaaaa	aattagcaga	agatattaat	aaagacagaa	aaaataatat	tgctgaccaa	1440
acggttattt	atcttttaag	tgaaagcttg	tcagatcctg	atagagtatc	aaatgttact	1500
gttagccacg	atgttttacc	taatatacaag	gcaatcaaaa	atagcacaac	tgccgggactc	1560
atgcagtcag	actcctacgg	gggtggaacg	gctaacatgg	agtttcaaac	gttaacaagc	1620
ttaccttttt	ataatttttc	ttcttcagta	tctgttcttt	attcagaagt	ctttcctaaa	1680
atggccaaac	ctcatacgat	tagtgagttt	taccaaggaa	aaaatcgtat	tgcgatgcat	1740
cctgctagtg	ctaacaattt	taatagaaaa	acagtttata	gtaatttagg	tttttccaaa	1800
ttcttagctc	tatcgggttc	taaggataag	tttaagaaca	ttgaaaatgt	cggttttattg	1860
actagcgata	aaactgtcta	taataatatt	ttatctttta	ttaatcctag	tgaaagccaa	1920
tttttctcag	ttattacaat	gcaaaatcat	attccttggt	catccgatta	tcctgaagaa	1980
attgttgctg	aaggaaaaaa	tttcacggaa	gaagaaaaatc	acaacctaac	aagttatgct	2040
cggttattat	cgtttactga	taaggaaaca	agagcatttt	tagaaaaatt	aacacaaatt	2100
aacaagccta	tcacagtggg	gttttacgga	gatcattttac	ccggtttata	tcctgatagt	2160
gcttttaaca	agcatattga	aaataaatatc	cttactgatt	attttatttg	gagtaatggg	2220
actaacgaga	aaaaaaatca	tccgcttatc	aactcaagtg	attttactgc	agctttattt	2280
gagcatctg	attcaaaagt	atcaccttac	tatgctttgt	taacagaggt	actgaataaa	2340
gctatgtctg	ataaatcacc	agatagtcct	gaagttaaag	ctatttcagaa	tgatttataaa	2400
aatatccaat	acgatgtgac	tataggaaaa	ggttaccctt	tgaaacacaa	aacttttttt	2460
aagatatcac	gttaa					2475

<210> SEQ ID NO 450

<211> LENGTH: 824

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 450

Met	Ile	Lys	Asp	Thr	Phe	Leu	Lys	Thr	Asn	Trp	Leu	Asn	Ile	Ser	His
1				5					10					15	
His	Ile	Ile	Leu	Leu	Val	Phe	Gly	Phe	Tyr	Phe	Ser	Phe	Tyr	Ser	Leu
			20					25					30		
Ala	Lys	Glu	Leu	Val	Ser	Ser	Thr	Ala	Gln	Pro	Val	Asn	Tyr	Tyr	Ala
		35					40					45			
His	Leu	Leu	Asn	Val	Ser	Phe	Val	Gly	Tyr	Ile	Ile	Ser	Leu	Ile	Gly
	50					55					60				
Leu	Ser	Tyr	Tyr	Leu	Ser	Arg	Gln	Val	Ser	Arg	Gln	Leu	Phe	Leu	Lys
65					70					75					80
Thr	Ser	Phe	Ile	Val	Ile	Ser	Tyr	Leu	Ile	Val	Ser	Tyr	Trp	Val	Gln
				85					90					95	
Ile	Thr	Gln	His	Leu	Asn	Asp	Lys	Arg	Phe	Asp	Ile	Trp	Ser	Leu	Thr
			100					105					110		
Lys	Asn	Gln	Phe	Tyr	Gln	Phe	Gln	Ala	Leu	Pro	Ser	Leu	Leu	Ile	Ile
		115					120					125			
Leu	Val	Met	Ala	Thr	Leu	Ile	Lys	Ile	Leu	Ala	Ala	Tyr	Phe	Ala	Ile
	130					135					140				
Glu	Lys	Asp	Arg	Phe	Gly	Leu	Leu	Gly	Tyr	Gln	Gly	Asn	Thr	Phe	Ser
145					150					155					160
Val	Ala	Leu	Ile	Leu	Ala	Val	Val	Pro	Ile	Asn	Asp	Ile	His	Leu	Leu
				165					170					175	
Lys	Leu	Ile	Ser	Ser	Arg	Phe	Ser	Glu	Leu	Val	Thr	Ala	Gly	Asn	Ser
			180					185					190		
Gln	Ile	Ala	Leu	Leu	Lys	Ile	Ser	Gly	Leu	Leu	Ile	Val	Leu	Leu	Val
	195						200					205			
Ile	Phe	Ala	Thr	Ile	Ile	Tyr	Val	Val	Leu	Asn	Ala	Leu	Lys	His	Leu
	210					215						220			
Lys	Ser	Asn	Lys	Pro	Ser	Phe	Ser	Val	Ala	Ala	Thr	Thr	Ser	Leu	Phe
225					230					235					240
Leu	Ala	Leu	Val	Phe	Asn	Tyr	Thr	Phe	Gln	Tyr	Gly	Val	Lys	Gly	Asp
				245					250					255	
Glu	Ala	Leu	Leu	Gly	Tyr	Tyr	Val	Phe	Pro	Gly	Ala	Thr	Leu	Phe	Gln
		260					265						270		
Ile	Val	Ala	Ile	Thr	Leu	Val	Ala	Leu	Leu	Ala	Tyr	Val	Ile	Thr	Asn
	275						280					285			
Arg	Tyr	Trp	Pro	Thr	Thr	Phe	Phe	Leu	Leu	Ile	Leu	Gly	Thr	Ile	Ile
	290					295					300				
Ser	Val	Val	Asn	Asp	Leu	Lys	Glu	Ser	Met	Arg	Ser	Glu	Pro	Leu	Leu
305					310					315					320
Val	Thr	Asp	Phe	Val	Trp	Leu	Gln	Glu	Leu	Gly	Leu	Val	Thr	Ser	Phe
				325					330					335	
Val	Lys	Lys	Ser	Val	Ile	Val	Glu	Met	Val	Val	Gly	Leu	Ala	Ile	Cys
			340					345					350		
Ile	Val	Val	Ala	Trp	Tyr	Leu	His	Gly	Arg	Val	Leu	Ala	Gly	Lys	Leu
	355						360					365			
Phe	Met	Ser	Pro	Val	Lys	Arg	Ala	Ser	Ala	Val	Leu	Gly	Leu	Phe	Ile
	370					375					380				
Val	Ser	Cys	Ser	Met	Leu	Ile	Pro	Phe	Ser	Tyr	Glu	Lys	Glu	Gly	Lys
385					390					395					400
Ile	Leu	Ser	Gly	Leu	Pro	Ile	Ile	Ser	Ala	Leu	Asn	Asn	Asp	Asn	Asp
				405					410					415	


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<400> SEQUENCE: 451
atgtataaag tttcaattat ttgcaccaat tataacaaag ctccttggat atctgatgca      60
cttgacagtt ttttaagcca agtgacagat tttgaggttg aaattattgt tattgatgat      120
gcttctacag atgactcacg agagatttta aagagttatc aaaaaaagtc ttcaggaaaa      180
attaaattac tctttaacga aactaatatt ggaataacaa agacttggat aaaagcatgc      240
ctttatgcaa aaggcaaata tattgctaga tgtgatgggtg atgattactg gacggatagt      300
tttaaactcc aaaaacaagt tgatgtctta gaagcttcca aacggtcacg atgggtgtaat      360
actgattttg actttgtaaa tagtcaaggc gacttattat atgctaatagc tttttcatct      420
gggtcatacac ctttgacaga tacttacgaa aaagtttttag ccttaaaaagg gatgacgatg      480
gcatcgacat ggtagttga tgctgattta atgagacaag taaaccaaaa aatcaatgta      540
gatacaccag acgatacttt tgatattcaa ctagagttat ttcaactgac tcaactgacc      600
tatattaaag actcaacgac gatttatcgc atgacaaccg attctgattc aagacctact      660
gatacaccaa aaatgattta tcgtattcaa aaactacttg atactcagtt aaattactta      720
aaaaagtata atcaggtaga tacaaaagaa gtgtctgaac tattattaca acaagatgct      780
aagcaagaaa tacgaattca tgagttgagt tgctttattc aagaattaca acaaactatc      840
gtagataaaaa caaagcagca agaaacacgt gaagtggagt tgcaaaatgt catagaagaa      900
caaaaaaatc aactatctga attaagacaa caataccatg ccattattaa ttcacgtcaa      960
tggaataaca cgtctaagct cattgctttt attaggagaa aaaaatga      1008

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<210> SEQ ID NO 452
<211> LENGTH: 335
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 452

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Met Tyr Lys Val Ser Ile Ile Cys Thr Asn Tyr Asn Lys Ala Pro Trp
1          5          10          15
Ile Ser Asp Ala Leu Asp Ser Phe Leu Ser Gln Val Thr Asp Phe Glu
20          25          30
Val Glu Ile Ile Val Ile Asp Asp Ala Ser Thr Asp Asp Ser Arg Glu
35          40          45
Ile Leu Lys Ser Tyr Gln Lys Lys Ser Ser Gly Lys Ile Lys Leu Leu
50          55          60
Phe Asn Glu Thr Asn Ile Gly Ile Thr Lys Thr Trp Ile Lys Ala Cys
65          70          75          80
Leu Tyr Ala Lys Gly Lys Tyr Ile Ala Arg Cys Asp Gly Asp Asp Tyr
85          90          95
Trp Thr Asp Ser Phe Lys Leu Gln Lys Gln Val Asp Val Leu Glu Ala
100         105         110
Ser Lys Arg Ser Arg Trp Cys Asn Thr Asp Phe Asp Phe Val Asn Ser
115         120         125
Gln Gly Asp Leu Leu Tyr Ala Asn Ala Phe Ser Ser Gly His Thr Pro
130         135         140
Leu Thr Asp Thr Tyr Glu Lys Val Leu Ala Leu Lys Gly Met Thr Met
145         150         155         160
Ala Ser Thr Trp Leu Val Asp Ala Asp Leu Met Arg Gln Val Asn Gln
165         170         175
Lys Ile Asn Val Asp Thr Pro Asp Asp Thr Phe Asp Ile Gln Leu Glu
180         185         190
Leu Phe Gln Leu Thr Gln Leu Thr Tyr Ile Lys Asp Ser Thr Thr Ile
195         200         205
Tyr Arg Met Thr Thr Asp Ser Asp Ser Arg Pro Thr Asp Thr Pro Lys
210         215         220
Met Ile Tyr Arg Ile Gln Lys Leu Leu Asp Thr Gln Leu Asn Tyr Leu
225         230         235         240
Lys Lys Tyr Asn Gln Val Asp Thr Lys Glu Val Ser Glu Leu Leu Leu
245         250         255
Gln Gln Asp Ala Lys Gln Glu Ile Arg Ile His Glu Leu Ser Cys Phe

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Gly	Thr	Met	Met	Ile	Thr	His	Ala	Leu	Ala	Glu	Glu	Trp	Thr	Thr	Cys	
				165					170						175	
Asp	Gly	Leu	Leu	Met	His	Asp	Trp	Tyr	Leu	Ala	Leu	Leu	Ala	Ser	Ala	
				180				185						190		
Ile	Gly	Lys	Leu	Val	Tyr	Leu	Asp	Ile	Pro	Thr	Glu	Leu	Tyr	Arg	Gln	
		195					200						205			
His	Asp	Ala	Asn	Val	Leu	Gly	Ala	Arg	Thr	Trp	Ser	Lys	Arg	Met	Lys	
	210					215					220					
Asn	Trp	Leu	Thr	Pro	His	His	Leu	Val	Asn	Lys	Tyr	Trp	Trp	Leu	Ile	
225					230					235					240	
Thr	Ser	Ser	Gln	Lys	Gln	Ala	Gln	Leu	Leu	Leu	Asp	Leu	Pro	Leu	Lys	
				245					250						255	
Pro	Asn	Asp	His	Glu	Leu	Val	Thr	Ala	Tyr	Val	Ser	Leu	Leu	Asp	Met	
			260					265						270		
Pro	Phe	Thr	Lys	Arg	Leu	Ala	Thr	Leu	Lys	Arg	Tyr	Gly	Phe	Arg	Lys	
		275					280					285				
Asn	Arg	Ile	Phe	His	Thr	Phe	Ile	Phe	Arg	Ser	Leu	Val	Val	Thr	Leu	
	290					295					300					
Phe	Gly	Tyr	Arg	Arg	Lys											
305					310											

<210> SEQ ID NO 455
 <211> LENGTH: 1077
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 455

atgttttttag	cgcttaatga	aatgaaacaa	tccaaattgc	ggtatggttt	gattgctggt	60
ttgctatggt	tggttgccta	tttgatgttc	tttttgtcag	gattggcctt	tggtttgatg	120
caggagaacc	gctcggcggt	tgatcttttg	aaagctgaca	gtgttttact	agccaaggat	180
gctgacgcta	ccttgacctt	atcacagggt	tccagagctc	aagaaaatca	aataacagca	240
gacaaggtag	ctcctcttgc	tcaactcaat	accgtggcgt	ggtcagttaa	aaatcctaag	300
gatgccgaca	aagttaaggt	tagccttttc	gggattgatt	ctaatagctt	tattcgtcct	360
aacattgtaa	aaggtcgttt	atttaagact	aacaaagagg	ttgttttggg	tcaaagcctt	420
gcaaaagagg	aagcttttgc	gattggcaag	gactttttaca	catcgagttc	tagtcaagca	480
ttaactatcg	ttggttatac	tcaaaaatgt	agatttagtg	ttgcaccagt	ggtttatatg	540
aatttggaag	cttttgaaac	attaaaatat	ggagaaccac	taccaaaga	taagcaagtt	600
gttaatgctt	ttatcactaa	aggaagttaa	acagattatc	ctaaaaaaga	cttccaaaaa	660
ttagatatta	aaacctttat	tactaaatta	cctgggttata	gcgctcaact	tttaactttt	720
ggctttatga	ttagttttct	tgctcattatt	tcagctatta	ttattggtat	ttttatgtat	780
attttgacta	ttcaaaaagg	acctattttt	gggattatga	aagcgcaagg	aattttctaac	840
aaaacgatta	cgaccgctgt	gcttatgcag	acattctttt	tgagtttttt	aggtagtggt	900
ttagggttgc	taggtacttg	gctgacatca	ttattattac	caacagtagt	accttttcaa	960
agcaattggg	ttttgtattt	ggctatatcc	gtagtatga	tctgttttgc	tctattaggg	1020
accttatttt	ctgtttttta	cattatacga	attgatcctt	tgaaagcaat	tggatag	1077

<210> SEQ ID NO 456
 <211> LENGTH: 358
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 456

Met	Phe	Leu	Ala	Leu	Asn	Glu	Met	Lys	Gln	Ser	Lys	Leu	Arg	Tyr	Gly	
1				5					10					15		
Leu	Ile	Ala	Gly	Leu	Leu	Cys	Leu	Val	Ala	Tyr	Leu	Met	Phe	Phe	Leu	
			20					25					30			
Ser	Gly	Leu	Ala	Phe	Gly	Leu	Met	Gln	Glu	Asn	Arg	Ser	Ala	Val	Asp	
		35					40					45				
Leu	Trp	Lys	Ala	Asp	Ser	Val	Leu	Leu	Ala	Lys	Asp	Ala	Asp	Ala	Thr	

50	55	60
Leu Thr Leu Ser Gln Val Ser Arg Ala Gln Glu Asn Gln Ile Thr Ala		
65	70	75
Asp Lys Val Ala Pro Leu Ala Gln Leu Asn Thr Val Ala Trp Ser Val		80
	85	90
Lys Asn Pro Lys Asp Ala Asp Lys Val Lys Val Ser Leu Phe Gly Ile		95
	100	105
Asp Ser Asn Ser Phe Ile Arg Pro Asn Ile Val Lys Gly Arg Leu Phe		110
	115	120
Lys Thr Asn Lys Glu Val Val Leu Asp Gln Ser Leu Ala Lys Glu Glu		125
	130	135
Ala Phe Ala Ile Gly Lys Asp Phe Tyr Thr Ser Ser Ser Gln Ala		140
145	150	155
Leu Thr Ile Val Gly Tyr Thr Gln Asn Ala Arg Phe Ser Val Ala Pro		160
	165	170
Val Val Tyr Met Asn Leu Glu Ala Phe Glu Thr Leu Lys Tyr Gly Glu		175
	180	185
Pro Leu Pro Lys Asp Lys Gln Val Val Asn Ala Phe Ile Thr Lys Gly		190
	195	200
Ser Leu Thr Asp Tyr Pro Lys Lys Asp Phe Gln Lys Leu Asp Ile Lys		205
	210	215
Thr Phe Ile Thr Lys Leu Pro Gly Tyr Ser Ala Gln Leu Leu Thr Phe		220
225	230	235
Gly Phe Met Ile Ser Phe Leu Val Ile Ile Ser Ala Ile Ile Ile Gly		240
	245	250
Ile Phe Met Tyr Ile Leu Thr Ile Gln Lys Ala Pro Ile Phe Gly Ile		255
	260	265
Met Lys Ala Gln Gly Ile Ser Asn Lys Thr Ile Thr Thr Ala Val Leu		270
	275	280
Met Gln Thr Phe Phe Leu Ser Phe Leu Gly Ser Gly Leu Gly Leu Leu		285
	290	295
Gly Thr Trp Leu Thr Ser Leu Leu Leu Pro Thr Val Val Pro Phe Gln		300
305	310	315
Ser Asn Trp Phe Leu Tyr Leu Ala Ile Phe Val Ser Met Ile Cys Phe		320
	325	330
Ala Leu Leu Gly Thr Leu Phe Ser Val Phe Asn Ile Ile Arg Ile Asp		335
	340	345
Pro Leu Lys Ala Ile Gly		350
355		

<210> SEQ ID NO 457

<211> LENGTH: 483

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 457

atgccttact tactaagtcg acacgacagt atcgaaatcg ctatcaaacg gataatgctt	60
atcgtaactt taagcccagc aggttggcac cgattgcacc acttaaaagg aagttatgat	120
cacgcggttg atagagggca tttgctaggt tatgctttag ttggtggact gaaaggtttt	180
gatgcttcta ctggtaatcc tgataatatt gccactcaac taagttgggc taatcaagca	240
aataaaccct acttgacagg tcagaattac tatgaagggt tagtacgtcg tgctttagat	300
aaggggcatc gcgtccgcta ccgtgtcacc ctactttatg atggtgataa tctactagcc	360
agcggtagcc atttggaggc taaatcctct gatgacagct tgacttttaa cgtgtttgtt	420
ccaaatgtcc aagcaggatt gaccgctgac tatcggacgg gacaaatagc tatcaatctc	480
taa	483

<210> SEQ ID NO 458

<211> LENGTH: 160

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 458

```
Met Pro Tyr Leu Leu Ser Arg His Asp Ser Ile Glu Ile Ala Ile Lys
 1           5           10           15
Arg Ile Met Leu Ile Val Thr Leu Ser Pro Ala Gly Trp His Arg Leu
 20           25           30
His His Leu Lys Gly Ser Tyr Asp His Ala Val Asp Arg Gly His Leu
 35           40           45
Leu Gly Tyr Ala Leu Val Gly Gly Leu Lys Gly Phe Asp Ala Ser Thr
 50           55           60
Gly Asn Pro Asp Asn Ile Ala Thr Gln Leu Ser Trp Ala Asn Gln Ala
 65           70           75           80
Asn Lys Pro Tyr Leu Thr Gly Gln Asn Tyr Tyr Glu Gly Leu Val Arg
 85           90           95
Arg Ala Leu Asp Lys Gly His Arg Val Arg Tyr Arg Val Thr Leu Leu
100          105          110
Tyr Asp Gly Asp Asn Leu Leu Ala Ser Gly Ser His Leu Glu Ala Lys
115          120          125
Ser Ser Asp Asp Ser Leu Thr Phe Asn Val Phe Val Pro Asn Val Gln
130          135          140
Ala Gly Leu Thr Ala Asp Tyr Arg Thr Gly Gln Ile Ala Ile Asn Leu
145          150          155          160
```

<210> SEQ ID NO 459

<211> LENGTH: 495

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 459

```
atgtcaatca catttggtga actcgttggg aattttattc tagtaacagg ttctgtaatc      60
gtcttggttac tcttgatcaa aaaattcgct tggggtgcga ttgaatcgat ttacagaca      120
cgctcacaac aaatctctcg agatattgat caggctgagc aatcacgtct aagtgtcaa      180
cagtttagagg caaaaagtca agctaacccta gatgctagtc gtttacaagc aagtaaaatc      240
attagtgatg ccaaagaaat tggtaatta caagggtgata aattggtggc agaagctact      300
gatgaagcaa aacgcttgaa agaaaaagcg ttgacagata ttgaacaaag caaatcagac      360
gctattttcag cagtcaaaac agaaatgtct gatttaacgg ttcttttagc ggaaaaaatt      420
atgggagcca atcttgataa gacggcgcaa agccagctta ttgacagtta tcttgatgac      480
ttaggagaag cttaa                                         495
```

<210> SEQ ID NO 460

<211> LENGTH: 164

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 460

```
Met Ser Ile Thr Phe Gly Glu Leu Val Gly Asn Phe Ile Leu Val Thr
 1           5           10           15
Gly Ser Val Ile Val Leu Leu Leu Leu Ile Lys Lys Phe Ala Trp Gly
 20           25           30
Ala Ile Glu Ser Ile Leu Gln Thr Arg Ser Gln Gln Ile Ser Arg Asp
 35           40           45
Ile Asp Gln Ala Glu Gln Ser Arg Leu Ser Ala Gln Gln Leu Glu Ala
 50           55           60
Lys Ser Gln Ala Asn Leu Asp Ala Ser Arg Leu Gln Ala Ser Lys Ile
 65           70           75           80
Ile Ser Asp Ala Lys Glu Ile Gly Gln Leu Gln Gly Asp Lys Leu Val
 85           90           95
Ala Glu Ala Thr Asp Glu Ala Lys Arg Leu Lys Glu Lys Ala Leu Thr
```

			100					105					110				
Asp	Ile	Glu	Gln	Ser	Lys	Ser	Asp	Ala	Ile	Ser	Ala	Val	Lys	Thr	Glu		
		115					120					125					
Met	Ser	Asp	Leu	Thr	Val	Leu	Leu	Ala	Glu	Lys	Ile	Met	Gly	Ala	Asn		
	130					135					140						
Leu	Asp	Lys	Thr	Ala	Gln	Ser	Gln	Leu	Ile	Asp	Ser	Tyr	Leu	Asp	Asp		
145					150					155					160		
Leu	Gly	Glu	Ala														

<210> SEQ ID NO 461

<211> LENGTH: 717

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 461

atggaagaag	ctaaaatacc	tatgctgaag	cttgggtccaa	taaccttttaa	tttgacccta	60
cttgcgtgtt	gtattgtcac	aattgcgatt	gtctttgcct	ttgttttttg	ggcaagtcgc	120
caaatgaaat	tgaaaccaga	agggaagcaa	actgcttttag	aatattttaat	cagttttgtg	180
gatggtattg	gagaagagca	cttagatcat	aatctacaaa	aatcttattc	gctgttactc	240
tttaccattt	ttctctttgt	ggctgtcgct	aataatttag	ggttatttac	taagttagag	300
acagttaatg	gctataacct	atggacctcg	ccaacagcca	atctggcttt	tgaccttgc	360
ctatctcttt	ttattacctt	aatggtacac	attgaagggg	ttagacggcg	tggcttggtt	420
gcccatttga	aacgtttggc	tacaccgtgg	ccaatgactc	cgatgaattt	attagaagag	480
ttcacaaatt	tcttatcact	tgccattagg	ttattcggta	atatctttgc	cggggaagtt	540
gttacagggt	tgattgttca	actggccaat	tatcgagttt	attggtggcc	gattgctttc	600
ctagtcaata	tggcgtggac	agccttttca	gtctttattt	cctgcataca	ggctttcgtt	660
ttcacaaaac	tgacagcgac	ctatctagga	aagaaagtca	atgaatcaga	agaataa	717

<210> SEQ ID NO 462

<211> LENGTH: 238

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 462

Met	Glu	Glu	Ala	Lys	Ile	Pro	Met	Leu	Lys	Leu	Gly	Pro	Ile	Thr	Phe
1				5					10					15	
Asn	Leu	Thr	Leu	Leu	Ala	Val	Cys	Ile	Val	Thr	Ile	Ala	Ile	Val	Phe
			20					25					30		
Ala	Phe	Val	Phe	Trp	Ala	Ser	Arg	Gln	Met	Lys	Leu	Lys	Pro	Glu	Gly
		35				40					45				
Lys	Gln	Thr	Ala	Leu	Glu	Tyr	Leu	Ile	Ser	Phe	Val	Asp	Gly	Ile	Gly
	50				55					60					
Glu	Glu	His	Leu	Asp	His	Asn	Leu	Gln	Lys	Ser	Tyr	Ser	Leu	Leu	Leu
65				70					75					80	
Phe	Thr	Ile	Phe	Leu	Phe	Val	Ala	Val	Ala	Asn	Asn	Leu	Gly	Leu	Phe
			85					90					95		
Thr	Lys	Leu	Glu	Thr	Val	Asn	Gly	Tyr	Asn	Leu	Trp	Thr	Ser	Pro	Thr
		100					105					110			
Ala	Asn	Leu	Ala	Phe	Asp	Leu	Ala	Leu	Ser	Leu	Phe	Ile	Thr	Leu	Met
	115					120					125				
Val	His	Ile	Glu	Gly	Val	Arg	Arg	Gly	Leu	Val	Ala	His	Leu	Lys	
	130				135				140						
Arg	Leu	Ala	Thr	Pro	Trp	Pro	Met	Thr	Pro	Met	Asn	Leu	Leu	Glu	Glu
145			150					155						160	
Phe	Thr	Asn	Phe	Leu	Ser	Leu	Ala	Ile	Arg	Leu	Phe	Gly	Asn	Ile	Phe
			165					170				175			
Ala	Gly	Glu	Val	Val	Thr	Gly	Leu	Ile	Val	Gln	Leu	Ala	Asn	Tyr	Arg
		180					185					190			
Val	Tyr	Trp	Trp	Pro	Ile	Ala	Phe	Leu	Val	Asn	Met	Ala	Trp	Thr	Ala

	195						200					205							
Phe	Ser	Val	Phe	Ile	Ser	Cys	Ile	Gln	Ala	Phe	Val	Phe	Thr	Lys	Leu				
	210						215					220							
Thr	Ala	Thr	Tyr	Leu	Gly	Lys	Lys	Val	Asn	Glu	Ser	Glu	Glu						
225						230					235								

<210> SEQ ID NO 463
 <211> LENGTH: 1128
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 463

atggttttat	ttcatttaat	caaaaaagaa	agtttacaga	tttttagaaa	ccgaacagcc	60
ttattgatga	tgggtgatttt	tccaattttg	atgatcggtta	ttttaagttt	tgccttttaa	120
tcaagtttta	atactgcgac	aacagtcctt	aaattgacca	ttcgttacca	attagagggt	180
gaaaaaacgg	attaccagaa	aaattttctt	gcttttttaa	aagtttttaa	ccaaaaactt	240
catttagaga	ctaaacctag	taattctctt	gaaaaagatc	gacaaagggt	cagtgaagga	300
gccttaacgg	ctgtttttaga	agtgaagaag	aatcagacca	ttaagggttat	tactaataat	360
attaatcagc	aaaatgcaga	tttgatcaat	atgctagtaa	aaaattatgt	tgataatgct	420
aaaacttatg	actcgatagc	agctctttat	cctcaacaat	taaatcatat	cagaaagcga	480
agtgtggact	atgttaaggt	cagttcaata	cagacaagta	aaggaatgac	atcagctgat	540
tattatgcta	tttccatggt	taccatgatt	actttttata	gtatgatgtc	tgcgatgaac	600
cttgttttgt	cagatcggtc	acaacggatt	acaaatcgta	ttcacttaac	aggagtttct	660
ccaagttttt	tgggtctttg	gaaattaata	ggtgctatgt	tagcaacaac	tggtcaattg	720
agtcttttat	acattttttac	aagggttggt	ttacgagtta	attggggcac	taatgagtgg	780
atgcttattg	gtataacagc	ctccttagtc	tatctctctg	tagctatagg	tatcgggcta	840
ggtataagca	ttaaaaaatga	ggctttttta	acggttgcac	ccaatactat	tattcctata	900
ttcgcccttt	taggaggcag	ttacgttcca	ttgacaacat	tacacagctc	tattattaat	960
caattgtcga	atatactctcc	tattaaatgg	gttaatgata	gtttgttcta	tcttattttt	1020
ggtgggtcaat	ataatccgat	tcctgtaact	ttgatcggtta	atattagtat	cggaacaatt	1080
tttataatat	tggcattgat	aggtatgaga	aagcaggtga	cgacatga		1128

<210> SEQ ID NO 464
 <211> LENGTH: 375
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 464

Met	Val	Leu	Phe	His	Leu	Ile	Lys	Lys	Glu	Ser	Leu	Gln	Ile	Phe	Arg
1				5					10					15	
Asn	Arg	Thr	Ala	Leu	Leu	Met	Met	Val	Ile	Phe	Pro	Ile	Leu	Met	Ile
			20					25					30		
Val	Ile	Leu	Ser	Phe	Ala	Phe	Lys	Ser	Ser	Phe	Asn	Thr	Ala	Thr	Thr
		35					40					45			
Val	Pro	Lys	Leu	Thr	Ile	Arg	Tyr	Gln	Leu	Glu	Gly	Glu	Lys	Thr	Asp
	50					55				60					
Tyr	Gln	Lys	Asn	Phe	Leu	Ala	Phe	Leu	Lys	Val	Leu	Asn	Gln	Lys	Leu
65				70					75					80	
His	Leu	Glu	Thr	Lys	Pro	Ser	Asn	Ser	Leu	Glu	Lys	Asp	Arg	Gln	Arg
			85					90					95		
Val	Ser	Glu	Gly	Ala	Leu	Thr	Ala	Val	Leu	Glu	Val	Lys	Lys	Asn	Gln
		100						105					110		
Thr	Ile	Lys	Val	Ile	Thr	Asn	Asn	Ile	Asn	Gln	Gln	Asn	Ala	Asp	Leu
	115					120						125			
Ile	Asn	Met	Leu	Val	Lys	Asn	Tyr	Val	Asp	Asn	Ala	Lys	Thr	Tyr	Asp
	130					135				140					
Ser	Ile	Ala	Ala	Leu	Tyr	Pro	Gln	Gln	Leu	Asn	His	Ile	Arg	Lys	Arg
145				150						155				160	
Ser	Val	Asp	Tyr	Val	Lys	Val	Ser	Ser	Ile	Gln	Thr	Ser	Lys	Gly	Met

				165				170					175				
Thr	Ser	Ala	Asp	Tyr	Tyr	Ala	Ile	Ser	Met	Phe	Thr	Met	Ile	Thr	Phe		
			180					185					190				
Tyr	Ser	Met	Met	Ser	Ala	Met	Asn	Leu	Val	Leu	Ser	Asp	Arg	Gln	Gln		
		195					200					205					
Arg	Ile	Thr	Asn	Arg	Ile	His	Leu	Thr	Gly	Val	Ser	Pro	Ser	Phe	Leu		
	210				215						220						
Val	Phe	Gly	Lys	Leu	Ile	Gly	Ala	Met	Leu	Ala	Thr	Thr	Val	Gln	Leu		
225				230					235					240			
Ser	Leu	Leu	Tyr	Ile	Phe	Thr	Arg	Phe	Val	Leu	Arg	Val	Asn	Trp	Gly		
			245					250					255				
Thr	Asn	Glu	Trp	Met	Leu	Ile	Gly	Ile	Thr	Ala	Ser	Leu	Val	Tyr	Leu		
	260						265						270				
Ser	Val	Ala	Ile	Gly	Ile	Gly	Leu	Gly	Ile	Ser	Ile	Lys	Asn	Glu	Ala		
	275					280						285					
Phe	Leu	Thr	Val	Ala	Ser	Asn	Thr	Ile	Ile	Pro	Ile	Phe	Ala	Phe	Leu		
290				295						300							
Gly	Gly	Ser	Tyr	Val	Pro	Leu	Thr	Thr	Leu	His	Ser	Ser	Ile	Ile	Asn		
305				310					315					320			
Gln	Leu	Ser	Asn	Ile	Ser	Pro	Ile	Lys	Trp	Val	Asn	Asp	Ser	Leu	Phe		
			325					330					335				
Tyr	Leu	Ile	Phe	Gly	Gly	Gln	Tyr	Asn	Pro	Ile	Pro	Val	Thr	Leu	Ile		
		340					345					350					
Val	Asn	Ile	Ser	Ile	Gly	Thr	Ile	Phe	Ile	Ile	Leu	Ala	Leu	Ile	Gly		
	355					360					365						
Met	Arg	Lys	Gln	Val	Thr	Thr											
	370					375											

<210> SEQ ID NO 465

<211> LENGTH: 672

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 465

atgcctttgt	ccatccaatg	ccttaatctt	tgttttttgt	tggttaacttt	ttgtccttca	60
attcctatgc	aagctatttt	tggaaggaa	gatagtgggt	atgcatttaa	tttaattgggt	120
tttctaagag	caactctgat	ttatgacatt	ttggctttgg	taagtattta	tgttttgtca	180
cctcaaataa	ccttgtctct	tgaaagtatt	gatagtaaga	cgttctttat	gggacttgta	240
ttttgcgtct	tgatagtact	gattgaactc	gttttcttac	atggtttacg	ttgttggcaa	300
aaaaagcaat	ggcttcctgc	aactttctcg	tttgtaggaa	cgacaaatga	ttgggtctaag	360
attggctatc	ctttattact	agctttatct	gaagagacga	tttatcgttt	tttgtggttt	420
aatatattag	cttttcaatg	gcatttacca	acaattattg	ttttaattgt	aactagtttt	480
tgctatgctt	taaatcactt	attgatgggg	aaatccattt	tttatgctaa	gttggttaaca	540
ggcatcattt	atggtagtat	ttacatgctg	actagtcaat	tgtggttggt	tgtgataatg	600
catgtaggag	gtaacttgct	agttgagtgt	cttagccatc	ttcaaacaaa	aaagaagaag	660
gaggtgacat	ga					672

<210> SEQ ID NO 466

<211> LENGTH: 223

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 466

Met	Pro	Leu	Ser	Ile	Gln	Cys	Leu	Asn	Leu	Cys	Phe	Leu	Leu	Val	Thr
1			5					10					15		
Phe	Cys	Pro	Ser	Ile	Pro	Met	Gln	Ala	Ile	Phe	Gly	Lys	Glu	Asp	Ser
		20					25				30				
Gly	Tyr	Ala	Phe	Asn	Leu	Ile	Gly	Phe	Leu	Arg	Ala	Thr	Leu	Ile	Tyr
	35					40					45				

Asp	Ile	Leu	Ala	Leu	Val	Ser	Ile	Tyr	Val	Leu	Ser	Pro	Gln	Ile	Thr
50						55				60					
Leu	Ser	Leu	Glu	Ser	Ile	Asp	Ser	Lys	Thr	Phe	Phe	Met	Gly	Leu	Val
65					70					75				80	
Phe	Cys	Val	Leu	Ile	Val	Leu	Ile	Glu	Leu	Val	Phe	Leu	His	Gly	Leu
				85					90					95	
Arg	Cys	Trp	Gln	Lys	Lys	Gln	Trp	Leu	Pro	Ala	Thr	Phe	Ser	Phe	Val
			100					105					110		
Gly	Thr	Thr	Asn	Asp	Trp	Ser	Lys	Ile	Gly	Tyr	Pro	Leu	Leu	Leu	Ala
		115				120						125			
Leu	Phe	Glu	Glu	Thr	Ile	Tyr	Arg	Phe	Leu	Trp	Phe	Asn	Ile	Leu	Ala
130					135						140				
Phe	Gln	Trp	His	Leu	Pro	Thr	Ile	Ile	Val	Leu	Ile	Val	Thr	Ser	Phe
145					150					155					160
Cys	Tyr	Ala	Leu	Asn	His	Leu	Leu	Met	Gly	Lys	Ser	Ile	Phe	Tyr	Ala
				165					170					175	
Lys	Leu	Val	Thr	Gly	Ile	Ile	Tyr	Gly	Ser	Ile	Tyr	Met	Leu	Thr	Ser
			180					185						190	
Gln	Leu	Trp	Leu	Val	Val	Ile	Met	His	Val	Gly	Gly	Asn	Leu	Leu	Val
		195				200						205			
Glu	Cys	Leu	Ser	His	Leu	Gln	Thr	Lys	Lys	Lys	Lys	Glu	Val	Thr	
210						215						220			

<210> SEQ ID NO 467

<211> LENGTH: 759

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 467

atgaaattat	ctaaacaaaa	ggcaagtttg	cttaccgctg	ttttactggt	acttttctctt	60
tctataacga	caataactgt	tgacgcagct	agggtagcaa	cttatccgaa	tgtatcccat	120
gcaaacacac	attataaaaa	tactgtttct	agtaagctct	taccttttac	tgctaattat	180
cagttacaac	ttggtgagtt	ggataacctt	aaccgcgcta	ccttttcaca	tatccaactg	240
caagatagac	acgaaactaa	agatgtacgc	actaaaataa	attatgaccc	tgtgggatgg	300
cacaactatc	aattttccata	cggagatggc	tcaaaatctt	catgggtaat	gaatcgtggg	360
catctagtcg	gatatcaatt	ttgtggatta	aacgatgaac	caagaaattt	agtggcaatg	420
acagcctggc	taaacacagg	tgcttattca	ggagcaaag	acagcaatcc	tgaagggatg	480
ttatactatg	aaaaccgttt	agattcttgg	cttgcaactc	accctgactt	ttggctagat	540
tataaaagtca	ctcctatata	tagtggcaat	gaagtagtgc	ctcgacaaat	tgaattacag	600
tatgttggaa	ttgattcatc	tggtgagttg	cttactataa	ggctaaatag	taataaagaa	660
agtattgatg	aaaatggtgt	tactacagta	atcttagaaa	actctgctcc	aaatatcaac	720
cttgactatt	taaatggaac	tgccactcct	aaaaactaa			759

<210> SEQ ID NO 468

<211> LENGTH: 252

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 468

Met	Lys	Leu	Ser	Lys	Gln	Lys	Ala	Ser	Leu	Leu	Thr	Ala	Val	Leu	Leu
1				5					10					15	
Leu	Leu	Ser	Leu	Ser	Ile	Thr	Thr	Ile	Thr	Val	Asp	Ala	Ala	Arg	Val
			20					25					30		
Arg	Thr	Tyr	Pro	Asn	Val	Ser	His	Ala	Asn	Thr	His	Tyr	Lys	Asn	Thr
		35				40					45				
Val	Ser	Ser	Lys	Leu	Leu	Pro	Phe	Thr	Ala	Asn	Tyr	Gln	Leu	Gln	Leu
	50					55				60					
Gly	Glu	Leu	Asp	Asn	Leu	Asn	Arg	Ala	Thr	Phe	Ser	His	Ile	Gln	Leu
65				70						75				80	

Gln	Asp	Arg	His	Glu	Thr	Lys	Asp	Val	Arg	Thr	Lys	Ile	Asn	Tyr	Asp
				85					90				95		
Pro	Val	Gly	Trp	His	Asn	Tyr	Gln	Phe	Pro	Tyr	Gly	Asp	Gly	Ser	Lys
			100					105					110		
Ser	Ser	Trp	Val	Met	Asn	Arg	Gly	His	Leu	Val	Gly	Tyr	Gln	Phe	Cys
		115					120					125			
Gly	Leu	Asn	Asp	Glu	Pro	Arg	Asn	Leu	Val	Ala	Met	Thr	Ala	Trp	Leu
	130					135					140				
Asn	Thr	Gly	Ala	Tyr	Ser	Gly	Ala	Asn	Asp	Ser	Asn	Pro	Glu	Gly	Met
145					150					155					160
Leu	Tyr	Tyr	Glu	Asn	Arg	Leu	Asp	Ser	Trp	Leu	Ala	Leu	His	Pro	Asp
			165						170					175	
Phe	Trp	Leu	Asp	Tyr	Lys	Val	Thr	Pro	Ile	Tyr	Ser	Gly	Asn	Glu	Val
			180					185					190		
Val	Pro	Arg	Gln	Ile	Glu	Leu	Gln	Tyr	Val	Gly	Ile	Asp	Ser	Ser	Gly
		195					200					205			
Glu	Leu	Leu	Thr	Ile	Arg	Leu	Asn	Ser	Asn	Lys	Glu	Ser	Ile	Asp	Glu
	210					215					220				
Asn	Gly	Val	Thr	Thr	Val	Ile	Leu	Glu	Asn	Ser	Ala	Pro	Asn	Ile	Asn
225					230					235					240
Leu	Asp	Tyr	Leu	Asn	Gly	Thr	Ala	Thr	Pro	Lys	Asn				
				245					250						

<210> SEQ ID NO 469

<211> LENGTH: 267

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 469

atgaataaac	gcattaagaa	aaaacgtaaa	ctagaaacag	cagttgtgat	gcttggtgca	60
gaaaatgcca	tgcaggttga	agcaattaaa	aatcaaaaaca	aacaaatcat	ggagctaaaa	120
tcaatcgttc	aacgaaacgc	tctggcaaca	aacgaagagt	tagcgactgt	taaagctgct	180
actttagata	accaatcagt	tatcaaggca	attggtgaca	cggttgacta	tattaagaaa	240
aactacaaac	ggaagtgggg	gaaataa				267

<210> SEQ ID NO 470

<211> LENGTH: 88

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 470

Met	Asn	Lys	Arg	Ile	Lys	Lys	Lys	Arg	Lys	Leu	Glu	Thr	Ala	Val	Val
1				5				10					15		
Met	Leu	Val	Ala	Glu	Asn	Ala	Met	Gln	Val	Glu	Ala	Ile	Lys	Asn	Gln
			20				25					30			
Asn	Lys	Gln	Ile	Met	Glu	Leu	Lys	Ser	Ile	Val	Gln	Arg	Asn	Ala	Leu
		35				40					45				
Ala	Thr	Asn	Glu	Glu	Leu	Ala	Thr	Val	Lys	Ala	Ala	Thr	Leu	Asp	Asn
	50				55					60					
Gln	Ser	Val	Ile	Lys	Ala	Ile	Gly	Asp	Thr	Val	Asp	Tyr	Ile	Lys	Lys
65				70					75					80	
Asn	Tyr	Lys	Arg	Lys	Trp	Gly	Lys								
				85											

<210> SEQ ID NO 471

<211> LENGTH: 849

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 471

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atgagaagaa aaataaaaacc tattgtttgt ctagtcttct ttattttact ggcaatggta      60
ttgattatcg gaaaaagaca agctaatacat gcgaaacaaa aagaagttga agacgctaag      120
agtcataattc ctattgcaac cagtaatcct ggtaaagcaa aaactagcac ttctgaaacc      180
gaagacttta ttttaaattcc tattgtttgat gtttccggct ggcaactccc tgaagaaatt      240
gattatgaca cattgtcacg tcacatctct ggcgcaattg tacgtgtcta tggaggatcg      300
caaattacag ctcataacaa cgctgctttt acaactggaa ttgacaaatc ttttaaaacg      360
catatcaaag aatttcaaaa acgaaatgtt cctgtagctg tttacagtta cgcacttggt      420
cgtagtacta aagagatgaa agaagaggcc cgagctttct acaaaaacgc tgctccctat      480
aatccaactt actactggat tgatgtcgaa gaagccacta tgaaagatat gaataaaggc      540
gtaacagcct tccgagaaga gcttaaaaaa cttggtgctg aaaatgttgg tctctatatt      600
ggaacttatt ttatggcaga acaagatatt tcaacaaaag gtttcgattc tgtatggatt      660
ccgacttatg gtagtgattc tggctattat gaggctgctc ctaatacaac cttagattac      720
gatttacacc aatacacctc acaaggttat ctcagtgggt ttaacaatgc tttagattta      780
aatcaaattg ccgtaacaaa agacactaaa aaaacgtttg agaagttatt tggcaactcc      840
aacaattaa

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<210> SEQ ID NO 472

<211> LENGTH: 282

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 472

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Met Arg Arg Lys Ile Lys Pro Ile Val Val Leu Val Phe Phe Ile Leu
1           5           10          15
Leu Ala Met Val Leu Ile Ile Gly Lys Arg Gln Ala Asn His Ala Lys
20          25          30
Gln Lys Glu Val Glu Asp Ala Lys Ser His Ile Pro Ile Ala Thr Ser
35          40          45
Asn Pro Gly Lys Ala Lys Thr Ser Thr Ser Glu Thr Glu Asp Phe Ile
50          55          60
Leu Asn Pro Ile Val Asp Val Ser Gly Trp Gln Leu Pro Glu Glu Ile
65          70          75          80
Asp Tyr Asp Thr Leu Ser Arg His Ile Ser Gly Ala Ile Val Arg Val
85          90          95
Tyr Gly Gly Ser Gln Ile Thr Ala His Asn Asn Ala Ala Phe Thr Thr
100         105         110
Gly Ile Asp Lys Ser Phe Lys Thr His Ile Lys Glu Phe Gln Lys Arg
115         120         125
Asn Val Pro Val Ala Val Tyr Ser Tyr Ala Leu Gly Arg Ser Thr Lys
130         135         140
Glu Met Lys Glu Glu Ala Arg Ala Phe Tyr Lys Asn Ala Ala Pro Tyr
145         150         155         160
Asn Pro Thr Tyr Tyr Trp Ile Asp Val Glu Glu Ala Thr Met Lys Asp
165         170         175
Met Asn Lys Gly Val Thr Ala Phe Arg Glu Glu Leu Lys Lys Leu Gly
180         185         190
Ala Glu Asn Val Gly Leu Tyr Ile Gly Thr Tyr Phe Met Ala Glu Gln
195         200         205
Asp Ile Ser Thr Lys Gly Phe Asp Ser Val Trp Ile Pro Thr Tyr Gly
210         215         220
Ser Asp Ser Gly Tyr Tyr Glu Ala Ala Pro Asn Thr Thr Leu Asp Tyr
225         230         235         240
Asp Leu His Gln Tyr Thr Ser Gln Gly Tyr Leu Ser Gly Phe Asn Asn
245         250         255
Ala Leu Asp Leu Asn Gln Ile Ala Val Thr Lys Asp Thr Lys Lys Thr
260         265         270
Phe Glu Lys Leu Phe Gly Asn Ser Asn Asn
275         280

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<210> SEQ ID NO 473
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 473
atgggctaaaa aaacaaaact caaaaaaaccc ttagtagaac aaatcctcga taaggctaatt      60
attgctcatc aaggactcaa gcttaatgct ttagaaggcg actttccaga tgatcttcaa      120
ccatcagata ttacaagac acttgctctg actggtgac aaacagggtcc tctaattggc      180
attattccat taacagaaca cttatcagaa aaacaattgg caaaagtatc aggtaacaaa      240
aaagtgtcca tggttcctca aaaagacttg caaaagacaa caggctatat tcacgggtgcc      300
aataatcctg ttgggattcg tcaaaaacat tcatatccta tttttattga ccaaactgca      360
ctggaaaaag gtcaaataat cgtttcagct ggtgaagttg ggcgttctat aaagatttct      420
agccaggctc tagctgattt cgttggcgca agctttgctg atttaaagaa gagaaaatga      480

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<210> SEQ ID NO 474
<211> LENGTH: 159
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 474
Met Ala Lys Lys Thr Lys Leu Lys Lys Thr Leu Val Glu Gln Ile Leu
1      5      10      15
Asp Lys Ala Asn Ile Ala His Gln Gly Leu Lys Leu Asn Ala Leu Glu
20     25     30
Gly Asp Phe Pro Asp Asp Leu Gln Pro Ser Asp Ile Tyr Lys Thr Leu
35     40     45
Ala Leu Thr Gly Asp Gln Thr Gly Pro Leu Ile Gly Ile Ile Pro Leu
50     55     60
Thr Glu His Leu Ser Glu Lys Gln Leu Ala Lys Val Ser Gly Asn Lys
65     70     75     80
Lys Val Ser Met Val Pro Gln Lys Asp Leu Gln Lys Thr Thr Gly Tyr
85     90     95
Ile His Gly Ala Asn Asn Pro Val Gly Ile Arg Gln Lys His Ser Tyr
100    105    110
Pro Ile Phe Ile Asp Gln Thr Ala Leu Glu Lys Gly Gln Ile Ile Val
115    120    125
Ser Ala Gly Glu Val Gly Arg Ser Ile Lys Ile Ser Ser Gln Ala Leu
130    135    140
Ala Asp Phe Val Gly Ala Ser Phe Ala Asp Leu Lys Lys Arg Lys
145    150    155

```

```

<210> SEQ ID NO 475
<211> LENGTH: 408
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 475
atggacttag ttggaatctc actgatgatt attgcactcg catttggtgc tttggtgatt      60
ttcttgatta ttgtattaaa gaaagtctca gaaacaattg atgaagccaa aaaaacgatt      120
tctgtattga caagtgatgt taatgtgaca cttcatcaaa ctaatgatat ttagcaaaaa      180
gctaatatcc ttgttgaaga tgtaaatggt aaagtagcaa ccatcgatcc actgtttggt      240
gctattgctg atttgtcaga aagtctttca gatttaaata gtcaagcaag gcattttggg      300
caaaaagcaa ctaatgctac aggtaatgtt tcaaaagctg gaaaattagc attagtgtgt      360
aaagtagcct caaaagtatt tggaaaaaaa ggagaaaagc atgaataa      408

```

```

<210> SEQ ID NO 476
<211> LENGTH: 135
<212> TYPE: PRT

```

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 476

```
Met Asp Leu Val Gly Ile Ser Leu Met Ile Ile Ala Leu Ala Phe Val
 1          5          10          15
Ala Leu Val Ile Phe Leu Ile Ile Val Leu Lys Lys Val Ser Glu Thr
 20          25          30
Ile Asp Glu Ala Lys Lys Thr Ile Ser Val Leu Thr Ser Asp Val Asn
 35          40          45
Val Thr Leu His Gln Thr Asn Asp Ile Leu Ala Lys Ala Asn Ile Leu
 50          55          60
Val Glu Asp Val Asn Gly Lys Val Ala Thr Ile Asp Pro Leu Phe Val
 65          70          75          80
Ala Ile Ala Asp Leu Ser Glu Ser Leu Ser Asp Leu Asn Ser Gln Ala
 85          90          95
Arg His Phe Gly Gln Lys Ala Thr Asn Ala Thr Gly Asn Val Ser Lys
100         105         110
Ala Gly Lys Leu Ala Leu Val Gly Lys Val Ala Ser Lys Val Phe Gly
115         120         125
Lys Lys Gly Glu Lys His Glu
130         135
```

<210> SEQ ID NO 477

<211> LENGTH: 780

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 477

```
atgatcaatc ccattgcctt aaaatgtggt ccactagcca tccactggta tgctctatgt      60
atcttgtcag gacttgtttt ggcggtttac ttagcatcaa aagaagcacc caaaaaagga      120
atatcatctg atgctatttt cgattttatt ctgattgctt ttccacttgc tattgttgggt      180
gcaagaattt actatgttat ttttgaatgg tcttattatg tcaagcattt agatgaaatc      240
atagccattt ggaatggcgg tattgctatt tatggcggtc tcattacagg agctcttgta      300
cttttggtt actgttataa caaggtgctc aatcccattc attttttaga tattgccgca      360
ccaagtgtca tggtcgctca agctatcggt cgctggggaa attttatcaa ccaagaagcc      420
tatggtaaaag ctgtgagcca gttaaattac ttaccaagct ttattcaaaa gcaaatgttt      480
atagaggggaa gttaccgcat tccgaccttt ctctatgaat cactttggaa tcttttgggc      540
tttgtcatta ttatgatgtg gcgtcgtaag ccaaaaagtc tattagatgg agaaatcttt      600
gcattttact taatttggtg tggtagtggg agactagtca ttgaagggtat gcgaacagat      660
agtcttatgt ttttaggtat tcgcatctcc caatatgtgt ctgccttatt aattattatt      720
ggcttaaatct ttgttataaa aagacgtcgt caaaaaggaa tttcttatta tcaagaataa      780
```

<210> SEQ ID NO 478

<211> LENGTH: 259

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 478

```
Met Ile Asn Pro Ile Ala Leu Lys Cys Gly Pro Leu Ala Ile His Trp
 1          5          10          15
Tyr Ala Leu Cys Ile Leu Ser Gly Leu Val Leu Ala Val Tyr Leu Ala
 20          25          30
Ser Lys Glu Ala Pro Lys Lys Gly Ile Ser Ser Asp Ala Ile Phe Asp
 35          40          45
Phe Ile Leu Ile Ala Phe Pro Leu Ala Ile Val Gly Ala Arg Ile Tyr
 50          55          60
Tyr Val Ile Phe Glu Trp Ser Tyr Tyr Val Lys His Leu Asp Glu Ile
 65          70          75          80
Ile Ala Ile Trp Asn Gly Gly Ile Ala Ile Tyr Gly Gly Leu Ile Thr
 85          90          95
```

Gly	Ala	Leu	Val	Leu	Leu	Ala	Tyr	Cys	Tyr	Asn	Lys	Val	Leu	Asn	Pro
			100					105					110		
Ile	His	Phe	Leu	Asp	Ile	Ala	Ala	Pro	Ser	Val	Met	Val	Ala	Gln	Ala
		115				120					125				
Ile	Gly	Arg	Trp	Gly	Asn	Phe	Ile	Asn	Gln	Glu	Ala	Tyr	Gly	Lys	Ala
	130				135						140				
Val	Ser	Gln	Leu	Asn	Tyr	Leu	Pro	Ser	Phe	Ile	Gln	Lys	Gln	Met	Phe
145				150					155					160	
Ile	Glu	Gly	Ser	Tyr	Arg	Ile	Pro	Thr	Phe	Leu	Tyr	Glu	Ser	Leu	Trp
			165					170					175		
Asn	Leu	Leu	Gly	Phe	Val	Ile	Ile	Met	Met	Trp	Arg	Arg	Lys	Pro	Lys
		180						185					190		
Ser	Leu	Leu	Asp	Gly	Glu	Ile	Phe	Ala	Phe	Tyr	Leu	Ile	Trp	Tyr	Gly
	195				200						205				
Ser	Gly	Arg	Leu	Val	Ile	Glu	Gly	Met	Arg	Thr	Asp	Ser	Leu	Met	Phe
210					215						220				
Leu	Gly	Ile	Arg	Ile	Ser	Gln	Tyr	Val	Ser	Ala	Leu	Leu	Ile	Ile	Ile
225				230						235				240	
Gly	Leu	Ile	Phe	Val	Ile	Lys	Arg	Arg	Arg	Gln	Lys	Gly	Ile	Ser	Tyr
			245					250					255		
Tyr	Gln	Glu													

<210> SEQ ID NO 479

<211> LENGTH: 1863

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 479

atgacgtatc	aagaaactgc	caaggctatt	ttagcggcgg	ttggtggcaa	aacaaatatt	60
caacgtgtga	cacactgtgt	aacacgtcta	cgcttagtac	tgaaaaatga	tgagaaagtt	120
aaagatcagc	aagtcaaaagc	catttcaa	gtgattggcg	tgatgcgcaa	aaacggccag	180
taccaaatta	tcttgggcaa	tgatgtcaat	aattattacc	aagccttttt	aagcctaggg	240
cattttgaca	atcaagatga	agatcattct	tcaaaagcga	aaggaagtat	ccttgagcgc	300
ttgattgaaa	ccattgctgg	cgtgattaca	ccgctgattc	cagcccttct	tggtggtgga	360
atgctcaaag	tggtgggaat	cttgcttcc	atgcttggct	tagcgagtgc	ggactctcaa	420
accgttgcct	ttattaactt	cttggcgat	gcggcttatt	attttatgcc	tgcatgatt	480
gcctattcag	cagcggcgcg	ctttaaagg	acacctgttt	tagcagcgac	gatcgagg	540
attttattgc	atcctgcctt	tggtgcaatg	gtagcagaag	gtaaaccatt	gactttattt	600
ggagcaccag	tcactcctgc	tagctatggc	tcactgttta	ttcccatttt	gatgatggtt	660
tacttgatgc	aatacattga	aaaatgggtc	aatcgcttgg	tgccaagcgt	gatgaaaagc	720
ttcttacagc	caacctta	cattttgatt	tctggctttt	tggtcttagt	ggttgtaggt	780
cctcttggtg	tgattattgg	tcaagggtta	tctaatacca	tgctcgctat	ttatcatgtg	840
gctccgtggc	tagcacttgc	tattttggga	gcgattatgc	cgcttgttgt	catgacgggg	900
atgcactggg	cttttgcacc	aatctttttg	gccgcttcgg	tcgcaacacc	agatgtcttg	960
attttaccag	caatgttggc	ttctaatttg	gctcaaggag	ccgcatcttt	ggctgttgcc	1020
tttaaaacaa	agcagaaaca	aacacgtcaa	gttgcccttg	ccgcggggat	ttcagctttg	1080
ctggcaggta	tcacggaacc	ggcactttat	ggggtcacac	tgaaatttaa	aaagccactc	1140
tatgcagcca	tgatttcagg	tggtctggtt	ggagccttta	ttggttttgt	caatattgct	1200
tcttatacct	ttgtcgta	ttctattatt	ggtttaccac	agtacatcaa	cccatcaggc	1260
ggagctaatt	ttacaaatgc	tttgattgcc	ggaactgcga	cgatttgtgt	agccttcagt	1320
ttgacttggt	tcatgggaat	tgatgaagag	tcccaaagc	aagtgaagtgt	tgacgagat	1380
atgtcacaag	ttaagagcgg	cttgtcaacc	aaacaaacgt	tgtatgctcc	aatgacagg	1440
gagatgcttt	ttctatcaga	agttcctgat	gaaacctttt	cttccaagtt	attaggagaa	1500
ggatttgcca	tattaccaag	cgaagggtgag	gtctatgccc	cctttgatgg	tgaagtcac	1560
actttctttc	caaccaagca	tgctgttgcc	ttaaaaaaca	cacgtggtgt	ggaagtcttg	1620
attctatgtc	gtattgatac	ggttgagtta	aaagggcaag	gtttcgagca	gttagtgtct	1680
gttggcgatg	tcgtgaaacg	aggccaggca	cttctaaaaa	tggaatttga	tttcattact	1740
tcaaaaggct	attcactcat	cagtcctgtg	gtcgtgacca	attcggctga	gcagttggag	1800

attattattc aagatgacaa aaaaatggtg actaaagagg acgctttggt agtcatttta 1860
taa 1863

```
<210> SEQ ID NO 480
<211> LENGTH: 620
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 480
```

Met	Thr	Tyr	Gln	Glu	Thr	Ala	Lys	Ala	Ile	Leu	Ala	Ala	Val	Gly	Gly
1				5					10					15	
Lys	Thr	Asn	Ile	Gln	Arg	Val	Thr	His	Cys	Val	Thr	Arg	Leu	Arg	Leu
			20					25					30		
Val	Leu	Lys	Asn	Asp	Glu	Lys	Val	Lys	Asp	Gln	Gln	Val	Lys	Ala	Ile
		35					40					45			
Ser	Asn	Val	Ile	Gly	Val	Met	Arg	Lys	Asn	Gly	Gln	Tyr	Gln	Ile	Ile
	50					55					60				
Leu	Gly	Asn	Asp	Val	Asn	Asn	Tyr	Tyr	Gln	Ala	Phe	Leu	Ser	Leu	Gly
65				70						75					80
His	Phe	Asp	Asn	Gln	Asp	Glu	Asp	His	Ser	Ser	Lys	Ala	Lys	Gly	Ser
			85					90						95	
Ile	Leu	Glu	Arg	Leu	Ile	Glu	Thr	Ile	Ala	Gly	Val	Ile	Thr	Pro	Leu
			100					105					110		
Ile	Pro	Ala	Leu	Leu	Gly	Gly	Gly	Met	Leu	Lys	Val	Val	Gly	Ile	Leu
		115					120					125			
Leu	Pro	Met	Leu	Gly	Leu	Ala	Ser	Ala	Asp	Ser	Gln	Thr	Val	Ala	Phe
	130					135					140				
Ile	Asn	Phe	Phe	Gly	Asp	Ala	Ala	Tyr	Tyr	Phe	Met	Pro	Val	Met	Ile
145				150						155					160
Ala	Tyr	Ser	Ala	Ala	Ala	Arg	Phe	Lys	Val	Thr	Pro	Val	Leu	Ala	Ala
			165					170						175	
Thr	Ile	Ala	Gly	Ile	Leu	Leu	His	Pro	Ala	Phe	Val	Ala	Met	Val	Ala
			180					185					190		
Glu	Gly	Lys	Pro	Leu	Thr	Leu	Phe	Gly	Ala	Pro	Val	Thr	Pro	Ala	Ser
		195					200					205			
Tyr	Gly	Ser	Ser	Val	Ile	Pro	Ile	Leu	Met	Met	Val	Tyr	Leu	Met	Gln
	210					215					220				
Tyr	Ile	Glu	Lys	Trp	Val	Asn	Arg	Leu	Val	Pro	Ser	Val	Met	Lys	Ser
225				230						235					240
Phe	Leu	Gln	Pro	Thr	Leu	Ile	Ile	Leu	Ile	Ser	Gly	Phe	Leu	Ala	Leu
			245					250						255	
Val	Val	Val	Gly	Pro	Leu	Gly	Val	Ile	Ile	Gly	Gln	Gly	Leu	Ser	Asn
			260					265					270		
Thr	Met	Leu	Ala	Ile	Tyr	His	Val	Ala	Pro	Trp	Leu	Ala	Leu	Ala	Ile
		275					280					285			
Leu	Gly	Ala	Ile	Met	Pro	Leu	Val	Val	Met	Thr	Gly	Met	His	Trp	Ala
	290					295					300				
Phe	Ala	Pro	Ile	Phe	Leu	Ala	Ala	Ser	Val	Ala	Thr	Pro	Asp	Val	Leu
305				310						315					320
Ile	Leu	Pro	Ala	Met	Leu	Ala	Ser	Asn	Leu	Ala	Gln	Gly	Ala	Ala	Ser
			325					330					335		
Leu	Ala	Val	Ala	Phe	Lys	Thr	Lys	Gln	Lys	Gln	Thr	Arg	Gln	Val	Ala
			340					345					350		
Leu	Ala	Ala													

385					390					395				400	
Ser	Tyr	Thr	Phe	Val	Val	Pro	Ser	Ile	Ile	Gly	Leu	Pro	Gln	Tyr	Ile
				405					410					415	
Asn	Pro	Ser	Gly	Gly	Ala	Asn	Phe	Thr	Asn	Ala	Leu	Ile	Ala	Gly	Thr
			420					425					430		
Ala	Thr	Ile	Val	Leu	Ala	Phe	Ser	Leu	Thr	Trp	Phe	Met	Gly	Ile	Asp
		435					440					445			
Glu	Glu	Ser	Pro	Lys	Gln	Val	Ser	Val	Ala	Ala	Asp	Met	Ser	Gln	Val
	450					455					460				
Lys	Ser	Gly	Leu	Ser	Thr	Lys	Gln	Thr	Leu	Tyr	Ala	Pro	Met	Thr	Gly
465					470					475					480
Glu	Met	Leu	Phe	Leu	Ser	Glu	Val	Pro	Asp	Glu	Thr	Phe	Ser	Ser	Lys
			485					490						495	
Leu	Leu	Gly	Glu	Gly	Phe	Ala	Ile	Leu	Pro	Ser	Glu	Gly	Glu	Val	Tyr
		500						505					510		
Ala	Pro	Phe	Asp	Gly	Glu	Val	Ile	Thr	Phe	Phe	Pro	Thr	Lys	His	Ala
		515					520					525			
Val	Ala	Leu	Lys	Asn	Thr	Arg	Gly	Val	Glu	Val	Leu	Ile	His	Val	Gly
	530					535					540				
Ile	Asp	Thr	Val	Glu	Leu	Lys	Gly	Gln	Gly	Phe	Glu	Gln	Leu	Val	Ser
545					550					555					560
Val	Gly	Asp	Val	Val	Lys	Arg	Gly	Gln	Ala	Leu	Leu	Lys	Met	Asp	Ile
			565					570						575	
Asp	Phe	Ile	Thr	Ser	Lys	Gly	Tyr	Ser	Leu	Ile	Ser	Pro	Val	Val	Val
		580						585					590		
Thr	Asn	Ser	Ala	Glu	Gln	Leu	Glu	Ile	Ile	Ile	Gln	Asp	Asp	Lys	Lys
	595					600					605				
Met	Val	Thr	Lys	Glu	Asp	Ala	Leu	Leu	Val	Ile	Leu				
	610					615					620				

<210> SEQ ID NO 481

<211> LENGTH: 1368

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 481

atgtcacatc	atcaacaaac	cgtttcaaaa	caaacaatta	tggcgattat	cgccatagca	60
ctcattgggtt	tttcaggaat	tttgtctgaa	accagtatga	atgtcacctt	cccgacactg	120
atgtcagtct	atcagttacc	cttaaatagc	ttgcaatgga	tgacgaccat	ttattttacta	180
gcagtggcga	ttatgatgac	cacttcgggt	acactgaaaa	aaaatgtgcg	ggaaagaccc	240
ctctttttta	tggccacagg	tctttttaca	tttggcacca	tcttggccgt	tctgacccag	300
tcctttgcga	tcatgttgct	agcccgcatt	tttcaaggca	ttggtactgg	tctggtaatg	360
cctcagatgt	ttaatattat	tttagagcgt	gtcccaatgc	ataaggtagg	tctattttatg	420
ggatttgctg	gtcttattat	tagcttagca	cctgcttttg	ggcctactta	tgggggcttt	480
atgattagcc	attttagttg	gcaatggatt	tttatctgta	tactccctgt	accactgatt	540
gcagggtattc	tagcttatta	ttacctgaa	gattctccag	taagcgaaaa	agtacccttt	600
gactgggttg	cattttattgc	actatcgatt	agcttaactt	ctgccttatt	agctattact	660
agtctagaaa	acggcagtg	taatttgtat	tacttagggc	tttttattct	cagctttatc	720
ctcttcctct	acaagaatct	cacagctaag	caaccctttc	ttgatattcg	cattctcaaa	780
attccctctc	taaccttttg	cctgattccc	ttttttgtct	tccagctgat	taatttaggc	840
ataaattttc	taacgcaaaa	ctttattgtc	atggaaaaga	ttgctaatag	ttctcaagct	900
ggtatggtgt	tactacctgg	taccttactc	ggagctctac	tagcacctgc	ttttggtaaa	960
ctttatgatc	aaaaaaggagc	aagactttcg	ctttatttag	gaaatgcctt	atttagttta	1020
tcattgatta	ttatgacact	tcaaacaaga	cattttatgc	ttttaccatt	cactctttta	1080
tatattttat	tcacgtttgg	gcgtaacatg	ggctttaata	atagcttagc	cacggctatt	1140
cgagaattgc	ctgccgagaa	aaatgccgat	gccacggcca	tttttcagat	agtcagcaa	1200
tttgctggcg	ctctaggaac	tgctatggca	tcactgatag	caaatagtca	agcagaattc	1260
acaagcgggtg	tccagtctgt	ctaccttctc	tttactat	ttgctctact	tgattttatc	1320

tttttctttg ctatgtttta ccatttaggg aaaaaaggat tagcctaa

1368

<210> SEQ ID NO 482

<211> LENGTH: 455

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 482

Met	Ser	His	His	Gln	Gln	Thr	Val	Ser	Lys	Gln	Thr	Ile	Met	Ala	Ile	1	5	10	15
Ile	Ala	Ile	Ala	Leu	Ile	Gly	Phe	Ser	Gly	Ile	Leu	Ser	Glu	Thr	Ser	20	25	30	
Met	Asn	Val	Thr	Phe	Pro	Thr	Leu	Met	Ser	Val	Tyr	Gln	Leu	Pro	Leu	35	40	45	
Asn	Ser	Leu	Gln	Trp	Met	Thr	Thr	Ile	Tyr	Leu	Leu	Ala	Val	Ala	Ile	50	55	60	
Met	Met	Thr	Thr	Ser	Ala	Thr	Leu	Lys	Lys	Asn	Val	Arg	Glu	Arg	Pro	65	70	75	80
Leu	Phe	Phe	Met	Ala	Thr	Gly	Leu	Phe	Thr	Phe	Gly	Thr	Ile	Leu	Ala	85	90	95	
Val	Leu	Thr	Gln	Ser	Phe	Ala	Ile	Met	Leu	Leu	Ala	Arg	Ile	Phe	Gln	100	105	110	
Gly	Ile	Gly	Thr	Gly	Leu	Val	Met	Pro	Gln	Met	Phe	Asn	Ile	Ile	Leu	115	120	125	
Glu	Arg	Val	Pro	Met	His	Lys	Val	Gly	Leu	Phe	Met	Gly	Phe	Ala	Gly	130	135	140	
Leu	Ile	Ile	Ser	Leu	Ala	Pro	Ala	Phe	Gly	Pro	Thr	Tyr	Gly	Gly	Phe	145	150	155	160
Met	Ile	Ser	His	Phe	Ser	Trp	Gln	Trp	Ile	Phe	Ile	Cys	Ile	Leu	Pro	165	170	175	
Val	Pro	Leu	Ile	Ala	Gly	Ile	Leu	Ala	Tyr	Tyr	Tyr	Leu	Glu	Asp	Ser	180	185	190	
Pro	Val	Ser	Glu	Lys	Val	Pro	Phe	Asp	Trp	Leu	Ala	Phe	Ile	Ala	Leu	195	200	205	
Ser	Ile	Ser	Leu	Thr	Ser	Ala	Leu	Leu	Ala	Ile	Thr	Ser	Leu	Glu	Asn	210	215	220	
Gly	Ser	Val	Asn	Leu	Tyr	Tyr	Leu	Gly	Leu	Phe	Ile	Leu	Ser	Phe	Ile	225	230	235	240
Leu	Phe	Leu	Tyr	Lys	Asn	Leu	Thr	Ala	Lys	Gln	Pro	Phe	Leu	Asp	Ile	245	250	255	
Arg	Ile	Leu	Lys	Ile	Pro	Ser	Leu	Thr	Phe	Gly	Leu	Ile	Pro	Phe	Phe	260	265	270	
Val	Phe	Gln	Leu	Ile	Asn	Leu	Gly	Ile	Asn	Phe	Leu	Thr	Pro	Asn	Phe	275	280	285	
Ile	Val	Met	Glu	Lys	Ile	Ala	Asn	Ser	Ser	Gln	Ala	Gly	Met	Val	Leu	290	295	300	
Leu	Pro	Gly	Thr	Leu	Leu	Gly	Ala	Leu	Leu	Ala	Pro	Ala	Phe	Gly	Lys	305	310	315	320
Leu	Tyr	Asp	Gln	Lys	Gly	Ala	Arg	Leu	Ser	Leu	Tyr	Leu	Gly	Asn	Ala	325	330	335	
Leu	Phe	Ser	Leu	Ser	Leu	Ile	Ile	Met	Thr	Leu	Gln	Thr	Arg	His	Phe	340	345	350	
Met	Leu	Leu	Pro	Phe	Thr	Leu	Leu	Tyr	Ile	Leu	Phe	Thr	Phe	Gly	Arg	355	360	365	
Asn	Met	Gly	Phe	Asn	Asn	Ser	Leu	Ala	Thr	Ala	Ile	Arg	Glu	Leu	Pro	370	375	380	
Ala	Glu	Lys	Asn	Ala	Asp	Ala	Thr	Ala	Ile	Phe	Gln	Met	Met	Gln	Gln	385	390	395	400

Phe	Ala	Gly	Ala	Leu	Gly	Thr	Ala	Met	Ala	Ser	Leu	Ile	Ala	Asn	Ser
				405					410					415	
Gln	Ala	Glu	Phe	Thr	Ser	Gly	Val	Gln	Ser	Val	Tyr	Leu	Leu	Phe	Thr
			420					425					430		
Ile	Phe	Ala	Leu	Leu	Asp	Phe	Ile	Phe	Phe	Phe	Ala	Met	Phe	Tyr	His
		435					440					445			
Leu	Gly	Lys	Lys	Gly	Leu	Ala									
	450					455									

<210> SEQ ID NO 483
 <211> LENGTH: 1095
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 483

ttgactcaac	taaaaactca	atatccctcg	ctcatcatag	acgctagctt	catcaccttg	60
gcggcaaatg	caacgggtcaa	gccccaggat	aagacctaca	ataccgtcaa	tcttctcaac	120
agatttttcc	ttatctggct	tgatgttgcc	tccaggggct	tgtcgcatca	ccacgttttg	180
tcccatccat	ttaaggactg	gatgaccaac	atgttagatt	ttccctacca	tcatgagttt	240
atagagttcc	ttggacggtg	gactcatatc	cttatagccc	tgcccaaaag	gcaccatggt	300
caagtcgaca	ccgcaattcc	aaggatatctt	ctggtaacca	tcagagagaa	gacagggatt	360
gtaaaattaa	ccactgtgca	aaatacagcg	ttcactaccc	agtcgaatca	actcaaaaaa	420
caatacgggc	agttcttggt	aacagaatct	aataactggt	gtgcatgccc	aggctgtgat	480
agaccactca	ttctaaccag	tggcaactta	gcagcagaaa	attacgaggt	ttcagccatt	540
gaaaaagata	aggacgctga	agcactgaat	ctgatagccc	tctgcccaga	tggtttttta	600
acctatcaag	cagataggcg	caaaaaaatt	gtaacaactc	taaaaaatgt	taaaaagatt	660
ctagtctctg	cacataacag	ccaacaagcg	atctctgata	tgaagttaga	cagtgggaatt	720
gtttcagttt	tgactagtct	caataaacta	aaatgtgatg	aatataatat	ctcctatgac	780
tcgaagcaat	tgactgataa	gatatcacct	gagaacaatc	gtacgcttta	tcaattgggt	840
aaaaaccaag	ttattgataa	ctacttaacc	attcaaaaaa	tcacgtaaaa	tttggacaaa	900
caaggaaaaa	ttgattacga	gaaaaatcaa	tatcaaacgc	gatcgatgta	taaaaagtta	960
aaagcagcca	agcataataa	tctggctatt	ttcaataacta	tttcggaaaa	actccatctg	1020
gctacactac	aggacatcta	cttctgtcag	atgattgtct	cttactttat	ccaaaaatgc	1080
gaggtacttg	aataa					1095

<210> SEQ ID NO 484
 <211> LENGTH: 364
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 484

Met	Thr	Gln	Leu	Lys	Thr	Gln	Tyr	Pro	Ser	Leu	Ile	Ile	Asp	Ala	Ser
1				5					10					15	
Phe	Ile	Thr	Leu	Ala	Ala	Asn	Ala	Thr	Val	Lys	Pro	Gln	Asp	Lys	Thr
			20					25					30		
Tyr	Asn	Thr	Val	Asn	Leu	Leu	Asn	Arg	Phe	Phe	Leu	Ile	Trp	Leu	Asp
		35					40					45			
Val	Ala	Ser	Arg	Gly	Leu	Ser	His	His	His	Val	Leu	Ser	His	Pro	Phe
	50					55					60				
Lys	Asp	Trp	Met	Thr	Asn	Met	Leu	Asp	Phe	Pro	Tyr	His	His	Glu	Phe
65					70				75					80	
Ile	Glu	Phe	Leu	Gly	Arg	Trp	Thr	His	Ile	Leu	Ile	Ala	Leu	Pro	Lys
			85					90					95		
Arg	His	His	Gly	Gln	Val	Asp	Thr	Ala	Ile	Pro	Arg	Tyr	Leu	Leu	Val
			100					105					110		
Thr	Ile	Arg	Glu	Lys	Thr	Gly	Ile	Val	Lys	Leu	Thr	Thr	Val	Gln	Asn
		115				120						125			
Thr	Ala	Phe	Thr	Thr	Gln	Ser	Asn	Gln	Leu	Lys	Lys	Gln	Tyr	Gly	Gln
	130					135						140			

Phe	Leu	Leu	Thr	Glu	Ser	Asn	Asn	Cys	Cys	Ala	Cys	Pro	Gly	Cys	Asp
145					150					155					160
Arg	Pro	Leu	Ile	Leu	Thr	Ser	Gly	Asn	Leu	Ala	Ala	Glu	Asn	Tyr	Glu
				165					170						175
Val	Ser	Ala	Ile	Glu	Lys	Asp	Lys	Asp	Ala	Glu	Ala	Leu	Asn	Leu	Ile
			180					185					190		
Ala	Leu	Cys	Pro	Asp	Gly	Phe	Leu	Thr	Tyr	Gln	Ala	Asp	Arg	Arg	Lys
	195						200					205			
Lys	Ile	Val	Thr	Thr	Leu	Lys	Asn	Val	Lys	Lys	Ile	Leu	Val	Ser	Ala
	210					215					220				
His	Asn	Ser	Gln	Gln	Ala	Ile	Ser	Asp	Met	Lys	Leu	Asp	Ser	Gly	Ile
225					230					235					240
Val	Ser	Val	Leu	Thr	Ser	Leu	Asn	Lys	Leu	Lys	Cys	Asp	Glu	Tyr	Asn
			245						250					255	
Ile	Ser	Tyr	Asp	Ser	Lys	Gln	Leu	Thr	Asp	Lys	Ile	Ser	Pro	Glu	Asn
			260					265					270		
Asn	Arg	Thr	Leu	Tyr	Gln	Leu	Val	Lys	Asn	Gln	Val	Ile	Asp	Asn	Tyr
	275						280					285			
Leu	Thr	Ile	Gln	Lys	Ile	Ile	Val	Asn	Leu	Asp	Lys	Gln	Gly	Lys	Ile
	290					295					300				
Asp	Tyr	Glu	Lys	Ile	Gln	Tyr	Gln	Thr	Arg	Ser	Met	Tyr	Lys	Lys	Leu
305					310					315					320
Lys	Ala	Ala	Lys	His	Asn	Asn	Leu	Ala	Ile	Phe	Asn	Thr	Ile	Ser	Glu
				325					330					335	
Lys	Leu	His	Leu	Ala	Thr	Leu	Gln	Asp	Ile	Tyr	Phe	Cys	Gln	Met	Ile
			340					345					350		
Val	Ser	Tyr	Phe	Ile	Gln	Lys	Cys	Glu	Val	Leu	Glu				
		355					360								

<210> SEQ ID NO 485

<211> LENGTH: 1353

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 485

atgactagag	atatcattgg	aaacttatcc	acatttgaat	tagcgatcct	tatcttactt	60
gtttttgttg	ctttttactt	tatccatctt	gcggtgcgtg	attaccgaaa	tgcacgtatt	120
attcggatga	tgagccataa	aatccgagac	ttgattaatg	gtcgctatac	tgatataatc	180
gacgaaaaag	cagacattga	gttaatggag	ctttcagacc	agttaaata	cctgtcagat	240
gtttttcgct	tgacgcatga	aaatcttgcc	caagaaaaaa	atcgcttggc	aagtattttg	300
gcttatatgt	cagatgggtg	acttgctaca	gaccggtctg	gtaaaatcat	catgattaac	360
gagacagctc	gcaagcaatt	aaatttaagt	aaagaagagg	cactaaagaa	aaacattaca	420
gatttgttag	aagggtgatac	ttcatatacc	taccgtgatt	tggtatccaa	aacaccagt	480
gtaactgtta	atagccgaaa	tgatatgggt	gagtttgtct	cattacgctt	gcgctttgcg	540
ttgaatagga	gagagagtgg	ttttatttcg	ggcttggttg	tggtgctcca	tgacaccaca	600
gaacaggaaa	aagaagaacg	tgaacgccgt	ctttttgtct	ctaataagta	tcataaatta	660
aggacccctt	taacttcggt	taaaatcctac	ttggaggctc	ttgatgaagg	tgactttaaa	720
gaagatatgt	ctccaagttt	cataaaaagtt	tctcttgatg	aaactaatcg	gatgatgcgt	780
atgatttcag	atctttttaa	cctgtctcgg	attgataatc	aagtaacca	attagcagta	840
gagatgacta	attttactgc	ttttataact	tctattttaa	acagatttga	tttggttaaa	900
aatcagcata	caggtacagg	aaaagtctat	gaaattgtaa	gagattaccc	tattacctct	960
gtctggattg	aaattgataa	tgataaaaatg	acacagggtta	tcgagaatat	tttgaacaat	1020
gccattaagt	attctccaga	tggtggaaaa	attacagtcc	gtatgaaaac	aacagatacc	1080
caattaatta	tttccatttc	agaccaagga	ctaggtatcc	ctaaaacaga	tttgctctct	1140
atttttgatc	ggttctatcg	tgtagacaag	gcaagaagtc	gtgcccaagg	agggaccggt	1200
ctaggccttg	ccattgctaa	agaaatcatc	aagcagcacc	atggccttat	ctgggctaag	1260
agtgactatg	gtaaaggatc	gacctttact	attgtcttgc	cttatgaaaa	agatgcagcc	1320
atctatgaag	aatggggagga	agatgtagac	taa			1353

<210> SEQ ID NO 486
 <211> LENGTH: 450
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 486

Met	Thr	Arg	Asp	Ile	Ile	Gly	Asn	Leu	Ser	Thr	Phe	Glu	Leu	Ala	Ile	1	5	10	15
Leu	Ile	Leu	Leu	Val	Phe	Val	Ala	Phe	Tyr	Phe	Ile	His	Leu	Ala	Val	20	25	30	
Arg	Asp	Tyr	Arg	Asn	Ala	Arg	Ile	Ile	Arg	Met	Met	Ser	His	Lys	Ile	35	40	45	
Arg	Asp	Leu	Ile	Asn	Gly	Arg	Tyr	Thr	Asp	Ile	Ile	Asp	Glu	Lys	Ala	50	55	60	
Asp	Ile	Glu	Leu	Met	Glu	Leu	Ser	Asp	Gln	Leu	Asn	Asp	Leu	Ser	Asp	65	70	75	80
Val	Phe	Arg	Leu	Thr	His	Glu	Asn	Leu	Ala	Gln	Glu	Lys	Asn	Arg	Leu	85	90	95	
Ala	Ser	Ile	Leu	Ala	Tyr	Met	Ser	Asp	Gly	Val	Leu	Ala	Thr	Asp	Arg	100	105	110	
Ser	Gly	Lys	Ile	Ile	Met	Ile	Asn	Glu	Thr	Ala	Arg	Lys	Gln	Leu	Asn	115	120	125	
Leu	Ser	Lys	Glu	Glu	Ala	Leu	Lys	Lys	Asn	Ile	Thr	Asp	Leu	Leu	Glu	130	135	140	
Gly	Asp	Thr	Ser	Tyr	Thr	Tyr	Arg	Asp	Leu	Val	Ser	Lys	Thr	Pro	Val	145	150	155	160
Val	Thr	Val	Asn	Ser	Arg	Asn	Asp	Met	Gly	Glu	Phe	Val	Ser	Leu	Arg	165	170	175	
Leu	Arg	Phe	Ala	Leu	Asn	Arg	Arg	Glu	Ser	Gly	Phe	Ile	Ser	Gly	Leu	180	185	190	
Val	Val	Val	Leu	His	Asp	Thr	Thr	Glu	Gln	Glu	Lys	Glu	Glu	Arg	Glu	195	200	205	
Arg	Arg	Leu	Phe	Val	Ser	Asn	Val	Ser	His	Glu	Leu	Arg	Thr	Pro	Leu	210	215	220	
Thr	Ser	Val	Lys	Ser	Tyr	Leu	Glu	Ala	Leu	Asp	Glu	Gly	Ala	Leu	Lys	225	230	235	240
Glu	Asp	Ile	Ala	Pro	Ser	Phe	Ile	Lys	Val	Ser	Leu	Asp	Glu	Thr	Asn	245	250	255	
Arg	Met	Met	Arg	Met	Ile	Ser	Asp	Leu	Leu	Asn	Leu	Ser	Arg	Ile	Asp	260	265	270	
Asn	Gln	Val	Thr	Gln	Leu	Ala	Val	Glu	Met	Thr	Asn	Phe	Thr	Ala	Phe	275	280	285	
Ile	Thr	Ser	Ile	Leu	Asn	Arg	Phe	Asp	Leu	Val	Lys	Asn	Gln	His	Thr	290	295	300	
Gly	Thr	Gly	Lys	Val	Tyr	Glu	Ile	Val	Arg	Asp	Tyr	Pro	Ile	Thr	Ser	305	310	315	320
Val	Trp	Ile	Glu	Ile	Asp	Asn	Asp	Lys	Met	Thr	Gln	Val	Ile	Glu	Asn	325	330	335	
Ile	Leu	Asn	Asn	Ala	Ile	Lys	Tyr	Ser	Pro	Asp	Gly	Gly	Lys	Ile	Thr	340	345	350	
Val	Arg	Met	Lys	Thr	Thr	Asp	Thr	Gln	Leu	Ile	Ile	Ser	Ile	Ser	Asp	355	360	365	
Gln	Gly	Leu	Gly	Ile	Pro	Lys	Thr	Asp	Leu	Pro	Leu	Ile	Phe	Asp	Arg	370	375	380	
Phe	Tyr	Arg	Val	Asp	Lys	Ala	Arg	Ser	Arg	Ala	Gln	Gly	Gly	Thr	Gly	385	390	395	400
Leu	Gly	Leu	Ala	Ile	Ala	Lys	Glu	Ile	Ile	Lys	Gln	His	His	Gly	Phe				

				405					410					415			
Ile	Trp	Ala	Lys	Ser	Asp	Tyr	Gly	Lys	Gly	Ser	Thr	Phe	Thr	Ile	Val		
			420						425					430			
Leu	Pro	Tyr	Glu	Lys	Asp	Ala	Ala	Ile	Tyr	Glu	Glu	Trp	Glu	Glu	Asp		
			435				440						445				
Val	Asp																
	450																

<210> SEQ ID NO 487

<211> LENGTH: 1335

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 487

atgcgtatag	gtctattcac	agatacctat	tttcacacaag	tttcaggagt	cgctactagt	60
attcgtacgt	taaaagaaga	gctagaaaaa	gaaggtcacg	aagtttatat	tttcaccact	120
actgatagag	atgtcaaacy	ctttgaagac	ccgaccatta	ttcgactgcc	aagtgttcct	180
tttgtgtcat	ttacggatag	acgtgtgggt	tatcgtggcc	tcatttcgtc	atacaaaatt	240
gcaaaacact	ataatcttga	tattattcat	acgcaaactg	agtttagctt	aggcttatta	300
gggaaaatga	taggcaaagc	tttgcggaatt	cctgttgtcc	atacttacca	tacccaatat	360
gaggactacg	tgagttatat	tgccaacgga	aaaatcattc	gaccaagtat	ggcacaacct	420
cttccttaggg	gctatttgaa	ggatttggat	ggggttatct	gccaagtag	gattgtcctc	480
aatcttctag	aaggttacga	agttactatc	cctaagcggg	ttatcccaac	aggcattcct	540
ttggaaaaaat	atattcgtga	tgacatcaca	gcagaagaag	taaccaactt	aaaagcagaa	600
ttgggcatg	ctggtgatga	aacctatgta	ttgagtttgt	cacggatttc	ttatgaaaaa	660
aatattcaag	ctatcatcaa	tcagatgcca	gctatttttg	ctgaaaatgc	caagataaaag	720
cttattattg	taggaaatgg	cccctatttg	caagatttga	aacacttggc	gatgcagtta	780
gaggttgaca	aacacgtgac	ctttacaggc	atggtgcctc	atgataaggt	tgctctgtac	840
tataaggctt	gtgatttctt	tatctcagca	tcaactagtg	agactcaggg	cttgacctat	900
attgaaagtt	tggctagtgg	cactcctatt	attgctcatg	gcaatcctta	tttagatgat	960
gtggtgactg	ataaaaatgtt	tggcactctt	tattacgctg	aaacagattt	aactgatgct	1020
attattgatg	ccatactaaa	aacaccagtt	atggataaac	ggttattagc	aaaaaaacgt	1080
tatgaaatct	cagcacagca	ctttggaaaa	tctatttaca	cgttctattt	agatacgtaa	1140
attgctagaa	atagcaaaag	agctcaaaaag	ctgagtcctt	atcttaataca	ttctggtaaa	1200
agtagttctc	taaaattagt	gcaagggtgct	attcacttgc	ctaaacgtgc	tgctaagggtc	1260
acagctatca	cctcagtaaa	agtagtcaag	gctcctatca	agctgggtcca	tgctatcaaa	1320
gatttttctgg	attaa					1335

<210> SEQ ID NO 488

<211> LENGTH: 444

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 488

Met	Arg	Ile	Gly	Leu	Phe	Thr	Asp	Thr	Tyr	Phe	Pro	Gln	Val	Ser	Gly
1				5					10					15	
Val	Ala	Thr	Ser	Ile	Arg	Thr	Leu	Lys	Glu	Glu	Leu	Glu	Lys	Glu	Gly
			20					25					30		
His	Glu	Val	Tyr	Ile	Phe	Thr	Thr	Thr	Asp	Arg	Asp	Val	Lys	Arg	Phe
			35				40					45			
Glu	Asp	Pro	Thr	Ile	Ile	Arg	Leu	Pro	Ser	Val	Pro	Phe	Val	Ser	Phe
	50					55				60					
Thr	Asp	Arg	Arg	Val	Val	Tyr	Arg	Gly	Leu	Ile	Ser	Ser	Tyr	Lys	Ile
65				70					75					80	
Ala	Lys	His	Tyr	Asn	Leu	Asp	Ile	Ile	His	Thr	Gln	Thr	Glu	Phe	Ser
			85					90					95		
Leu	Gly	Leu	Leu	Gly	Lys	Met	Ile	Gly	Lys	Ala	Leu	Arg	Ile	Pro	Val
			100					105					110		
Val	His	Thr	Tyr	His	Thr	Gln	Tyr	Glu	Asp	Tyr	Val	Ser	Tyr	Ile	Ala

gtcattcctg	ctcaagttcg	ccaaatggtc	aatggtaacc	accgaaaaa	tcttattttc	660
ccaggataca	ttaaagggga	tgtttatgaa	ggtgccatga	ctgggtgcaga	tgcctttttc	720
tttccaagtc	gtgaagaaac	agaaggcatt	gttgtcttag	aagccttggc	cagtcgccag	780
caccttgttt	tacgtgatat	accagtttac	tacggatggg	ttgatcaaag	tagtgcgga	840
ttagcaaccg	atataccagg	ttttatagaa	gctctgaaaa	aagtcttttc	tgggtgccagc	900
aacaaagttg	aagctggtta	caaggttgcc	cagagtcgtc	gcctagaaac	ggttggccat	960
gccttagtag	atgtctataa	aaaagtaatg	gagttataa			999

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<210> SEQ ID NO 490
<211> LENGTH: 332
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 490
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Met	Lys	Val	Leu	Leu	Tyr	Leu	Glu	Ala	Glu	Asn	Tyr	Leu	Arg	Lys	Ser
1				5					10					15	
Gly	Ile	Gly	Arg	Ala	Ile	Lys	His	Gln	Ala	Lys	Ala	Leu	Ser	Leu	Val
			20					25					30		
Gly	Gln	His	Phe	Thr	Thr	Asn	Pro	Arg	Glu	Thr	Tyr	Asp	Leu	Val	His
		35				40					45				
Leu	Asn	Thr	Tyr	Gly	Leu	Lys	Ser	Trp	Leu	Leu	Met	Ile	Lys	Ala	Gln
	50					55					60				
Lys	Ala	Gly	Lys	Lys	Val	Ile	Met	His	Gly	His	Ser	Thr	Glu	Glu	Asp
65				70					75						80
Phe	Arg	Asn	Ser	Phe	Ile	Phe	Ser	Asn	Leu	Leu	Ser	Pro	Trp	Phe	Lys
				85				90					95		
Lys	Tyr	Leu	Cys	His	Phe	Tyr	Asn	Lys	Ala	Asp	Ala	Ile	Ile	Thr	Pro
			100					105					110		
Thr	Leu	Tyr	Ser	Lys	Ser	Leu	Ile	Glu	Ser	Tyr	Gly	Val	Lys	Ser	Pro
		115					120					125			
Ile	Phe	Ala	Val	Ser	Asn	Gly	Ile	Asp	Leu	Glu	Gln	Tyr	Gly	Ala	Asp
	130					135					140				
Pro	Lys	Lys	Glu	Ala	Ala	Phe	Arg	Arg	Tyr	Phe	Asp	Ile	Lys	Glu	Gly
145				150						155					160
Glu	Lys	Val	Val	Met	Gly	Ala	Gly	Leu	Phe	Phe	Leu	Arg	Lys	Gly	Ile
				165					170					175	
Asp	Asp	Phe	Val	Lys	Val	Ala	Gln	Ala	Met	Pro	Asp	Val	Arg	Phe	Ile
			180					185				190			
Trp	Phe	Gly	Glu	Thr	Asn	Lys	Trp	Val	Ile	Pro	Ala	Gln	Val	Arg	Gln
		195					200					205			
Met	Val	Asn	Gly	Asn	His	Pro	Lys	Asn	Leu	Ile	Phe	Pro	Gly	Tyr	Ile
	210					215					220				
Lys	Gly	Asp	Val	Tyr	Glu	Gly	Ala	Met	Thr	Gly	Ala	Asp	Ala	Phe	Phe
225				230						235					240
Phe	Pro	Ser	Arg	Glu	Glu	Thr	Glu	Gly	Ile	Val	Val	Leu	Glu	Ala	Leu
				245					250					255	
Ala	Ser	Arg	Gln	His	Leu	Val	Leu	Arg	Asp	Ile	Pro	Val	Tyr	Tyr	Gly
			260					265					270		
Trp	Val	Asp	Gln	Ser	Ser	Ala	Glu	Leu	Ala	Thr	Asp	Ile	Pro	Gly	Phe
		275					280					285			
Ile	Glu	Ala	Leu	Lys	Lys	Val	Phe	Ser	Gly	Ala	Ser	Asn	Lys	Val	Glu
	290					295					300				
Ala	Gly	Tyr	Lys	Val	Ala	Gln	Ser	Arg	Arg	Leu	Glu	Thr	Val	Gly	His
305				310						315					320
Ala	Leu	Val	Asp	Val	Tyr	Lys	Lys	Val	Met	Glu	Leu				
				325					330						

<210> SEQ ID NO 491

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<211> LENGTH: 987
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 491
  ttgaaatatc tcagcttttg tgttacaatt gccctaaaat tccatttgaa agaaaagtct      60
  atgacactac tatctatcat tgtcccctgc tttaatgaag aagcaaacat tctccccttat      120
  tttgaagaaa tgcatacaact agaaacgtcc atgaccaacc aacttgcttt tgaatacatt      180
  tttattgatg atggttctaa ggataacacc ttgggtattt tgcgtgagct agctgctcgc      240
  tttccaaatg tgcattatct gtctttttca cgccattttg gcaaggaagc tgggctctta      300
  gctggactaa aagaagccaa aggcaattac attactgtga tggatgtgga tctgcaagat      360
  ccacccgaac ttttgccaat tatgtacgct aagctaaaag aaggttatga catcgttggc      420
  accaggcgcc aaaatagaca aggagaacca ctaattcggt caatgtgttc gaatctattt      480
  tatggactga tcaaacactt atcagatact gaaatgggtca atggagtctg ggattatcgg      540
  ttaatgacca gacaagtcgt tgatagcatt cttgagttgg gagagggtta tcgtttttca      600
  aaaggggatct tttcgtgggt tggttatcgt atcacctatc ttagttttga aaaccaaaaa      660
  cgcaaatatg gaaaaagtgc ttggcatttt ttgggagttgc tccgatattc tttagatggc      720
  tttatcaact tttcagaaat gccgttaacc attgctacct ggacaggggac tttcagcttt      780
  ttgatttcta ttttcgccat cttatttatc attatcagaa agatactctt tgggtatcct      840
  gtctctgggt gggccagcac tgtctctatt attttattca tgggaggcat tcagctcttt      900
  tgcattgggt ttattggaaa atatatttca aaaatattcc ttgaaactaa aaaaaggcct      960
  ctctatatta tcaaagaaaa acattaa
                                         987

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<210> SEQ ID NO 492
<211> LENGTH: 328
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 492
  Met Lys Tyr Leu Ser Phe Cys Val Thr Ile Ala Leu Lys Phe His Leu
  1          5          10          15
  Lys Glu Lys Ser Met Thr Leu Leu Ser Ile Ile Val Pro Cys Phe Asn
  20        25        30
  Glu Glu Ala Asn Ile Leu Pro Tyr Phe Glu Glu Met His Gln Leu Glu
  35        40        45
  Thr Ser Met Thr Asn Gln Leu Ala Phe Glu Tyr Ile Phe Ile Asp Asp
  50        55        60
  Gly Ser Lys Asp Asn Thr Leu Gly Ile Leu Arg Glu Leu Ala Ala Arg
  65        70        75        80
  Phe Pro Asn Val His Tyr Leu Ser Phe Ser Arg His Phe Gly Lys Glu
  85        90        95
  Ala Gly Leu Leu Ala Gly Leu Lys Glu Ala Lys Gly Asn Tyr Ile Thr
  100       105       110
  Val Met Asp Val Asp Leu Gln Asp Pro Pro Glu Leu Leu Pro Ile Met
  115       120       125
  Tyr Ala Lys Leu Lys Glu Gly Tyr Asp Ile Val Gly Thr Arg Arg Gln
  130       135       140
  Asn Arg Gln Gly Glu Pro Leu Ile Arg Ser Met Cys Ser Asn Leu Phe
  145       150       155       160
  Tyr Gly Leu Ile Lys His Leu Ser Asp Thr Glu Met Val Asn Gly Val
  165       170       175
  Arg Asp Tyr Arg Leu Met Thr Arg Gln Val Val Asp Ser Ile Leu Glu
  180       185       190
  Leu Gly Glu Val Asn Arg Phe Ser Lys Gly Ile Phe Ser Trp Val Gly
  195       200       205
  Tyr Arg Ile Thr Tyr Leu Ser Phe Glu Asn Gln Lys Arg Lys Tyr Gly
  210       215       220
  Lys Ser Arg Trp His Phe Trp Glu Leu Leu Arg Tyr Ser Leu Asp Gly
  225       230       235       240

```


Phe	Ile	Asn	Phe	Ser	Glu	Met	Pro	Leu	Thr	Ile	Ala	Thr	Trp	Thr	Gly
				245					250					255	
Thr	Phe	Ser	Phe	Leu	Ile	Ser	Ile	Phe	Ala	Ile	Leu	Phe	Ile	Ile	Ile
			260					265					270		
Arg	Lys	Ile	Leu	Phe	Gly	Asp	Pro	Val	Ser	Gly	Trp	Ala	Ser	Thr	Val
		275				280					285				
Ser	Ile	Ile	Leu	Phe	Met	Gly	Gly	Ile	Gln	Leu	Phe	Cys	Met	Gly	Ile
	290					295				300					
Ile	Gly	Lys	Tyr	Ile	Ser	Lys	Ile	Phe	Leu	Glu	Thr	Lys	Lys	Arg	Pro
305					310					315					320
Leu	Tyr	Ile	Ile	Lys	Glu	Lys	His								
				325											

<210> SEQ ID NO 493

<211> LENGTH: 1194

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 493

gtgaactggc	gacaaaatct	aaaagtggct	tggcttggta	acttctttac	tggggcaagc	60
ttttcacttg	ttatgccttt	tatggctcta	tatgtggaaa	atttaggtac	tccgacagaa	120
ttagtagaat	actatgctgg	tctggcagtt	gctgtgacgg	cacttgcttc	agctttattt	180
gctcctgttt	gggggaagtt	ggctgatcgt	tatggccgaa	aacctatgat	gctgcgagcc	240
agttttgtta	tgacattttac	aatgggtggt	ttagctatta	ttcctaattgt	gttttggtta	300
ctcattttga	gattattaac	aggtgtctct	gcgggctatg	tgccaaatgc	cactgccttg	360
attgccagcc	aagccccaaa	agaggagtca	ggttatgctt	taggcacatt	agcaacagga	420
gtgacagcag	gcgctttaat	tggtccttta	ctagggggaa	ttttggcaga	gctattagga	480
attcgacaag	ttttcttatt	agttggtgtg	atattatttt	tatgttcctt	aatgacagct	540
gtttatgtta	aagaagagtt	taagccgggt	aggcgctttg	agatgatacc	tacaaaagtc	600
attttaaaac	aggtaaaaaag	tccccagatt	atgcttggtt	tatttgtgac	tagtatgatt	660
attcaaattt	cagctcaatc	agtggccccc	attttatcat	tgtatattcg	tcactttggt	720
caaactcaca	acttaatgtt	tacttcaggc	ctggtagttt	cggccatggg	gttttctagc	780
ttattttagca	gttcttactt	aggaaaaatta	ggagatcgat	ttggcaatca	tcggttattg	840
ttagccgctt	tgtgttatag	ctttatcatg	tatttttagca	gtgccttagc	gcagaccagt	900
tttcaattag	gagtactacg	ctttgcttat	gggtttggtg	tgggcgcttt	gatgccaaagt	960
attaactcct	tactaactaa	gttaaacacca	aaagaaggta	tttctagagt	atttgcctat	1020
aatcaaatgt	ttagtaacct	tggccaagtc	attggccctt	ttattggatc	aaatgtggct	1080
gtagtgttag	gctaccgttc	tgttttttat	gtgactagtt	tgatttgtgt	tgtaatttta	1140
atatggagtt	tgattatatt	tcgaaaatat	attaaagtta	aggatattgt	gtga	1194

<210> SEQ ID NO 494

<211> LENGTH: 397

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 494

Met	Asn	Trp	Arg	Gln	Asn	Leu	Lys	Val	Ala	Trp	Leu	Gly	Asn	Phe	Phe
1				5					10					15	
Thr	Gly	Ala	Ser	Phe	Ser	Leu	Val	Met	Pro	Phe	Met	Ala	Leu	Tyr	Val
			20					25					30		
Glu	Asn	Leu	Gly	Thr	Pro	Thr	Glu	Leu	Val	Glu	Tyr	Tyr	Ala	Gly	Leu
	35					40					45				
Ala	Val	Ala	Val	Thr	Ala	Leu	Ala	Ser	Ala	Leu	Phe	Ala	Pro	Val	Trp
	50					55					60				
Gly	Lys	Leu	Ala	Asp	Arg	Tyr	Gly	Arg	Lys	Pro	Met	Met	Leu	Arg	Ala
65				70					75					80	
Ser	Phe	Val	Met	Thr	Phe	Thr	Met	Gly	Gly	Leu	Ala	Ile	Ile	Pro	Asn
				85					90					95	
Val	Phe	Trp	Leu	Leu	Ile	Leu	Arg	Leu	Leu	Thr	Gly	Val	Ser	Ala	Gly

			100					105				110					
Tyr	Val	Pro	Asn	Ala	Thr	Ala	Leu	Ile	Ala	Ser	Gln	Ala	Pro	Lys	Glu		
		115						120				125					
Glu	Ser	Gly	Tyr	Ala	Leu	Gly	Thr	Leu	Ala	Thr	Gly	Val	Thr	Ala	Gly		
		130					135					140					
Ala	Leu	Ile	Gly	Pro	Leu	Leu	Gly	Gly	Ile	Leu	Ala	Glu	Leu	Leu	Gly		
145					150				155						160		
Ile	Arg	Gln	Val	Phe	Leu	Leu	Val	Gly	Val	Ile	Leu	Phe	Leu	Cys	Ser		
			165					170						175			
Leu	Met	Thr	Ala	Val	Tyr	Val	Lys	Glu	Glu	Phe	Lys	Pro	Val	Arg	Arg		
		180						185					190				
Phe	Glu	Met	Ile	Pro	Thr	Lys	Val	Ile	Leu	Lys	Gln	Val	Lys	Ser	Pro		
		195					200					205					
Gln	Ile	Met	Leu	Gly	Leu	Phe	Val	Thr	Ser	Met	Ile	Ile	Gln	Ile	Ser		
	210					215					220						
Ala	Gln	Ser	Val	Ala	Pro	Ile	Leu	Ser	Leu	Tyr	Ile	Arg	His	Leu	Gly		
225				230					235						240		
Gln	Thr	His	Asn	Leu	Met	Phe	Thr	Ser	Gly	Leu	Val	Val	Ser	Ala	Met		
			245					250						255			
Gly	Phe	Ser	Ser	Leu	Phe	Ser	Ser	Ser	Tyr	Leu	Gly	Lys	Leu	Gly	Asp		
		260					265					270					
Arg	Phe	Gly	Asn	His	Arg	Leu	Leu	Leu	Ala	Ala	Leu	Cys	Tyr	Ser	Phe		
		275				280					285						
Ile	Met	Tyr	Phe	Ser	Ser	Ala	Leu	Ala	Gln	Thr	Ser	Phe	Gln	Leu	Gly		
	290					295					300						
Val	Leu	Arg	Phe	Ala	Tyr	Gly	Phe	Gly	Val	Gly	Ala	Leu	Met	Pro	Ser		
305				310					315					320			
Ile	Asn	Ser	Leu	Leu	Thr	Lys	Leu	Thr	Pro	Lys	Glu	Gly	Ile	Ser	Arg		
			325					330						335			
Val	Phe	Ala	Tyr	Asn	Gln	Met	Phe	Ser	Asn	Leu	Gly	Gln	Val	Ile	Gly		
		340						345					350				
Pro	Phe	Ile	Gly	Ser	Asn	Val	Ala	Val	Val	Leu	Gly	Tyr	Arg	Ser	Val		
		355				360					365						
Phe	Tyr	Val	Thr	Ser	Leu	Ile	Val	Phe	Val	Asn	Leu	Ile	Trp	Ser	Leu		
	370					375					380						
Ile	Ile	Phe	Arg	Lys	Tyr	Ile	Lys	Val	Lys	Asp	Ile	Val					
385					390					395							

<210> SEQ ID NO 495

<211> LENGTH: 855

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 495

atgtctatga	aattttttga	gggcttgatg	tcataccact	ttttacaaaa	tgcactgata	60
acggctgtag	tatttggtat	cgtctcaggt	gctgtagggg	gttttattat	ccttaggtca	120
atgtctctta	tgggtgatgc	catctcacac	gctgttttac	caggggttgc	tttgtcattt	180
atttttaggag	tcaatttttt	tattggagcg	attatttttg	ggttattagc	ttctgttatt	240
attacttata	tcaaggaaaa	ctctgtcatt	aaaggagata	cggctattgg	tatcaccttt	300
agctcttttt	tggcactggg	agtcattctg	ataggggtag	ccaatagttc	gacggactta	360
tttcatattt	tgtttgggaa	tatttttagct	gtgcaagata	gcgataagtg	gattactatt	420
gggtgtttcga	tttttgtttt	agtggttatt	agtctctttt	tcaaagaact	attattaaca	480
tcatttgatc	ctatcttagc	caaatacaatg	gggtgtgaagg	tcaatgcgta	tcattatttg	540
ttgatggccc	tattaacttt	agtggctgtt	acggcgatgc	aaagcgtggg	tactatcttg	600
attgttgcc	tattgattac	gccagcagcg	acagcttatt	tatatgctaa	tagcttaaaa	660
gtaatgtag	tgaatgcatc	tttactaggc	gctttagcat	cggttttagg	gctttatttg	720
ggctatacct	ttaatgttgc	cgcagggtca	agtatcgtac	tgacttctgc	gatgatgttt	780
ttgatcagtt	tctttgtttc	acccaagcaa	ggctacctta	aaagatggat	gcaaaaaaaaa	840

gaaaaaacac cttaa

855

<210> SEQ ID NO 496

<211> LENGTH: 284

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 496

```
Met Ser Met Lys Phe Phe Glu Gly Leu Met Ser Tyr His Phe Leu Gln
 1          5          10          15
Asn Ala Leu Ile Thr Ala Val Val Ile Gly Ile Val Ser Gly Ala Val
 20          25          30
Gly Cys Phe Ile Ile Leu Arg Ser Met Ser Leu Met Gly Asp Ala Ile
 35          40          45
Ser His Ala Val Leu Pro Gly Val Ala Leu Ser Phe Ile Leu Gly Val
 50          55          60
Asn Phe Phe Ile Gly Ala Ile Ile Phe Gly Leu Leu Ala Ser Val Ile
 65          70          75          80
Ile Thr Tyr Ile Lys Glu Asn Ser Val Ile Lys Gly Asp Thr Ala Ile
 85          90          95
Gly Ile Thr Phe Ser Ser Phe Leu Ala Leu Gly Val Ile Leu Ile Gly
100          105          110
Val Ala Asn Ser Ser Thr Asp Leu Phe His Ile Leu Phe Gly Asn Ile
115          120          125
Leu Ala Val Gln Asp Ser Asp Lys Trp Ile Thr Ile Gly Val Ser Ile
130          135          140
Phe Val Leu Val Val Ile Ser Leu Phe Phe Lys Glu Leu Leu Leu Thr
145          150          155          160
Ser Phe Asp Pro Ile Leu Ala Lys Ser Met Gly Val Lys Val Asn Ala
165          170          175
Tyr His Tyr Leu Leu Met Val Leu Leu Thr Leu Val Ala Val Thr Ala
180          185          190
Met Gln Ser Val Gly Thr Ile Leu Ile Val Ala Leu Leu Ile Thr Pro
195          200          205
Ala Ala Thr Ala Tyr Leu Tyr Ala Asn Ser Leu Lys Val Met Leu Val
210          215          220
Met Ser Ser Leu Leu Gly Ala Leu Ala Ser Val Leu Gly Leu Tyr Leu
225          230          235          240
Gly Tyr Thr Phe Asn Val Ala Ala Gly Ser Ser Ile Val Leu Thr Ser
245          250          255
Ala Met Met Phe Leu Ile Ser Phe Phe Val Ser Pro Lys Gln Gly Tyr
260          265          270
Leu Lys Arg Trp Met Gln Lys Lys Glu Lys Thr Pro
275          280
```

<210> SEQ ID NO 497

<211> LENGTH: 342

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 497

```
atgacactaa aaaaacacta ttatcttctc agcctgctag ctcttgtaac gggttggtgct      60
gcctttaaca caagccagag tgtcagtgca caagtttata gcaatgaagg gtatcaccag      120
catttgactg atgaaaaatc acacctgcaa tatagtaaag acaacgcaca acttcaattg      180
agaaatatcc ttgacggcta ccaaaatgac ctagggagac actactctag ctattattac      240
tacaacctaa gaaccgttat gggactatca agtgagcaag acattgaaaa acatatgaa      300
gagcttaaga acaagttaca tgatatgtac aatcattatt aa      342
```

<210> SEQ ID NO 498

<211> LENGTH: 113

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 498

```
Met Thr Leu Lys Lys His Tyr Tyr Leu Leu Ser Leu Leu Ala Leu Val
1           5           10           15
Thr Val Gly Ala Ala Phe Asn Thr Ser Gln Ser Val Ser Ala Gln Val
20           25           30
Tyr Ser Asn Glu Gly Tyr His Gln His Leu Thr Asp Glu Lys Ser His
35           40           45
Leu Gln Tyr Ser Lys Asp Asn Ala Gln Leu Gln Leu Arg Asn Ile Leu
50           55           60
Asp Gly Tyr Gln Asn Asp Leu Gly Arg His Tyr Ser Ser Tyr Tyr Tyr
65           70           75           80
Tyr Asn Leu Arg Thr Val Met Gly Leu Ser Ser Glu Gln Asp Ile Glu
85           90           95
Lys His Tyr Glu Glu Leu Lys Asn Lys Leu His Asp Met Tyr Asn His
100          105          110
Tyr
```

<210> SEQ ID NO 499

<211> LENGTH: 1383

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 499

```
atgacaaatt atgccattat tttagcagcg ggcaaaggga ctcgcatgac ttctgatctc 60
ccaaaagttc ttcataaagt atctggacta accatgcttg agcatgtttt tcgtagtgta 120
aaagcgatta gtcctgaaaa atccgtgacg gttattggtc acaaatcaga aatggtacgt 180
gctgtccttag cagatcaatc agcctttgtc catcaaacag agcagttagg aactggccat 240
gccgtgatga tggcagaaac acaactagaa ggactagaag ggcatacctt ggtgattgca 300
ggagatactc ccttgatcac tggagaaagc ctgaagagtc tgattgattt tcatgtgaat 360
cataaaaaatg tcgccactat tttaacagct acggctcaag atccatttgg ttatggtcgt 420
attgttcgca acaaagatgg cgaagtgatc aagattgttg agcaaaaaga cgccaatgag 480
tatgagcaac aattaaaga aatcaatata ggaacctatg tgtttgataa caagcgtctc 540
tttgaagcgc tcaaattgcat cactaccaac aatgctcaag gagagtatta cctgactgac 600
gttgtggcta tttttagagc aaacaaaaga aaggtaggag cctatatcct gagagacttc 660
aatgaaagtc tgggagtaaa tgatcgtgtg gccttagcaa tagctgaaac agtgatgcgt 720
cagcgcatta cccaaaaaca tatggtcaat ggggtgactt tccaaaatcc tgaaactgtt 780
tatattgaaa gcgatgttga gattgctcca gacgtcctta tcgaaggaaa tgtgacctta 840
aaagggcgta cacatatcgg ctcaggaact gtcttgacga atggtactta tattgtggat 900
tctgaaattg gtgataactg tgttgttacc aattcgatga tcgaatcatc tgtttttagct 960
gcaggagtta cggttgccc ttacgccac cttcgaccgg gaacgacctt agatagggaa 1020
gtccatatcg gtaactttgt cgaggatcaag ggttctcaca ttggtgaaaa aacaaaggct 1080
gggcatctga cttatatagg aaacgctcag gttgggtcct cagtcaatgt tggggctgga 1140
accatcactg tcaactacga cggccaaaac aaatatgaaa cagtcattgg agatcacgct 1200
tttattggga gcaactcgac tctcattgca cttttggaag ttggggatca cgctttaaca 1260
gcagcagggt caacgatatt aaaaacagtt cctatcgata gcattgctat tggtcgtagc 1320
cgccaagtca caaaagaagg ttatgccaaag cgcctagcgc atcacccaag tcgaagcaaa 1380
taa 1383
```

<210> SEQ ID NO 500

<211> LENGTH: 460

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 500

```
Met Thr Asn Tyr Ala Ile Ile Leu Ala Ala Gly Lys Gly Thr Arg Met
1           5           10           15
```

Thr	Ser	Asp	Leu	Pro	Lys	Val	Leu	His	Lys	Val	Ser	Gly	Leu	Thr	Met
			20					25					30		
Leu	Glu	His	Val	Phe	Arg	Ser	Val	Lys	Ala	Ile	Ser	Pro	Glu	Lys	Ser
		35					40					45			
Val	Thr	Val	Ile	Gly	His	Lys	Ser	Glu	Met	Val	Arg	Ala	Val	Leu	Ala
	50					55					60				
Asp	Gln	Ser	Ala	Phe	Val	His	Gln	Thr	Glu	Gln	Leu	Gly	Thr	Gly	His
65				70					75						80
Ala	Val	Met	Met	Ala	Glu	Thr	Gln	Leu	Glu	Gly	Leu	Glu	Gly	His	Thr
			85					90					95		
Leu	Val	Ile	Ala	Gly	Asp	Thr	Pro	Leu	Ile	Thr	Gly	Glu	Ser	Leu	Lys
			100				105					110			
Ser	Leu	Ile	Asp	Phe	His	Val	Asn	His	Lys	Asn	Val	Ala	Thr	Ile	Leu
		115					120					125			
Thr	Ala	Thr	Ala	Gln	Asp	Pro	Phe	Gly	Tyr	Gly	Arg	Ile	Val	Arg	Asn
	130					135					140				
Lys	Asp	Gly	Glu	Val	Ile	Lys	Ile	Val	Glu	Gln	Lys	Asp	Ala	Asn	Glu
145				150					155						160
Tyr	Glu	Gln	Gln	Leu	Lys	Glu	Ile	Asn	Thr	Gly	Thr	Tyr	Val	Phe	Asp
			165					170					175		
Asn	Lys	Arg	Leu	Phe	Glu	Ala	Leu	Lys	Cys	Ile	Thr	Thr	Asn	Asn	Ala
			180				185					190			
Gln	Gly	Glu	Tyr	Tyr	Leu	Thr	Asp	Val	Val	Ala	Ile	Phe	Arg	Ala	Asn
		195					200					205			
Lys	Glu	Lys	Val	Gly	Ala	Tyr	Ile	Leu	Arg	Asp	Phe	Asn	Glu	Ser	Leu
	210					215					220				
Gly	Val	Asn	Asp	Arg	Val	Ala	Leu	Ala	Ile	Ala	Glu	Thr	Val	Met	Arg
225				230					235						240
Gln	Arg	Ile	Thr	Gln	Lys	His	Met	Val	Asn	Gly	Val	Thr	Phe	Gln	Asn
			245					250					255		
Pro	Glu	Thr	Val	Tyr	Ile	Glu	Ser	Asp	Val	Glu	Ile	Ala	Pro	Asp	Val
			260				265					270			
Leu	Ile	Glu	Gly	Asn	Val	Thr	Leu	Lys	Gly	Arg	Thr	His	Ile	Gly	Ser
		275					280					285			
Gly	Thr	Val	Leu	Thr	Asn	Gly	Thr	Tyr	Ile	Val	Asp	Ser	Glu	Ile	Gly
	290					295					300				
Asp	Asn	Cys	Val	Val	Thr	Asn	Ser	Met	Ile	Glu	Ser	Ser	Val	Leu	Ala
305				310					315						320
Ala	Gly	Val	Thr	Val	Gly	Pro	Tyr	Ala	His	Leu	Arg	Pro	Gly	Thr	Thr
			325					330					335		
Leu	Asp	Arg	Glu	Val	His	Ile	Gly	Asn	Phe	Val	Glu	Val	Lys	Gly	Ser
			340				345					350			
His	Ile	Gly	Glu	Lys	Thr	Lys	Ala	Gly	His	Leu	Thr	Tyr	Ile	Gly	Asn
		355					360					365			
Ala	Gln	Val	Gly	Ser	Ser	Val	As								

```

<210> SEQ ID NO 501
<211> LENGTH: 1344
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 501
    ttgttttatgg aagaggatta taacaaaaga gaacctgaga agtttacgca atttctgcgc      60
    cgtcaaaagg tcgctctttt tgctgcattt tttggttatg tgtgtgctta cttgggtacgc      120
    aacaatttca aactaatgtc aaacactatt atggtgcaaa atggttgga caaggctcaa      180
    attgcgatct tgttatcgtg tttgaccgtt tcttatggct tagcaaaatt ctatatggga      240
    gccttagggg atcgtgtag cttgaggaag ctcttttcaa tcagcttggg tgcaagcgct      300
    ttgatttgta ttttaattgg ttttttcaat agttcaatgg tggtagtagg aatactgcta      360
    gtcttggtg gtgtcgtaca aggtgccttg gcacctgcct cacaagccat gattgccaat      420
    tattttccaa ataaaacacg cggcggagcc atcgctggat ggaacatttc tcaaaacatg      480
    ggatcagccc tcttgccatt aaccatcgcc ttgctcacca gtatgggctt ggtggtacca      540
    gctaattggca atattttact tgccttttta atccctggcg ttttagtggt cttgtttgct      600
    ttgtgttgct ggaagcttgg cggtgataac cctgagtctg agggacttga ctctcttcga      660
    acgatgtatg gtgatgcggg cgagtcagct gttgccagtg aagaagaaaa gcataacctg      720
    tcttattggc aactcatctg gaaatacgtt ttttgtaacc cgtcgtctct acttgttgct      780
    gctgtcaatg tggcccttta ttttgttcgt tttgggattg aagactggat gccgatctac      840
    ttgtcacaag tagccaatat gtcagaggct catatccatt ttgcgatttc aatgtagtag      900
    tgggtcgcta ttccaggctc gctggtatgt gcgtggttag cggttcgta tcctaataaa      960
    atggccaagg ttggggctat tgggcttttt gtgttagcgg ctattgtctt tgtctatgaa     1020
    cgcttgactg ccacaggtgc tccaaattat ttcttggtgc ttgttattgc aggtatttta     1080
    ggggtcattga tttatggccc acagttgatc gtgaatattt taacaatcaa ctttgttcct     1140
    ttaaatgttg caggaacagc gattggtttt gtaggagtaa cagcttatct catcggaat     1200
    atgggagcaa actggctgat gccgattttg gcagatgggt ttggctgggt ttggtcatat     1260
    attgtcgttg cagccttatc tgctttttca gcggttggtt atttgatttt agccaaacgt     1320
    gaggaagaaa tcatcaaaga ttag                                     1344

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<210> SEQ ID NO 502
<211> LENGTH: 447
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 502
    Met Phe Met Glu Glu Asp Tyr Asn Lys Arg Glu Pro Glu Lys Phe Thr
    1             5             10             15
    Gln Phe Leu Arg Arg Gln Lys Val Val Phe Phe Val Ala Phe Phe Gly
    20             25             30
    Tyr Val Cys Ala Tyr Leu Val Arg Asn Asn Phe Lys Leu Met Ser Asn
    35             40             45
    Thr Ile Met Val Gln Asn Gly Trp Asp Lys Ala Gln Ile Ala Ile Leu
    50             55             60
    Leu Ser Cys Leu Thr Val Ser Tyr Gly Leu Ala Lys Phe Tyr Met Gly
    65             70             75             80
    Ala Leu Gly Asp Arg Val Ser Leu Arg Lys Leu Phe Ser Ile Ser Leu
    85             90             95
    Gly Ala Ser Ala Leu Ile Cys Ile Leu Ile Gly Phe Phe Asn Ser Ser
    100            105            110
    Met Val Val Leu Gly Ile Leu Leu Val Leu Cys Gly Val Val Gln Gly
    115            120            125
    Ala Leu Ala Pro Ala Ser Gln Ala Met Ile Ala Asn Tyr Phe Pro Asn
    130            135            140
    Lys Thr Arg Gly Gly Ala Ile Ala Gly Trp Asn Ile Ser Gln Asn Met
    145            150            155            160
    Gly Ser Ala Leu Leu Pro Leu Thr Ile Ala Leu Leu Thr Ser Met Gly
    165            170            175
    Leu Val Val Pro Ala Asn Gly Asn Ile Leu Leu Ala Phe Leu Ile Pro

```

			180					185				190					
Gly	Val	Leu	Val	Phe	Leu	Phe	Ala	Leu	Cys	Cys	Trp	Lys	Leu	Gly	Gly		
		195					200					205					
Asp	Asn	Pro	Glu	Ser	Glu	Gly	Leu	Asp	Ser	Leu	Arg	Thr	Met	Tyr	Gly		
		210				215					220						
Asp	Ala	Gly	Glu	Ser	Ala	Val	Ala	Ser	Glu	Glu	Glu	Lys	His	Asn	Leu		
225					230					235					240		
Ser	Tyr	Trp	Gln	Leu	Ile	Trp	Lys	Tyr	Val	Phe	Cys	Asn	Pro	Ser	Leu		
			245						250					255			
Leu	Leu	Val	Ala	Ala	Val	Asn	Val	Ala	Leu	Tyr	Phe	Val	Arg	Phe	Gly		
		260						265					270				
Ile	Glu	Asp	Trp	Met	Pro	Ile	Tyr	Leu	Ser	Gln	Val	Ala	Asn	Met	Ser		
		275					280					285					
Glu	Ala	His	Ile	His	Phe	Ala	Ile	Ser	Met	Leu	Glu	Trp	Val	Ala	Ile		
	290					295					300						
Pro	Gly	Ser	Leu	Val	Phe	Ala	Trp	Leu	Ala	Val	Arg	Tyr	Pro	Asn	Lys		
305					310					315					320		
Met	Ala	Lys	Val	Gly	Ala	Ile	Gly	Leu	Phe	Val	Leu	Ala	Ala	Ile	Val		
			325					330						335			
Phe	Val	Tyr	Glu	Arg	Leu	Thr	Ala	Thr	Gly	Ala	Pro	Asn	Tyr	Phe	Leu		
		340						345					350				
Leu	Leu	Val	Ile	Ala	Gly	Ile	Leu	Gly	Ser	Leu	Ile	Tyr	Gly	Pro	Gln		
	355					360					365						
Leu	Ile	Val	Asn	Ile	Leu	Thr	Ile	Asn	Phe	Val	Pro	Leu	Asn	Val	Ala		
	370					375					380						
Gly	Thr	Ala	Ile	Gly	Phe	Val	Gly	Val	Thr	Ala	Tyr	Leu	Ile	Gly	Asn		
385				390				395						400			
Met	Gly	Ala	Asn	Trp	Leu	Met	Pro	Ile	Leu	Ala	Asp	Gly	Phe	Gly	Trp		
			405					410					415				
Phe	Trp	Ser	Tyr	Ile	Val	Val	Ala	Ala	Leu	Ser	Ala	Phe	Ser	Ala	Val		
		420						425				430					
Gly	Tyr	Leu	Ile	Leu	Ala	Lys	Arg	Glu	Glu	Glu	Ile	Ile	Lys	Asp			
	435					440					445						

<210> SEQ ID NO 503

<211> LENGTH: 615

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 503

atgaaaaaaaa	cattaacctt	gctactggca	ctctttgcc	tcggggtaac	tagtagcgct	60
agagcggagg	atgaacagaa	taagtttata	cttgatggat	tacaggaaaa	agtaaaagaa	120
gtagtggtat	cagatttttc	tggtggagaa	tctaaaatca	aagtctggct	tcctcaagct	180
tggtcgggtca	aaattttctag	agaacattca	ccaaaatcaa	gcattttctaa	ttctggagaa	240
caaaaacctt	taagcaatag	ctcagagaat	aaagaaggct	aatttttctaa	aagattacct	300
tatggtaccc	aacatactat	taaattatca	tcccaactta	caaaagggtga	gagagtcact	360
ttgacattca	gagatgaaga	tttttgggga	gcaggttact	gcttctatag	agattcacta	420
tccataaaaag	aagacaaaaca	atacgaagaa	gaaattaaga	aaattgagga	tgacctagag	480
agacaagatc	ttgaaaaatga	tgactagag	atgtttaaaa	aacaaaccga	aagagaggct	540
aataaacctt	ggcatcagcg	gttaagcgaa	aacatccaag	atcagtgggtg	gaactttaag	600
ggactgtttc	agtga					615

<210> SEQ ID NO 504

<211> LENGTH: 204

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 504

Met Lys Lys Thr Leu Thr Leu Leu Leu Ala Leu Phe Ala Ile Gly Val

1				5					10					15			
Thr	Ser	Ser	Val	Arg	Ala	Glu	Asp	Glu	Gln	Asn	Lys	Phe	Ile	Leu	Asp		
			20					25					30				
Gly	Leu	Gln	Glu	Lys	Val	Lys	Glu	Val	Ser	Val	Ser	Asp	Phe	Ser	Val		
		35					40					45					
Gly	Glu	Ser	Lys	Ile	Lys	Val	Trp	Leu	Pro	Gln	Ala	Trp	Ser	Val	Lys		
	50				55					60							
Ile	Ser	Arg	Glu	His	Ser	Pro	Lys	Ser	Ser	Ile	Ser	Asn	Ser	Gly	Glu		
65				70				75						80			
Gln	Lys	Pro	Leu	Ser	Asn	Ser	Ser	Glu	Asn	Lys	Glu	Gly	Gln	Phe	Ser		
			85					90					95				
Lys	Arg	Leu	Pro	Tyr	Gly	Thr	Gln	His	Thr	Ile	Lys	Leu	Ser	Ser	Gln		
		100					105						110				
Leu	Thr	Lys	Gly	Glu	Arg	Val	Thr	Leu	Thr	Phe	Arg	Asp	Glu	Asp	Phe		
	115						120					125					
Trp	Gly	Ala	Gly	Tyr	Cys	Phe	Tyr	Arg	Asp	Ser	Leu	Ser	Ile	Lys	Glu		
	130					135				140							
Asp	Lys	Gln	Tyr	Glu	Glu	Glu	Ile	Lys	Lys	Ile	Glu	Asp	Asp	Leu	Glu		
145				150				155						160			
Arg	Gln	Asp	Leu	Glu	Asn	Asp	Ala	Leu	Glu	Met	Phe	Lys	Lys	Gln	Thr		
			165					170						175			
Glu	Arg	Glu	Ala	Asn	Lys	Pro	Trp	His	Gln	Arg	Leu	Ser	Glu	Asn	Ile		
		180					185						190				
Gln	Asp	Gln	Trp	Trp	Asn	Phe	Lys	Gly	Leu	Phe	Gln						
	195						200										

<210> SEQ ID NO 505

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 505

atgaaaaaaaaa	cactattatt	aagtactgct	gttttgacgc	tagccggtac	tgtcgcacctta	60
ttaactcatt	ctgtagatgc	atcgacttat	tcttactaca	gcactagtca	ttttttaaga	120
caagatggaa	gagagactct	tagagaagct	aaatatgcgg	cagagttaca	aattagaaac	180
ttgttaagtc	agtatcatat	taatggaaaa	gaatataata	attatttcag	atattattat	240
agacaagcta	tgcaagctag	aaatatagac	gaagttaata	aaatcattga	agatttagaa	300
aaaaaacttgc	aagcacaata	a				321

<210> SEQ ID NO 506

<211> LENGTH: 106

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 506

Met	Lys	Lys	Thr	Leu	Leu	Leu	Ser	Thr	Ala	Val	Leu	Thr	Leu	Ala	Gly
1				5				10					15		
Thr	Val	Ala	Leu	Leu	Thr	His	Ser	Val	Asp	Ala	Ser	Thr	Tyr	Ser	Tyr
		20					25					30			
Tyr	Ser	Thr	Ser	His	Phe	Leu	Arg	Gln	Asp	Gly	Arg	Glu	Thr	Leu	Arg
	35					40				45					
Glu	Ala	Lys	Tyr	Ala	Ala	Glu	Leu	Gln	Ile	Arg	Asn	Leu	Leu	Ser	Gln
	50					55				60					
Tyr	His	Ile	Asn	Gly	Lys	Glu	Tyr	Asn	Asn	Tyr	Phe	Arg	Tyr	Tyr	Tyr
65				70				75						80	
Arg	Gln	Ala	Met	Gln	Ala	Arg	Asn	Ile	Asp	Glu	Val	Asn	Lys	Ile	Ile
			85				90						95		
Glu	Asp	Leu	Glu	Lys	Asn	Leu	Gln	Ala	Gln						
	100						105								


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<210> SEQ ID NO 507
<211> LENGTH: 633
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 507
atgaaaaaga cattaacttt gctactggca ctctttgcca tcggggtaac tagtagcgtc      60
agagcgggagg atgaacaaaag tagtacacaa aagccagtaa aatttgattt ggatggacct      120
caacaaaaaaa ttaaagatta tagtggcaac acaatcactc tagaagactt atatgttggg      180
agtaaagtag taaaaatata tatccctcaa ggatgggtggg tataatcttta cagacaatgt      240
gatcataaca gtaaagaacg aggaatttta gctagtccta ttctcgaaaa aaatataaca      300
aaaacagatc cttatcgtca atattataca ggagtacctt atattcttaa cttaggagaa      360
gatcctttga agaaaggaga aaaattaact ttctcattta aaggagaaga cggattttat      420
gtcggtagct atatctatag agactctgat actataaaaa aagaaaaaga agctgaagaa      480
gcacttcaaa aaaaggaaga ggaaaagcaa caaaaacagc tagaagaaag catgctaaag      540
cagataagag aagaagacca taaaccttgg catcagcggc taagtgaag catccaagat      600
cagtgggtgga actttaaggg actgtttcag tga                                     633

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<210> SEQ ID NO 508
<211> LENGTH: 210
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 508
Met Lys Lys Thr Leu Thr Leu Leu Leu Ala Leu Phe Ala Ile Gly Val
1          5          10          15
Thr Ser Ser Val Arg Ala Glu Asp Glu Gln Ser Ser Thr Gln Lys Pro
20          25          30
Val Lys Phe Asp Leu Asp Gly Pro Gln Gln Lys Ile Lys Asp Tyr Ser
35          40          45
Gly Asn Thr Ile Thr Leu Glu Asp Leu Tyr Val Gly Ser Lys Val Val
50          55          60
Lys Ile Tyr Ile Pro Gln Gly Trp Trp Val Tyr Leu Tyr Arg Gln Cys
65          70          75          80
Asp His Asn Ser Lys Glu Arg Gly Ile Leu Ala Ser Pro Ile Leu Glu
85          90          95
Lys Asn Ile Thr Lys Thr Asp Pro Tyr Arg Gln Tyr Tyr Thr Gly Val
100         105         110
Pro Tyr Ile Leu Asn Leu Gly Glu Asp Pro Leu Lys Lys Gly Glu Lys
115         120         125
Leu Thr Phe Ser Phe Lys Gly Glu Asp Gly Phe Tyr Val Gly Ser Tyr
130         135         140
Ile Tyr Arg Asp Ser Asp Thr Ile Lys Lys Glu Lys Glu Ala Glu Glu
145         150         155         160
Ala Leu Gln Lys Lys Glu Glu Glu Lys Gln Gln Lys Gln Leu Glu Glu
165         170         175
Ser Met Leu Lys Gln Ile Arg Glu Glu Asp His Lys Pro Trp His Gln
180         185         190
Arg Leu Ser Glu Ser Ile Gln Asp Gln Trp Trp Asn Phe Lys Gly Leu
195         200         205
Phe Gln
210

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<210> SEQ ID NO 509
<211> LENGTH: 384
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 509

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gtgttgagca	gtcccactgt	tttaaaacaa	ttttctgcta	taattgggat	aatcccttta	60
gtagtcaggc	cacctctgat	aggggtggct	tttttgggtt	ttagtgaccc	gtgtgttgag	120
aaaggagcat	ttatgccaga	aaagaaagt	ttgcccgtcc	taagcatagt	ggtgagtttt	180
gtctgcctgc	ttgatcata	cttctttttt	gctacttata	gttatctcta	cttaccgctt	240
gtagcaagta	gtctagctct	tatcggtctg	gtgcaaaaca	aaggcaggca	aaaggtgtgg	300
tcgctagctg	gactcgtcct	agctgctcta	gccgtggcag	tagtggccta	tgctactat	360
gacccaaccg	tcattccccta	ctaa				384

<210> SEQ ID NO 510
 <211> LENGTH: 127
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 510

Met	Leu	Ser	Ser	Pro	Thr	Val	Leu	Lys	Gln	Phe	Ser	Ala	Ile	Ile	Gly
1				5					10				15		
Ile	Ile	Pro	Leu	Val	Val	Arg	Pro	Pro	Leu	Ile	Gly	Val	Ala	Phe	Leu
			20					25				30			
Gly	Phe	Ser	Asp	Pro	Cys	Val	Glu	Lys	Gly	Ala	Phe	Met	Pro	Glu	Lys
		35				40					45				
Lys	Val	Leu	Pro	Val	Leu	Ser	Ile	Val	Val	Ser	Phe	Val	Cys	Leu	Leu
	50					55					60				
Asp	His	Ile	Phe	Phe	Phe	Ala	Thr	Tyr	Ser	Tyr	Leu	Tyr	Leu	Pro	Leu
65				70					75					80	
Val	Ala	Ser	Ser	Leu	Ala	Leu	Ile	Gly	Leu	Val	Gln	Asn	Lys	Gly	Arg
			85					90				95			
Gln	Lys	Val	Trp	Ser	Leu	Ala	Gly	Leu	Val	Leu	Ala	Ala	Leu	Ala	Val
		100					105					110			
Ala	Val	Val	Ala	Tyr	Ala	Tyr	Tyr	Asp	Pro	Thr	Val	Ile	Pro	Tyr	
		115					120					125			

<210> SEQ ID NO 511
 <211> LENGTH: 555
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 511

atgaaatgga	gtggtttttat	gaaaacaaaa	tcaaaacgct	ttttaaacct	agcaaccctt	60
tgcttgggccc	tactaggaac	aacttttgcta	atggcacatc	ccgtacaggc	ggaggtgata	120
tcaaaaagag	actatatgac	tcgcttcggg	ttaggcgatt	tagaagatga	ttcagctaac	180
tatccttcaa	atttagaagc	tagatataaa	ggatatttag	agggatatga	aaaaggctta	240
aaaggagatg	atatacccg	acggcccaag	attcagggtc	ctgaggatgt	tcagccatct	300
gaccatggcg	actatagaga	tggttatgag	gaaggatttg	gagaaggaca	acataaacgt	360
gatccattag	aaacagaagc	agaagatgat	tctcaaggag	gacgtcaaga	aggacgtcaa	420
ggacatcaag	aaggagcaga	ttctagtgat	ttgaacgttg	aagaaagcga	cggtttgtct	480
gttattgatg	aagtagttgg	agtaatttat	caagcattta	gtactatttg	gacataactta	540
agcggtttgt	tctaa					555

<210> SEQ ID NO 512
 <211> LENGTH: 184
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 512

Met	Lys	Trp	Ser	Gly	Phe	Met	Lys	Thr	Lys	Ser	Lys	Arg	Phe	Leu	Asn
1				5				10					15		
Leu	Ala	Thr	Leu	Cys	Leu	Ala	Leu	Leu	Gly	Thr	Thr	Leu	Leu	Met	Ala
		20					25					30			
His	Pro	Val	Gln	Ala	Glu	Val	Ile	Ser	Lys	Arg	Asp	Tyr	Met	Thr	Arg
		35					40					45			

Phe	Gly	Leu	Gly	Asp	Leu	Glu	Asp	Asp	Ser	Ala	Asn	Tyr	Pro	Ser	Asn	
50						55					60					
Leu	Glu	Ala	Arg	Tyr	Lys	Gly	Tyr	Leu	Glu	Gly	Tyr	Glu	Lys	Gly	Leu	
65					70					75					80	
Lys	Gly	Asp	Asp	Ile	Pro	Glu	Arg	Pro	Lys	Ile	Gln	Val	Pro	Glu	Asp	
				85					90					95		
Val	Gln	Pro	Ser	Asp	His	Gly	Asp	Tyr	Arg	Asp	Gly	Tyr	Glu	Glu	Gly	
			100					105					110			
Phe	Gly	Glu	Gly	Gln	His	Lys	Arg	Asp	Pro	Leu	Glu	Thr	Glu	Ala	Glu	
		115					120					125				
Asp	Asp	Ser	Gln	Gly	Gly	Arg	Gln	Glu	Gly	Arg	Gln	Gly	His	Gln	Glu	
	130					135					140					
Gly	Ala	Asp	Ser	Ser	Asp	Leu	Asn	Val	Glu	Glu	Ser	Asp	Gly	Leu	Ser	
145					150					155					160	
Val	Ile	Asp	Glu	Val	Val	Gly	Val	Ile	Tyr	Gln	Ala	Phe	Ser	Thr	Ile	
			165					170						175		
Trp	Thr	Tyr	Leu	Ser	Gly	Leu	Phe									
			180													

<210> SEQ ID NO 513
 <211> LENGTH: 1635
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 513

atgtcgacag	aaaaaaaaaca	actgacacaa	gaagaattga	tggttcaggg	agcagcctgg	60
tccacagctg	gtaatttcat	tagccgactt	ttgggagtg	tatacattat	tccctgggtac	120
atttggatgg	ggcaatacgc	gattcaagcc	aacgctcttt	tcaatatggg	gtataatggt	180
tatgcttatt	ttttattgat	ttcaaccaca	ggactcaatg	ttgcgattgc	taagcagggt	240
gccaagtaca	attccatggg	acaaactgag	catagctatc	aattaatccg	aagtacccta	300
aaactcatgc	ttggtctggg	ccttattttt	tcagccatta	tgtatctggg	ctctccttta	360
tttgcgagct	tatctggtgg	tgatgacaca	cttgttccca	ttatgcacag	cctttccttta	420
gcagttttta	tttttcctgt	aatgagtgtg	attcgaggca	tctttcaagg	ccacaataat	480
atcaagcctt	atgcagttag	tcagattgct	gagcaactca	ttcgggttat	ctggatgctt	540
ttgaccacct	tttttatcat	gaagtgggt	tctggtgatt	acgcttcagc	agtgaactcag	600
tcaacttttg	cagcctttat	cgggatgggtg	gctagtatgg	gtgttctggg	gtactatctt	660
tggaaacagg	gacttctagc	agctattttt	agtaagccag	atcatactgt	ttctattgat	720
atcaagggtc	tgttgcttga	aaccttaaaa	gaatccatcc	cctttatcgt	aacaggaagt	780
gccattcaag	cctttcaatt	gattgatcaa	tggacttttg	tcaatacgat	gactcttttt	840
acagattata	gccgttctca	attgcttggt	ttatttggtt	actttaacgc	aaaccagcc	900
aaaattacaa	tggtcttaat	tgcagtagca	gcatctattg	gtggtgtagg	tattgccttg	960
ttaactgaaa	attatgtcaa	aaaagacatg	aaagcagctg	ctcgtttaat	cattaacaac	1020
attgaaatgt	tagtgatgtt	tttgttacct	gctcttactg	gggcaattat	tttagcaaga	1080
cctctatatt	ctgtttttta	cggagctagc	gaggagcgtg	ccattcacct	ccttggtggcg	1140
gttctctttc	aaaccttgct	actggcgctt	tacaccctct	tttcaccgat	gcttcaagct	1200
ctttttgaaa	atcgaaaagc	gatttactac	tttgccatag	gtatcttgat	taagttagtt	1260
ttacagatac	cgcttattta	tttgctacat	gcttatgggtc	ccttactagc	gacgacgatt	1320
gcttttagtg	tgccgattta	tttgatgtat	cgacgcctat	atcagggttac	tcatttttaac	1380
cgcaaaactgt	tgcaaaaacg	tttattatta	accttaattg	aaaccttatt	aatgggactg	1440
gtcgtgtttg	tggccaactg	gctattgggc	tatgccttta	aaccgacagg	ccgcttgacc	1500
agccttcttt	acctcctcat	tattggtggc	ttgggaatga	cgttttacac	ggcactcacc	1560
ttgctgacgc	atcaactgga	taaattaatt	ggtagcaaag	ctagtcgcct	tcgtcagaaa	1620
ttaggctggc	attaa					1635

<210> SEQ ID NO 514
 <211> LENGTH: 544
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 514

Met	Ser	Thr	Glu	Lys	Lys	Gln	Leu	Thr	Gln	Glu	Glu	Leu	Met	Val	Gln	
1				5					10					15		
Gly	Ala	Ala	Trp	Ser	Thr	Ala	Gly	Asn	Phe	Ile	Ser	Arg	Leu	Leu	Gly	
			20					25					30			
Val	Leu	Tyr	Ile	Ile	Pro	Trp	Tyr	Ile	Trp	Met	Gly	Gln	Tyr	Ala	Ile	
		35					40					45				
Gln	Ala	Asn	Ala	Leu	Phe	Asn	Met	Gly	Tyr	Asn	Val	Tyr	Ala	Tyr	Phe	
	50					55				60						
Leu	Leu	Ile	Ser	Thr	Thr	Gly	Leu	Asn	Val	Ala	Ile	Ala	Lys	Gln	Val	
65					70					75					80	
Ala	Lys	Tyr	Asn	Ser	Met	Gly	Gln	Thr	Glu	His	Ser	Tyr	Gln	Leu	Ile	
			85						90					95		
Arg	Ser	Thr	Leu	Lys	Leu	Met	Leu	Gly	Leu	Gly	Leu	Ile	Phe	Ser	Ala	
			100					105					110			
Ile	Met	Tyr	Leu	Gly	Ser	Pro	Leu	Phe	Ala	Ser	Leu	Ser	Gly	Gly	Asp	
	115					120						125				
Asp	Thr	Leu	Val	Pro	Ile	Met	His	Ser	Leu	Ser	Leu	Ala	Val	Phe	Ile	
	130					135					140					
Phe	Pro	Val	Met	Ser	Val	Ile	Arg	Gly	Ile	Phe	Gln	Gly	His	Asn	Asn	
145					150					155					160	
Ile	Lys	Pro	Tyr	Ala	Val	Ser	Gln	Ile	Ala	Glu	Gln	Leu	Ile	Arg	Val	
				165					170					175		
Ile	Trp	Met	Leu	Leu	Thr	Thr	Phe	Phe	Ile	Met	Lys	Leu	Gly	Ser	Gly	
		180						185					190			
Asp	Tyr	Ala	Ser	Ala	Val	Thr	Gln	Ser	Thr	Phe	Ala	Ala	Phe	Ile	Gly	
	195					200						205				
Met	Val	Ala	Ser	Met	Gly	Val	Leu	Gly	Tyr	Tyr	Leu	Trp	Lys	Gln	Gly	
	210					215					220					
Leu	Leu	Ala	Ala	Ile	Phe	Ser	Lys	Pro	Asp	His	Thr	Val	Ser	Ile	Asp	
225					230					235					240	
Ile	Lys	Gly	Leu	Leu	Glu	Thr	Leu	Lys	Glu	Ser	Ile	Pro	Phe	Ile		
			245					250					255			
Val	Thr	Gly	Ser	Ala	Ile	Gln	Ala	Phe	Gln	Leu	Ile	Asp	Gln	Trp	Thr	
		260						265					270			
Phe	Val	Asn	Thr	Met	Thr	Leu	Phe	Thr	Asp	Tyr	Ser	Arg	Ser	Gln	Leu	
	275					280						285				
Leu	Val	Leu	Phe	Gly	Tyr	Phe	Asn	Ala	Asn	Pro	Ala	Lys	Ile	Thr	Met	
	290					295				300						
Val	Leu	Ile	Ala	Val	Ala	Ala	Ser	Ile	Gly	Gly	Val	Gly	Ile	Ala	Leu	
305					310					315					320	
Leu	Thr	Glu	Asn	Tyr	Val	Lys	Lys	Asp	Met	Lys	Ala	Ala	Ala	Arg	Leu	
			325					330					335			
Ile	Ile	Asn	Asn	Ile	Glu	Met	Leu	Val	Met	Phe	Leu	Leu	Pro	Ala	Leu	
		340						345					350			
Thr	Gly	Ala	Ile	Ile	Leu	Ala	Arg	Pro	Leu	Tyr	Ser	Val	Phe	Tyr	Gly	
	355					360						365				
Ala	Ser	Glu	Glu	Arg	Ala	Ile	His	Leu	Phe	Val	Ala	Val	Leu	Phe	Gln	
	370					375					380					
Thr	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Leu	Phe	Ser	Pro	Met	Leu	Gln	Ala	
385					390					395					400	
Leu	Phe	Glu	Asn	Arg	Lys	Ala	Ile	Tyr	Tyr	Phe	Ala	Tyr	Gly	Ile	Leu	
			405					410					415			
Ile	Lys	Leu	Val	Leu	Gln	Ile	Pro	Leu	Ile	Tyr	Leu	Leu	His	Ala	Tyr	
		420						425					430			
Gly	Pro	Leu	Leu	Ala	Thr	Thr	Ile	Ala	Leu	Val	Val	Pro	Ile	Tyr	Leu	
	435						440						445			

Met	Tyr	Arg	Arg	Leu	Tyr	Gln	Val	Thr	His	Phe	Asn	Arg	Lys	Leu	Leu
450						455					460				
Gln	Lys	Arg	Leu	Leu	Leu	Thr	Leu	Ile	Glu	Thr	Leu	Leu	Met	Gly	Leu
465						470					475				480
Val	Val	Phe	Val	Ala	Asn	Trp	Leu	Leu	Gly	Tyr	Ala	Phe	Lys	Pro	Thr
				485						490				495	
Gly	Arg	Leu	Thr	Ser	Leu	Leu	Tyr	Leu	Leu	Ile	Ile	Gly	Gly	Leu	Gly
			500					505					510		
Met	Thr	Val	Tyr	Thr	Ala	Leu	Thr	Leu	Leu	Thr	His	Gln	Leu	Asp	Lys
		515					520					525			
Leu	Ile	Gly	Ser	Lys	Ala	Ser	Arg	Leu	Arg	Gln	Lys	Leu	Gly	Trp	His
	530					535					540				

<210> SEQ ID NO 515

<211> LENGTH: 1053

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 515

gtgaaaacta	agcatccctt	tttgtgtctc	gagcgttttt	gcttaaaaaa	aacgcagata	60
atcactaagt	cacatatctt	ttggcttgct	tttgtgctac	ttagttttag	cttatgtgtt	120
gctattttact	gtcatctgcg	ctttggagcc	gttgctttat	cacatcagga	tcttaactct	180
attttatttg	gaaagcaaaa	cggccataaa	gccaatgttt	tactcgctat	acgattaccg	240
agactttttg	gtgctacctt	aactggctct	gcgttagctg	tttctggaac	tatcatgcaa	300
gcaatcacac	gtaatcctat	cgctgagcct	ggccttttag	gcattaatgc	tgagcagga	360
ctagccttgg	tactggctta	tgcgtttgta	cctcacttgc	actattccct	cattattctg	420
ctttcgttgt	tagggctctag	cctggcagca	accttagtct	ttggcctttc	ttatcaatct	480
ggcaaaggct	accatcagct	ccgccttgct	ttagcaggag	ctatggtttc	catactgcta	540
tcagcattag	gtcaagggtat	taccaattac	tatcatctgg	caaatgctgt	tatcggtcgg	600
caagcaggag	gtcctgtcgg	ggtcaattgg	caaatgatcg	gctatattgc	tcctcttatt	660
attccttagtc	tttgttttagc	ccagctatta	tcttatcacc	tgaccgtcct	tagtctaagt	720
gagtctcagg	caaaagctct	tgggcaaaaa	accaacttga	tcagtgcagt	ctttatgatt	780
ttggttctta	ttttatcatc	agcagctgta	gccattgctg	gaagcatttc	ttttatcggc	840
ttagtcattc	ctcatcttat	gaaacatttt	acacctcatc	attaccgata	ccttttgccg	900
ctttgtgcag	tttctggcgc	tagtttcacg	gtatgggttg	atattgcttg	tcgtaatctc	960
aatccgcctt	atgaaaacccc	tcttggggca	ttgggttagct	taattggttt	tccatgcttt	1020
ttatgggttaa	taagaagagg	aggccgctat	tga			1053

<210> SEQ ID NO 516

<211> LENGTH: 350

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 516

Met	Lys	Thr	Lys	His	Pro	Phe	Leu	Cys	Leu	Glu	Arg	Phe	Cys	Leu	Lys
1				5					10					15	
Lys	Thr	Gln	Ile	Ile	Thr	Lys	Ser	His	Ile	Phe	Trp	Leu	Val	Phe	Val
			20					25					30		
Leu	Leu	Ser	Phe	Ser	Leu	Cys	Val	Ala	Ile	Tyr	Cys	His	Leu	Arg	Phe
		35					40					45			
Gly	Ala	Val	Ala	Leu	Ser	His	Gln	Asp	Leu	Asn	Ser	Ile	Leu	Phe	Gly
	50					55				60					
Lys	Gln	Asn	Gly	His	Lys	Ala	Asn	Val	Leu	Leu	Ala	Ile	Arg	Leu	Pro
65					70					75				80	
Arg	Leu	Phe	Gly	Ala	Thr	Leu	Thr	Gly	Ser	Ala	Leu	Ala	Val	Ser	Gly
			85					90					95		
Thr	Ile	Met	Gln	Ala	Ile	Thr	Arg	Asn	Pro	Ile	Ala	Glu	Pro	Gly	Leu
		100						105				110			
Leu	Gly	Ile	Asn	Ala	Gly	Ala	Gly	Leu	Ala	Leu	Val	Leu	Ala	Tyr	Ala

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 518

```
Met Leu Phe Met Val Asn Lys Lys Arg Arg Pro Leu Leu Lys Ser Gln
 1           5           10           15
Arg His Leu Leu Arg Leu Tyr Thr Ser Leu Ile Leu Leu Leu Val Ser
 20           25           30
Leu Met Gly Leu Ala Leu Ser Leu Gly Glu Ser His Leu Ser Phe Leu
 35           40           45
Asp Leu Val His Val Phe Leu Gly Lys Ser Ser His Ala Ile Ser Phe
 50           55           60
Ile Val Ile Asn Ile Arg Leu Pro Arg Ile Leu Ala Ala Cys Leu Gly
 65           70           75           80
Gly Gly Ser Leu Ala Leu Ser Gly Leu Leu Leu Gln Arg Leu Thr Arg
 85           90           95
Asn Pro Leu Ala Asp Ser Gly Val Leu Gly Ile Thr Ile Gly Ala Gly
100           105           110
Ile Ser Leu Ala Ile Val Val Ser Phe Ser Phe Phe Glu Gln Ala His
115           120           125
Ile Ser His Tyr Leu Pro Leu Phe Ala Met Leu Gly Ala Ile Val Thr
130           135           140
Thr Phe Ser Val Tyr Trp Leu Ser Leu Thr Lys Gln Gly Gln Ile Asp
145           150           155           160
Pro Thr Arg Leu Ile Leu Thr Gly Val Ala Val Thr Thr Met Leu Ser
165           170           175
Ser Leu Met Val Ala Leu Val Gly His Ile Asn Arg Tyr Lys Val Asp
180           185           190
Leu Val Ile Asn Trp Leu Ser Gly Gln Leu Ile Gly Asp Asp Trp Pro
195           200           205
Thr Leu Ser Val Ile Ala Pro Leu Leu Leu Cys Phe Trp Leu Leu Thr
210           215           220
Tyr Ser Gln Ala His Phe Leu Asn Ile Met Gly Leu Ala Asp Asn Thr
225           230           235           240
Ala Ile Gly Leu Gly Leu Pro Leu Asn Arg Lys Arg Arg Leu Ile Leu
245           250           255
Val Leu Ala Ala Gly Leu Gly Ala Leu Ser Val Leu Leu Val Gly Asn
260           265           270
Ile Ser Phe Ile Gly Leu Ile Ala Gly His Phe Ser Thr Tyr Leu Val
275           280           285
Gly Ser Asn His Lys Ile Thr Ile Pro Ile Ser Ile Leu Ile Gly Met
290           295           300
Ile Leu Leu Leu Val Ala Asp Thr Val Gly Arg Val Tyr Leu Val Gly
305           310           315           320
Ser Asn Ile Gln Thr Gly Ile Leu Val Ser Leu Ile Gly Ala Pro Tyr
325           330           335
Phe Leu Tyr Leu Met Ala Lys Thr Lys
340           345
```

<210> SEQ ID NO 519

<211> LENGTH: 1374

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 519

```
atgaagtcac tatattat ttttaggagt tacattaaca tggaagaccc tgtgagtcag      60
tccttagtga ttcaattttt attgttagtt gttttaacct tgtaaagtgc ttttttttca      120
gccagtga aaa tggccttagt ttctctcaat cgttctcggg tggaacaaaa agcagcagac      180
gggtgataaaa aatacgctcg tttgttgcgg gtttagagg aacctaata ttttttatca      240
acgattcaag ttgggattac ctttattagt ttactatcag gagcaagttt atcagcttct      300
```

ttgggtaagg	tgatctcagg	ttggctaggt	aattcagcga	ccgcaaggac	agctgggtact	360
atcatctcct	tggttttctt	gacttatgtc	tctattgttt	taggagaatt	gtatccaaaa	420
cggattgcca	tgaacctcaa	agacaagttg	gcgattgttt	cagcccctat	tatcattggg	480
ttagggagac	tggttagtcc	ctttgtatgg	ctcttatcag	cttctactaa	tttactgagc	540
cgacttaccc	ctatgacctt	tgatgatgca	gatgagcaaa	tgacacgtga	tgaaatcgag	600
tatatgttat	caaaaagtga	ggcgaccctt	gatgctgaag	aaattgagat	gttgcaagga	660
gttttctcac	ttgatgaaat	gatggcgcgt	gaagtcatgg	tccaaggac	cgatgctttc	720
atgattgaca	ttaacgatga	tccgcttgaa	aatattcagg	aaatcttaaa	acaaagtttt	780
tcacgcattc	ctgtttatga	tgtggataaa	gataaaatta	tcggtctcat	ccacactaag	840
cgtctcttgg	agtcagggtt	ccgccaggga	tttgatcaga	ttaacatgcg	aaaaatgtta	900
caagaacctc	tttttgttcc	cgaaaccatt	ttttagatg	atctcttacg	ccagctgcgc	960
aatacccaaa	atcagatggc	tatttttgcta	gatgaatatg	gtgggtgtggc	aggacttgtg	1020
actttggaag	acttgcttga	agaaatcgtc	ggtgaaatcg	atgatgaaac	cgataaagca	1080
gaacaatttg	ttcattgagat	tggagacaat	acctatattg	ttgttggtac	tatgacttta	1140
aatgagttta	atgactattt	tgataccgaa	ctagaatcag	atgatgtaga	taccattgct	1200
ggttttttatt	tgacagggtat	cggaaccatt	ccaagccagg	agcaaaaaga	agcctacgaa	1260
atagataaca	aagacaaaaca	tttagttcta	atcaacgata	aagtcaaaga	tggccgtatt	1320
acgaaatttaa	aattaatcct	gtctaataata	gaacagatta	ttgaggaaga	ctag	1374

<210> SEQ ID NO 520

<211> LENGTH: 457

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 520

Met	Lys	Ser	Leu	Tyr	Tyr	Phe	Phe	Arg	Ser	Tyr	Ile	Asn	Met	Glu	Asp
1				5					10					15	
Pro	Val	Ser	Gln	Ser	Leu	Val	Ile	Gln	Phe	Leu	Leu	Leu	Val	Val	Leu
			20					25					30		
Thr	Leu	Leu	Asn	Ala	Phe	Phe	Ser	Ala	Ser	Glu	Met	Ala	Leu	Val	Ser
			35				40					45			
Leu	Asn	Arg	Ser	Arg	Val	Glu	Gln	Lys	Ala	Ala	Asp	Gly	Asp	Lys	Lys
	50					55					60				
Tyr	Ala	Arg	Leu	Leu	Arg	Val	Leu	Glu	Glu	Pro	Asn	His	Phe	Leu	Ser
65					70					75				80	
Thr	Ile	Gln	Val	Gly	Ile	Thr	Phe	Ile	Ser	Leu	Leu	Ser	Gly	Ala	Ser
			85					90					95		
Leu	Ser	Ala	Ser	Leu	Gly	Lys	Val	Ile	Ser	Gly	Trp	Leu	Gly	Asn	Ser
			100					105					110		
Ala	Thr	Ala	Arg	Thr	Ala	Gly	Thr	Ile	Ile	Ser	Leu	Val	Phe	Leu	Thr
			115				120					125			
Tyr	Val	Ser	Ile	Val	Leu	Gly	Glu	Leu	Tyr	Pro	Lys	Arg	Ile	Ala	Met
	130					135					140				
Asn	Leu	Lys	Asp	Lys	Leu	Ala	Ile	Val	Ser	Ala	Pro	Ile	Ile	Ile	Gly
145					150					155				160	
Leu	Gly	Arg	Leu	Val	Ser	Pro	Phe	Val	Trp	Leu	Leu	Ser	Ala	Ser	Thr
			165					170					175		
Asn	Leu	Leu	Ser	Arg	Leu	Thr	Pro	Met	Thr	Phe	Asp	Asp	Ala	Asp	Glu
			180					185					190		
Gln	Met	Thr	Arg	Asp	Glu	Ile	Glu	Tyr	Met	Leu	Ser	Lys	Ser	Glu	Ala
	195					200						205			
Thr	Leu	Asp	Ala	Glu	Glu	Ile	Glu	Met	Leu	Gln	Gly	Val	Phe	Ser	Leu
	210					215					220				
Asp	Glu	Met	Met	Ala	Arg	Glu	Val	Met	Val	Pro	Arg	Thr	Asp	Ala	Phe
225					230					235				240	
Met	Ile	Asp	Ile	Asn	Asp	Asp	Pro	Leu	Glu	Asn	Ile	Gln	Glu	Ile	Leu
			245					250					255		
Lys	Gln	Ser	Phe	Ser	Arg	Ile	Pro	Val	Tyr	Asp	Val	Asp	Lys	Asp	Lys

				260					265					270					
Ile	Ile	Gly	Leu	Ile	His	Thr	Lys	Arg	Leu	Leu	Glu	Ser	Gly	Phe	Arg				
		275					280					285							
Gln	Gly	Phe	Asp	Gln	Ile	Asn	Met	Arg	Lys	Met	Leu	Gln	Glu	Pro	Leu				
	290					295					300								
Phe	Val	Pro	Glu	Thr	Ile	Phe	Val	Asp	Asp	Leu	Leu	Arg	Gln	Leu	Arg				
305					310					315					320				
Asn	Thr	Gln	Asn	Gln	Met	Ala	Ile	Leu	Leu	Asp	Glu	Tyr	Gly	Gly	Val				
			325					330						335					
Ala	Gly	Leu	Val	Thr	Leu	Glu	Asp	Leu	Leu	Glu	Glu	Ile	Val	Gly	Glu				
		340						345					350						
Ile	Asp	Asp	Glu	Thr	Asp	Lys	Ala	Glu	Gln	Phe	Val	His	Glu	Ile	Gly				
	355					360				365									
Asp	Asn	Thr	Tyr	Ile	Val	Val	Gly	Thr	Met	Thr	Leu	Asn	Glu	Phe	Asn				
	370				375					380									
Asp	Tyr	Phe	Asp	Thr	Glu	Leu	Glu	Ser	Asp	Asp	Val	Asp	Thr	Ile	Ala				
385				390					395					400					
Gly	Phe	Tyr	Leu	Thr	Gly	Ile	Gly	Thr	Ile	Pro	Ser	Gln	Glu	Gln	Lys				
			405				410						415						
Glu	Ala	Tyr	Glu	Ile	Asp	Asn	Lys	Asp	Lys	His	Leu	Val	Leu	Ile	Asn				
		420				425						430							
Asp	Lys	Val	Lys	Asp	Gly	Arg	Ile	Thr	Lys	Leu	Lys	Leu	Ile	Leu	Ser				
	435				440					445									
Asn	Ile	Glu	Gln	Ile	Ile	Glu	Glu	Asp											
	450				455														

<210> SEQ ID NO 521

<211> LENGTH: 564

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 521

atgtcaaaaa	cacataaaat	gattatgatt	ggtatacttt	ctgcgatatc	atttctattg	60
atgctagtta	gctttgccat	tattccaggc	gcagcttttt	taaaaattga	atttagtatt	120
attcctgttt	tatttggttt	aatgattatg	gacttaaaga	gtgcttactt	aattttgtta	180
ttgaggtcct	tattgaaact	ctttttgaac	aatcgtgggg	ttaatgattt	tattggtctc	240
ccaatgaata	ttatcgctat	cgctttat	gtgacggctt	ttgccttagt	ttggaaccgt	300
caaaaaacgc	ttagtcaata	tgtatttgct	agcttactag	gcacagggtt	attaacgttt	360
ggcatgggtt	ttcttaatta	tacttttgcc	attcctttat	atgctatatt	tgcaaattatt	420
gatatcagag	cttatattgg	tgttactaag	tatatgatga	ctatgggttat	tccgtttaat	480
cttggtgaag	ggttgatatt	tgcaattacc	ttttattttg	tgtatattgc	aagtaaacca	540
attttagaaa	gatacttaca	ctaa				564

<210> SEQ ID NO 522

<211> LENGTH: 187

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 522

Met	Ser	Lys	Thr	His	Lys	Met	Ile	Met	Ile	Gly	Ile	Leu	Ser	Ala	Ile				
1			5				10			15									
Ser	Phe	Leu	Leu	Met	Leu	Val	Ser	Phe	Ala	Ile	Ile	Pro	Gly	Ala	Ala				
		20					25			30									
Phe	Leu	Lys	Ile	Glu	Phe	Ser	Ile	Ile	Pro	Val	Leu	Phe	Gly	Leu	Met				
	35				40					45									
Ile	Met	Asp	Leu	Lys	Ser	Ala	Tyr	Leu	Ile	Leu	Leu	Arg	Ser	Leu					
	50				55				60										
Leu	Lys	Leu	Phe	Leu	Asn	Asn	Arg	Gly	Val	Asn	Asp	Phe	Ile	Gly	Leu				
65				70					75					80					

Pro	Met	Asn	Ile	Ile	Ala	Ile	Ala	Leu	Phe	Val	Thr	Ala	Phe	Ala	Leu
				85					90					95	
Val	Trp	Asn	Arg	Gln	Lys	Thr	Leu	Ser	Gln	Tyr	Val	Phe	Ala	Ser	Leu
		100						105					110		
Leu	Gly	Thr	Gly	Leu	Leu	Thr	Phe	Gly	Met	Val	Val	Leu	Asn	Tyr	Thr
	115						120					125			
Phe	Ala	Ile	Pro	Leu	Tyr	Ala	Ile	Phe	Ala	Asn	Ile	Asp	Ile	Arg	Ala
	130					135					140				
Tyr	Ile	Gly	Val	Thr	Lys	Tyr	Met	Met	Thr	Met	Val	Ile	Pro	Phe	Asn
	145				150					155				160	
Leu	Val	Glu	Gly	Leu	Ile	Phe	Ala	Ile	Thr	Phe	Tyr	Phe	Val	Tyr	Ile
			165						170					175	
Ala	Ser	Lys	Pro	Ile	Leu	Glu	Arg	Tyr	Leu	His					
			180					185							

<210> SEQ ID NO 523

<211> LENGTH: 375

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 523

atgtctaaca	tatcattaat	catgattgcc	atacggtcag	cctcatgcgc	tggtgctgtc	60
aagctttctt	caagaatatc	actgtcatct	ttaccccaac	gttgtaagag	accaatatgc	120
cctttaataa	tcgcaaccgg	tggttcgtaat	tcattggctga	catcactaat	aaaacgtgat	180
tgcaacttag	tatgtgtctc	caatttgtct	aacatattgt	caaagataac	agacaattct	240
tcgatttcat	ctcctgacga	aatatctgag	cgcaggttta	aattattagg	attttcagag	300
atattacgca	tcacttcatg	taaattgtgt	aaaggcttca	aaaagcgccg	cgtagtaatt	360
aagatgatta	aatag					375

<210> SEQ ID NO 524

<211> LENGTH: 124

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 524

Met	Ser	Asn	Ile	Ser	Leu	Ile	Met	Ile	Ala	Ile	Arg	Ser	Ala	Ser	Cys
1			5						10				15		
Ala	Val	Ala	Val	Lys	Leu	Ser	Ser	Arg	Ile	Ser	Leu	Ser	Ser	Leu	Pro
			20					25					30		
Gln	Arg	Cys	Lys	Arg	Pro	Ile	Cys	Pro	Leu	Ile	Ile	Ala	Thr	Gly	Val
		35					40					45			
Arg	Asn	Ser	Trp	Leu	Thr	Ser	Leu	Ile	Lys	Arg	Asp	Cys	Asn	Leu	Val
	50					55				60					
Cys	Val	Ser	Asn	Leu	Ser	Asn	Ile	Leu	Ser	Lys	Ile	Thr	Asp	Asn	Ser
	65			70					75					80	
Ser	Ile	Ser	Ser	Pro	Asp	Glu	Ile	Ser	Glu	Arg	Arg	Phe	Lys	Leu	Leu
			85					90					95		
Gly	Phe	Ser	Glu	Ile	Leu	Arg	Ile	Thr	Ser	Cys	Lys	Leu	Cys	Lys	Gly
		100					105					110			
Phe	Lys	Lys	Arg	Arg	Val	Val	Ile	Lys	Met	Ile	Lys				
		115				120									

<210> SEQ ID NO 525

<211> LENGTH: 1503

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 525

atggaaaatc	agaaacaaaa	acagaagaaa	tataaaaatt	cgttaccaa	acgactatct	60
aatatctttt	ttgttctttt	tttctgcatt	ttctctgcct	ttacactgat	tgcttatagt	120

tcaacaaact	atttcttatt	gaagaaagaa	aagcagtcag	tctttcaagc	tgtaaattatt	180
gtagaggttc	gtctttctga	ggtggactct	aattttacat	tagagaactt	agcagaagtt	240
ttgtacaaaa	acgataaaac	acatctgaga	attgatgaca	gaaagggcag	tcgagtcatt	300
aggagtgagc	gcgatatcac	aaatactcta	gatgcgaatc	aagatattta	tgtctataac	360
attgataaac	agatgatttt	taccacagat	aacgaagaat	catctcctgg	cttgcattgg	420
cctatcggtc	gtgtgtatca	cgaccatata	gaagatcagt	atcgtgggtt	ttccatgaca	480
caaaagggtat	attctaatacg	gactggaaaa	tttgtgggct	atgttcaagt	ctttcatgat	540
ttaggcaatt	attatgtcat	tagagcaaga	ctgctgtttt	ggctactagt	tgttgagtta	600
tttggcacia	gcttagccta	tttaatacat	ttaattacta	cgcggcgctt	tttgaagcct	660
ttacacaatt	tacatgaagt	gatgcgtaat	atctctgaaa	atcctaataa	tttaaaccctg	720
cgctcagata	tttcgtcagg	agatgaaatc	gaagaattgt	ctgttatctt	tgacaatatg	780
ttagacaaat	tggagacaca	tactaagttg	caatcacggt	ttattagtga	tgtcagccat	840
gaattacgaa	caccggttgc	gattattaaa	gggcatattg	gtctcttaca	acgttggggt	900
aaagatgaca	gtgataattct	tgaagaaagc	ttgacagcaa	cagcgcatga	ggctgaccgt	960
atggcaaatca	tgattaatga	tatgttagac	atgattcgcg	tacaaggctc	atgttgagga	1020
catcaaaatg	atatgacagt	tttgggaagt	tctattgaaa	ctgttggttg	taattttaga	1080
gttttaagag	aagattttat	ctttacatgg	cagtcagaaa	atccaaaaac	gatagcccgt	1140
atttataaaa	atcattttga	gcaggctttg	atgattctga	ttgacaatgc	tgtgaagtat	1200
ttccgtaaa	aaaagaaaa	cgcgattaac	ctttcagtga	ctggcaaaca	agaagctatt	1260
gtagaggttc	aagataaagg	cgaaggaatt	tctaaagaag	atattgaaca	tatctttgaa	1320
cgcttttata	gaacggataa	atcacgtaat	cgaacaagta	cccaggctgg	attagggatt	1380
ggcttgtcta	ttctcaagca	aattgtagat	gggtatcatt	tacagatgaa	ggttgaaagt	1440
gaattaaatg	aaggttcagt	gtttatctta	catattcctt	tggcccagtc	taaagagagt	1500
tag						1503

<210> SEQ ID NO 526

<211> LENGTH: 500

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 526

Met	Glu	Asn	Gln	Lys	Gln	Lys	Lys	Tyr	Lys	Asn	Ser	Leu	Pro
1			5				10					15	
Lys	Arg	Leu	Ser	Asn	Ile	Phe	Phe	Val	Leu	Phe	Phe	Cys	Ile
		20					25				30		Phe
Ala	Phe	Thr	Leu	Ile	Ala	Tyr	Ser	Ser	Thr	Asn	Tyr	Phe	Leu
		35					40				45		Leu
Lys	Glu	Lys	Gln	Ser	Val	Phe	Gln	Ala	Val	Asn	Ile	Val	Arg
		50					55				60		Val
Leu	Ser	Glu	Val	Asp	Ser	Asn	Phe	Thr	Leu	Glu	Asn	Leu	Ala
65						70				75			80
Leu	Tyr	Lys	Asn	Asp	Lys	Thr	His	Leu	Arg	Ile	Asp	Asp	Arg
			85						90				95
Ser	Arg	Val	Ile	Arg	Ser	Glu	Arg	Asp	Ile	Thr	Asn	Thr	Leu
			100						105				110
Asn	Gln	Asp	Ile	Tyr	Val	Tyr	Asn	Ile	Asp	Lys	Gln	Met	Ile
		115					120					125	Phe
Thr	Asp	Asn	Glu	Glu	Ser	Ser	Pro	Gly	Leu	His	Gly	Pro	Ile
		130					135				140		Gly
Val	Tyr	His	Asp	His	Ile	Glu	Asp	Gln	Tyr	Arg	Gly	Phe	Ser
145						150				155			160
Gln	Lys	Val	Tyr	Ser	Asn	Arg	Thr	Gly	Lys	Phe	Val	Gly	Tyr
						165				170			175
Val	Phe	His	Asp	Leu	Gly	Asn	Tyr	Tyr	Val	Ile	Arg	Ala	Arg
			180						185				190
Phe	Trp	Leu	Leu	Val	Val	Glu	Leu	Phe	Gly	Thr	Ser	Leu	Ala
			195				200					205	Tyr
Ile	Ile	Leu	Ile	Thr	Thr	Arg	Arg	Phe	Leu	Lys	Pro	Leu	His

210	215	220
His Glu Val Met Arg Asn Ile Ser Glu Asn Pro Asn Asn Leu Asn Leu		
225	230	235
Arg Ser Asp Ile Ser Ser Gly Asp Glu Ile Glu Glu Leu Ser Val Ile		240
	245	250
Phe Asp Asn Met Leu Asp Lys Leu Glu Thr His Thr Lys Leu Gln Ser		255
	260	265
Arg Phe Ile Ser Asp Val Ser His Glu Leu Arg Thr Pro Val Ala Ile		270
	275	280
Ile Lys Gly His Ile Gly Leu Leu Gln Arg Trp Gly Lys Asp Asp Ser		285
	290	295
Asp Ile Leu Glu Glu Ser Leu Thr Ala Thr Ala His Glu Ala Asp Arg		300
305	310	315
Met Ala Ile Met Ile Asn Asp Met Leu Asp Met Ile Arg Val Gln Gly		320
	325	330
Ser Phe Glu Gly His Gln Asn Asp Met Thr Val Leu Glu Asp Ser Ile		335
	340	345
Glu Thr Val Val Gly Asn Phe Arg Val Leu Arg Glu Asp Phe Ile Phe		350
	355	360
Thr Trp Gln Ser Glu Asn Pro Lys Thr Ile Ala Arg Ile Tyr Lys Asn		365
	370	375
His Phe Glu Gln Ala Leu Met Ile Leu Ile Asp Asn Ala Val Lys Tyr		380
385	390	395
Ser Arg Lys Glu Lys Lys Ile Ala Ile Asn Leu Ser Val Thr Gly Lys		400
	405	410
Gln Glu Ala Ile Val Arg Val Gln Asp Lys Gly Glu Gly Ile Ser Lys		415
	420	425
Glu Asp Ile Glu His Ile Phe Glu Arg Phe Tyr Arg Thr Asp Lys Ser		430
	435	440
Arg Asn Arg Thr Ser Thr Gln Ala Gly Leu Gly Ile Gly Leu Ser Ile		445
	450	455
Leu Lys Gln Ile Val Asp Gly Tyr His Leu Gln Met Lys Val Glu Ser		460
465	470	475
Glu Leu Asn Glu Gly Ser Val Phe Ile Leu His Ile Pro Leu Ala Gln		480
	485	490
Ser Lys Glu Ser		495
	500	

<210> SEQ ID NO 527

<211> LENGTH: 297

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<220> FEATURE:

<221> NAME/KEY: Unsure

<222> LOCATION: (3)..(3)

<223> OTHER INFORMATION: unsure

<400> SEQUENCE: 527

ttntgtcgtt attatctttg ctttttagcg cccctagtag caagtttgat tcagttggct	60
atttctcgtc aaagagaata tctagctgat gctagttctg ttgaactaac aagaaatccc	120
caaggatga ttaaggctct tgaaaaattg cagttatctc agccaatgaa gcatcctgtt	180
gatgatgcta gtgcggcctt gtatattaat gagcctcgca aaaaaaggag cttcagttca	240
ttattcagca cccatcctcc tattgaggag aggattgaaa ggttaaaaaa catgtga	297

<210> SEQ ID NO 528

<211> LENGTH: 98

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

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<400> SEQUENCE: 528
Met Cys Arg Tyr Tyr Leu Cys Phe Leu Ala Pro Leu Val Ala Ser Leu
1           5           10           15
Ile Gln Leu Ala Ile Ser Arg Gln Arg Glu Tyr Leu Ala Asp Ala Ser
           20           25           30
Ser Val Glu Leu Thr Arg Asn Pro Gln Gly Met Ile Lys Ala Leu Glu
           35           40           45
Lys Leu Gln Leu Ser Gln Pro Met Lys His Pro Val Asp Asp Ala Ser
           50           55           60
Ala Ala Leu Tyr Ile Asn Glu Pro Arg Lys Lys Arg Ser Phe Ser Ser
65           70           75           80
Leu Phe Ser Thr His Pro Pro Ile Glu Glu Arg Ile Glu Arg Leu Lys
           85           90           95
Asn Met

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<210> SEQ ID NO 529
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<220> FEATURE:
<221> NAME/KEY: Unsure
<222> LOCATION: (41)..(41)
<223> OTHER INFORMATION: unsure
<400> SEQUENCE: 529

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atgctttatc aacagatttc acaaaataag caacgaacag ntgttttatt agttggtttc      60
ttcgctctct tagcacttat tggagcttca gcaggctatc tgctgttaga taattatgcc      120
atgggcttgg tccttgctct tgtcattggg gtgatttatg ctaccagtat gatttttcaa      180
tccaccagtc ttgtaatgag tatgaacaat gctagagaag ttacagaaaa agaggctcca      240
ggctttttcc atattgtcga ggatatggct atggtggccc agattccgat gccgagagtt      300
tttattattg aagatccttc tttaaatgct tttgcgacag gatctagccc tcaaaatgct      360
gctgttgcag caacgacagg tttacttgaa gtcatgaatc gtgaagaact tgaaggtgtt      420
atcggccatg aaattagcca catccgaaat tatgatatcc gtatttcgac tattgctgta      480
gctttggcga gtgctgttac cgttatttct agtatcggtg ggcgtatgct atggtatggt      540
ggcggttctc gcaggcaaag agatgacgga gatgatgatg ttttaagaat cattacatta      600
cttntgtgct ttattatctt tgctttttag      630

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<210> SEQ ID NO 530
<211> LENGTH: 209
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<220> FEATURE:
<221> NAME/KEY: UNSURE
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: unsure
<400> SEQUENCE: 530

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Met Leu Tyr Gln Gln Ile Ser Gln Asn Lys Gln Arg Thr Xaa Val Leu
1           5           10           15
Leu Val Gly Phe Phe Ala Leu Leu Ala Leu Ile Gly Ala Ser Ala Gly
           20           25           30
Tyr Leu Leu Leu Asp Asn Tyr Ala Met Gly Leu Val Leu Ala Leu Val
           35           40           45
Ile Gly Val Ile Tyr Ala Thr Ser Met Ile Phe Gln Ser Thr Ser Leu
           50           55           60
Val Met Ser Met Asn Asn Ala Arg Glu Val Thr Glu Lys Glu Ala Pro
65           70           75           80
Gly Phe Phe His Ile Val Glu Asp Met Ala Met Val Ala Gln Ile Pro
           85           90           95

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Met	Pro	Arg	Val	Phe	Ile	Ile	Glu	Asp	Pro	Ser	Leu	Asn	Ala	Phe	Ala
			100					105					110		
Thr	Gly	Ser	Ser	Pro	Gln	Asn	Ala	Ala	Val	Ala	Ala	Thr	Thr	Gly	Leu
		115					120					125			
Leu	Glu	Val	Met	Asn	Arg	Glu	Glu	Leu	Glu	Gly	Val	Ile	Gly	His	Glu
		130				135					140				
Ile	Ser	His	Ile	Arg	Asn	Tyr	Asp	Ile	Arg	Ile	Ser	Thr	Ile	Ala	Val
145					150				155					160	
Ala	Leu	Ala	Ser	Ala	Val	Thr	Val	Ile	Ser	Ser	Ile	Gly	Gly	Arg	Met
			165						170					175	
Leu	Trp	Tyr	Gly	Gly	Gly	Ser	Arg	Arg	Gln	Arg	Asp	Asp	Gly	Asp	Asp
		180						185					190		
Asp	Val	Leu	Arg	Ile	Ile	Thr	Leu	Leu	Xaa	Val	Val	Ile	Ile	Phe	Ala
		195					200					205			
Phe															

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<210> SEQ ID NO 531
<211> LENGTH: 558
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 531
atgccaacag ttttgattat cttagtcggt ttaggagtg c ttgcgctatg gttaatgatt      60
agttacaata gcctgggttaa atctcggatg cacacaaaag aagcttggag tcagattgat      120
gtgcaattaa agcgtcgttaa tgacttgatt ccaaattctta ttgaaaccgt aaagggatat      180
gctagctacg agcaaaagac atttgaaaaa atcactgatt tgcgtgcgcg tgttgcgaa      240
gcctcaactc ctcaagaaac catggcgggt tctaacgaat tgagtaaaca agtgaccagt      300
ttgtttgccg ttgctgaaaa ttaccagac ttaaaaagcta acgaaaactt cttgaaatta      360
caagaagagt tgaccaatac ggaaaaataaa atctcatatt ctcgtaact ctataattca      420
acaacgtcta attacaacct tcaattagaa tctttcccaa gcaatatcgc tggtaaatta      480
tttggtttta aaccaagtga attccttaca acaccagaag ctgaaaaaga agttccaaaa      540
gttgaattta acttttaa
558

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<210> SEQ ID NO 532
<211> LENGTH: 185
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 532
Met Pro Thr Val Leu Ile Ile Leu Val Val Leu Gly Val Leu Ala Leu
1          5          10          15
Trp Leu Met Ile Ser Tyr Asn Ser Leu Val Lys Ser Arg Met His Thr
20          25          30
Lys Glu Ala Trp Ser Gln Ile Asp Val Gln Leu Lys Arg Arg Asn Asp
35          40          45
Leu Ile Pro Asn Leu Ile Glu Thr Val Lys Gly Tyr Ala Ser Tyr Glu
50          55          60
Gln Lys Thr Phe Glu Lys Ile Thr Asp Leu Arg Ala Arg Val Ala Asn
65          70          75          80
Ala Ser Thr Pro Gln Glu Thr Met Ala Ala Ser Asn Glu Leu Ser Lys
85          90          95
Gln Val Thr Ser Leu Phe Ala Val Ala Glu Asn Tyr Pro Asp Leu Lys
100         105         110
Ala Asn Glu Asn Phe Leu Lys Leu Gln Glu Glu Leu Thr Asn Thr Glu
115         120         125
Asn Lys Ile Ser Tyr Ser Arg Gln Leu Tyr Asn Ser Thr Thr Ser Asn
130         135         140
Tyr Asn Leu Gln Leu Glu Ser Phe Pro Ser Asn Ile Ala Gly Lys Leu
145         150         155         160

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Phe	Gly	Phe	Lys	Pro	Ser	Glu	Phe	Leu	Gln	Thr	Pro	Glu	Ala	Glu	Lys
				165					170					175	
Glu	Val	Pro	Lys	Val	Glu	Phe	Asn	Phe							
			180					185							

<210> SEQ ID NO 533
 <211> LENGTH: 1215
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 533

atgaaaaaaa	tatatgattt	atgggtagg	gttagtctaa	tcaaaaaaat	aggtatcgg	60
gttgtaatat	gagtcattgt	gggcattttg	gctcctgatc	ttacagggtt	tagtatttta	120
ggaaagttaa	ttgttggtgg	tttaaaggct	atcgacacct	tgcttgattt	tgctttgggt	180
tccaagcta	tctcccatca	gaaaaaagg	aaacagacta	atatgacatt	aatcattggt	240
ctgtatttat	ttggtacctt	tgcgtcagct	ttagtagcag	tactgacagc	ttatctattc	300
cctttgacgt	tagtggttaa	tacacctgta	aatacagaat	tatcaccacc	tcaagggtgt	360
gctgaagtgt	ttcagtcact	tctattaaaa	ttagtgagta	atccgatcaa	tgcttttagct	420
actgccaatt	atattggtgt	gctatcatgg	gcaattattt	ttggactagc	attaaaggct	480
gcaagtaaa	aaacaaagca	tcttataaaa	acagcggcag	aagttacttc	acaaatagtt	540
gtttggatca	tcaatctggc	acctattggg	attatgagtc	tggtgttcac	tacgatttct	600
gaaaacgggt	ttggaatctt	atctgattat	gcttttttga	tactagtgtt	agtaggaaca	660
atgctttttg	tcgccttagt	ggttaatcca	cttattgcgg	ttttgattac	acgacaaaat	720
ccttatcccc	ttgtcttgag	atgtttacgt	gagtcaggct	ttacagcatt	tttcacacga	780
agttctgcag	ccaatattcc	agtcaatatg	caattatgcc	aaaaaattgg	attgagtaaa	840
gatacttatt	cagtggtcaat	tccacttgga	gcaactatta	atatgggtgg	ggcagcaatt	900
accatcaatg	tcctaacgct	tgctgctgta	cacacttttg	gtattcctat	tgatttttcta	960
acagccctct	tacttagcgt	tggtgctgct	gtctctgctt	gtggtgcttc	tggtgttgct	1020
gggggatcgt	tggtacttat	tcctgtagca	tgtagtttgt	ttggcatttc	aaatgatctt	1080
gcgatgcagg	tggttggtgt	tggttttatt	gttggtgtta	tccaggattc	ttgtgagaca	1140
gccttaaatt	cgtcaaccga	tggtcttttt	acagctattg	ctgaaaatgc	tttttggaag	1200
cgtaaaaaag	catag					1215

<210> SEQ ID NO 534
 <211> LENGTH: 404
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 534

Met	Lys	Lys	Ile	Tyr	Asp	Leu	Trp	Val	Arg	Val	Ser	Leu	Ile	Lys	Lys
1				5					10					15	
Ile	Gly	Ile	Gly	Val	Val	Ile	Gly	Val	Met	Leu	Gly	Ile	Leu	Ala	Pro
			20					25					30		
Asp	Leu	Thr	Gly	Phe	Ser	Ile	Leu	Gly	Lys	Leu	Phe	Val	Gly	Gly	Leu
		35					40				45				
Lys	Ala	Ile	Ala	Pro	Leu	Leu	Val	Phe	Ala	Leu	Val	Ser	Gln	Ala	Ile
		50				55					60				
Ser	His	Gln	Lys	Lys	Gly	Lys	Gln	Thr	Asn	Met	Thr	Leu	Ile	Ile	Val
65				70					75					80	
Leu	Tyr	Leu	Phe	Gly	Thr	Phe	Ala	Ser	Ala	Leu	Val	Ala	Val	Leu	Thr
			85					90						95	
Ala	Tyr	Leu	Phe	Pro	Leu	Thr	Leu	Val	Leu	Asn	Thr	Pro	Val	Asn	Thr
		100						105					110		
Glu	Leu	Ser	Pro	Pro	Gln	Gly	Val	Ala	Glu	Val	Phe	Gln	Ser	Leu	Leu
		115					120					125			
Leu	Lys	Leu	Val	Asp	Asn	Pro	Ile	Asn	Ala	Leu	Ala	Thr	Ala	Asn	Tyr
		130				135					140				
Ile	Gly	Val	Leu	Ser	Trp	Ala	Ile	Ile	Phe	Gly	Leu	Ala	Leu	Lys	Ala
145					150					155					160

Ala	Ser	Lys	Glu	Thr	Lys	His	Leu	Ile	Lys	Thr	Ala	Ala	Glu	Val	Thr
				165					170					175	
Ser	Gln	Ile	Val	Val	Trp	Ile	Ile	Asn	Leu	Ala	Pro	Ile	Gly	Ile	Met
			180					185					190		
Ser	Leu	Val	Phe	Thr	Thr	Ile	Ser	Glu	Asn	Gly	Val	Gly	Ile	Leu	Ser
		195					200				205				
Asp	Tyr	Ala	Phe	Leu	Ile	Leu	Val	Leu	Val	Gly	Thr	Met	Leu	Phe	Val
	210				215					220					
Ala	Leu	Val	Val	Asn	Pro	Leu	Ile	Ala	Val	Leu	Ile	Thr	Arg	Gln	Asn
225					230					235				240	
Pro	Tyr	Pro	Leu	Val	Leu	Arg	Cys	Leu	Arg	Glu	Ser	Gly	Leu	Thr	Ala
			245						250				255		
Phe	Phe	Thr	Arg	Ser	Ser	Ala	Ala	Asn	Ile	Pro	Val	Asn	Met	Gln	Leu
			260					265					270		
Cys	Gln	Lys	Ile	Gly	Leu	Ser	Lys	Asp	Thr	Tyr	Ser	Val	Ser	Ile	Pro
		275					280					285			
Leu	Gly	Ala	Thr	Ile	Asn	Met	Gly	Gly	Ala	Ala	Ile	Thr	Ile	Asn	Val
	290					295					300				
Leu	Thr	Leu	Ala	Ala	Val	His	Thr	Phe	Gly	Ile	Pro	Ile	Asp	Phe	Leu
305					310					315				320	
Thr	Ala	Leu	Leu	Leu	Ser	Val	Val	Ala	Ala	Val	Ser	Ala	Cys	Gly	Ala
			325					330					335		
Ser	Gly	Val	Ala	Gly	Gly	Ser	Leu	Leu	Leu	Ile	Pro	Val	Ala	Cys	Ser
			340				345					350			
Leu	Phe	Gly	Ile	Ser	Asn	Asp	Leu	Ala	Met	Gln	Val	Val	Gly	Val	Gly
		355				360				365					
Phe	Ile	Val	Gly	Val	Ile	Gln	Asp	Ser	Cys	Glu	Thr	Ala	Leu	Asn	Ser
	370					375				380					
Ser	Thr	Asp	Val	Leu	Phe	Thr	Ala	Ile	Ala	Glu	Asn	Ala	Phe	Trp	Lys
385				390						395				400	
Arg	Lys	Lys	Ala												

<210> SEQ ID NO 535

<211> LENGTH: 1371

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 535

atgaaacaaa	aaaatgtata	tatcgtcatt	ggattcatgc	tatttgcgct	atTTTTtggga	60
gcagcaaacc	tcattttacc	agctttttta	ggcatctact	cagggtcatca	gatttctatgg	120
tctatcattg	gtttttgttt	aactgggtgtc	tccttgccct	tactcggtgt	cattgctgtt	180
gctaaatctg	gatcaggcga	tggtgaaagt	ttggcacgcc	ccatctctaa	atgggatgca	240
atcttctatt	cttccatttt	gtatttatct	attggcccat	tttttgctat	tccaagaaca	300
ggagccactt	ctttttcagt	cggtatcgct	cctatccttag	gagataatac	aaccaataaa	360
gctattttatg	ctatactatt	ttttgggtctg	tcctacttcc	ttgctatcaa	acctagttaa	420
ctagctgaaa	atatcggaaa	atTTTTtaacg	ccaacgttgt	tagttgttat	ttctatTTTTg	480
ggtatcgcg	cctttgtcca	tcctgctgga	aattacgggtg	atgcttttaa	cgctgggggtc	540
ggtgttaata	atgcctttta	agattttcct	tttatagcag	gattaattca	aggttatggc	600
actatggatg	cactagcttc	tcttgTTTTt	gctatttttag	tcattgaggc	taccaaacaa	660
tttggcgcta	agacggacaa	agaaatgacc	aaaataaacac	ttattttctgg	ggctattgcc	720
atTTtgctat	tagcacttgt	ctatatcttt	gtcggctgta	ttggagcaac	atcacaatca	780
ttatttcctt	ttattgatgg	cagctttacc	cttcatggta	atccagttaa	tggcgggtcaa	840
atcctaagtc	atgcttctcg	tttttaccta	ggtggcatcg	gacaagcatt	tctagctgtt	900
gtgattttcc	tggcctgtct	aaccacttca	acaggcttaa	tcacgtcaag	tgctgaatac	960
ttccataaat	ttagtcctgc	tttatctcat	attgcttggg	caactatctt	tactttacta	1020
tcagctttct	tttatttttg	tggttatca	gtcattatca	actggtcagc	tcctgtttta	1080
ttccttttat	acccattaac	agtcgattta	atTTtccttg	ttttggcaca	aaaatgcttc	1140
aataatgatc	ctattgtcta	tcgaactaca	attgggtctaa	cctttatttc	tgccatattt	1200

gatgcactcc taacactatc acaaatgact ggattatttc atttaccaga agccgttgta	1260
acttttttcc aaaaaactgt tccactaggg caatttctcaa tgggatggat tatctttgct	1320
gctattgggtt ttttaatagg gcttatacta agtaaaacga agaaaagcta a	1371

<210> SEQ ID NO 536
 <211> LENGTH: 456
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 536

Met	Lys	Gln	Lys	Asn	Val	Tyr	Ile	Val	Ile	Gly	Phe	Met	Leu	Phe	Ala	
1				5					10					15		
Leu	Phe	Phe	Gly	Ala	Ala	Asn	Leu	Ile	Tyr	Pro	Ala	Phe	Leu	Gly	Ile	
			20					25					30			
Tyr	Ser	Gly	His	Gln	Ile	Leu	Trp	Ser	Ile	Ile	Gly	Phe	Cys	Leu	Thr	
		35					40					45				
Gly	Val	Ser	Leu	Pro	Leu	Leu	Gly	Val	Ile	Ala	Val	Ala	Lys	Ser	Gly	
	50					55					60					
Ser	Gly	Asp	Val	Glu	Ser	Leu	Ala	Arg	Pro	Ile	Ser	Lys	Trp	Tyr	Ala	
65				70						75					80	
Ile	Phe	Tyr	Ser	Ser	Ile	Leu	Tyr	Leu	Ser	Ile	Gly	Pro	Phe	Phe	Ala	
				85					90					95		
Ile	Pro	Arg	Thr	Gly	Ala	Thr	Ser	Phe	Ser	Val	Gly	Ile	Ala	Pro	Ile	
			100					105					110			
Leu	Gly	Asp	Asn	Thr	Thr	Asn	Lys	Ala	Ile	Tyr	Ala	Ile	Leu	Phe	Phe	
		115				120						125				
Gly	Leu	Ser	Tyr	Phe	Leu	Ala	Ile	Lys	Pro	Ser	Lys	Leu	Ala	Glu	Asn	
	130					135					140					
Ile	Gly	Lys	Phe	Leu	Thr	Pro	Thr	Leu	Leu	Val	Val	Ile	Ser	Ile	Leu	
145				150						155					160	
Val	Ile	Ala	Ser	Phe	Val	His	Pro	Ala	Gly	Asn	Tyr	Gly	Asp	Ala	Phe	
				165					170					175		
Asn	Ala	Gly	Val	Gly	Val	Asn	Asn	Ala	Phe	Lys	Asp	Phe	Pro	Phe	Ile	
			180					185					190			
Ala	Gly	Leu	Ile	Gln	Gly	Tyr	Gly	Thr	Met	Asp	Ala	Leu	Ala	Ser	Leu	
		195					200					205				
Val	Phe	Ala	Ile	Leu	Val	Ile	Glu	Ala	Thr	Lys	Gln	Phe	Gly	Ala	Lys	
	210					215					220					
Thr	Asp	Lys	Glu	Met	Thr	Lys	Ile	Thr	Leu	Ile	Ser	Gly	Ala	Ile	Ala	
225					230					235					240	
Ile	Leu	Leu	Leu	Ala	Leu	Val	Tyr	Ile	Phe	Val	Gly	Arg	Ile	Gly	Ala	
				245					250					255		
Thr	Ser	Gln	Ser	Leu	Phe	Pro	Phe	Ile	Asp	Gly	Ser	Phe	Thr	Leu	His	
			260					265					270			
Gly	Asn	Pro	Val	Asn	Gly	Gly	Gln	Ile	Leu	Ser	His	Ala	Ser	Arg	Phe	
		275				280						285				
Tyr	Leu	Gly	Gly	Ile	Gly	Gln	Ala	Phe	Leu	Ala	Val	Val	Ile	Phe	Leu	
	290					295					300					
Ala	Cys	Leu	Thr	Thr	Ser	Thr	Gly	Leu	Ile	Thr	Ser	Ser	Ala	Glu	Tyr	
305					310					315					320	
Phe	His	Lys	Leu	Val	Pro	Ala	Leu	Ser	His	Ile	Ala	Trp	Ala	Thr	Ile	
				325					330					335		
Phe	Thr	Leu	Leu	Ser	Ala	Phe	Phe	Tyr	Phe	Gly	Gly	Leu	Ser	Val	Ile	
			340					345					350			
Ile	Asn	Trp	Ser	Ala	Pro	Val	Leu	Phe	Leu	Leu	Tyr	Pro	Leu	Thr	Val	
		355					360					365				
Asp	Leu	Ile	Phe	Leu	Val	Leu	Ala	Gln	Lys	Cys	Phe	Asn	Asn	Asp	Pro	
	370					375						380				

Ile	Val	Tyr	Arg	Thr	Thr	Ile	Gly	Leu	Thr	Phe	Ile	Pro	Ala	Ile	Phe
385					390					395					400
Asp	Ala	Leu	Leu	Thr	Leu	Ser	Gln	Met	Thr	Gly	Leu	Phe	His	Leu	Pro
				405					410					415	
Glu	Ala	Val	Val	Thr	Phe	Phe	Gln	Lys	Thr	Val	Pro	Leu	Gly	Gln	Phe
			420				425						430		
Ser	Met	Gly	Trp	Ile	Ile	Phe	Ala	Ala	Ile	Gly	Phe	Leu	Ile	Gly	Leu
		435					440					445			
Ile	Leu	Ser	Lys	Thr	Lys	Lys	Ser								
	450					455									

<210> SEQ ID NO 537

<211> LENGTH: 663

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 537

atgtttatga	actcggatgg	tcatggagat	gcaggttggg	gcttagcgat	ttggaatact	60
ttatacatga	ccattgtgcc	ttttattgtt	gggggggcta	ttgggtctctt	attaggcttg	120
ttattagttt	taacaggacc	ggacggtggt	attgaaaaca	aaacgatttg	ttgggttatt	180
gataaagtta	cctctatttt	tagagccatt	ccttttggtta	ttttgattgc	tatttttagct	240
agctttacct	atttgctttt	aagaacaact	ttaggagcaa	cagcggcctt	ggtaccttta	300
acctttgcga	cttttccttt	ttatgcccgt	caggtccaag	ttgttttttc	agaattagac	360
aagggtgtta	ttgaagcagc	acaagcttca	ggtgctactt	tctgggatat	tgtcaaagtg	420
tatctcagtg	aaggtttacc	agatcttatt	cgtgtttcta	cagtcacctt	aatttcctta	480
gttggggaaa	ctgccatggc	aggagctatc	ggtgctggag	gattaggaaa	tgtagcgatt	540
tcttatgggt	ataatcggtt	taacaatgat	gtgacttggg	tagcgactat	tattattcct	600
ttaattattt	ttgctatcca	atttattggt	gatagcttga	ctagaagggt	tagtcataaa	660
taa						663

<210> SEQ ID NO 538

<211> LENGTH: 220

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 538

Met	Phe	Met	Asn	Ser	Asp	Gly	His	Gly	Asp	Ala	Gly	Trp	Gly	Leu	Ala
1			5						10					15	
Ile	Trp	Asn	Thr	Leu	Tyr	Met	Thr	Ile	Val	Pro	Phe	Ile	Val	Gly	Gly
			20					25					30		
Ala	Ile	Gly	Leu	Leu	Leu	Gly	Leu	Leu	Leu	Val	Leu	Thr	Gly	Pro	Asp
		35				40					45				
Gly	Val	Ile	Glu	Asn	Lys	Thr	Ile	Cys	Trp	Val	Ile	Asp	Lys	Val	Thr
	50				55					60					
Ser	Ile	Phe	Arg	Ala	Ile	Pro	Phe	Val	Ile	Leu	Ile	Ala	Ile	Leu	Ala
65				70					75					80	
Ser	Phe	Thr	Tyr	Leu	Leu	Leu	Arg	Thr	Thr	Leu	Gly	Ala	Thr	Ala	Ala
			85					90					95		
Leu	Val	Pro	Leu	Thr	Phe	Ala	Thr	Phe	Pro	Phe	Tyr	Ala	Arg	Gln	Val
		100					105					110			
Gln	Val	Val	Phe	Ser	Glu	Leu	Asp	Lys	Gly	Val	Ile	Glu	Ala	Ala	Gln
	115					120				125					
Ala	Ser	Gly	Ala	Thr	Phe	Trp	Asp	Ile	Val	Lys	Val	Tyr	Leu	Ser	Glu
	130					135				140					
Gly	Leu	Pro	Asp	Leu	Ile	Arg	Val	Ser	Thr	Val	Thr	Leu	Ile	Ser	Leu
145				150					155					160	
Val	Gly	Glu	Thr	Ala	Met	Ala	Gly	Ala	Ile	Gly	Ala	Gly	Gly	Leu	Gly
			165					170					175		
Asn	Val	Ala	Ile	Ser	Tyr	Gly	Tyr	Asn	Arg	Phe	Asn	Asn	Asp	Val	Thr

			180					185				190					
Trp	Val	Ala	Thr	Ile	Ile	Ile	Leu	Leu	Ile	Ile	Phe	Ala	Ile	Gln	Phe		
		195					200					205					
Ile	Gly	Asp	Ser	Leu	Thr	Arg	Arg	Phe	Ser	His	Lys						
	210					215					220						

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<210> SEQ ID NO 539
<211> LENGTH: 927
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 539
atggaatcga ttgataaatc taaatttcga tttgttgagc gcgatagtga agcctccgaa      60
gtgattgata cccctgctta ttcttactgg aaatcagtggt ttcgtcagtt tttttctaaa      120
aaatctacag tctttatgct cgtaatttta gtgacagtct tgatgatgag ctttatttat      180
ccaatgtttg ccaactacga ctttaatgac gttagtaata tcaatgactt ttcaaagcgt      240
tatatttggc caaatgcaga gtactgggtt ggaaccgaca aaaatgggca atctctgttt      300
gatggtgttt ggtatggggc acgtaattct attttaatct cagttatagc gacactaatt      360
aatatcacca ttggggtagt gttaggagcc atatggggag tttctaaagc atttgataaa      420
gttatgattg aaatttataa cattatctca aatatccctt ctatgcttat tatcattgtt      480
ttgacctatt cattaggtgc aggattttgg aatttgattc tagctttctg tatcactgga      540
tggattggtg tcgcctactc catccgtgtt caaatcttgc gttaccgtga tttagaatac      600
aaccttgcta gtcaaacttt gggaacacca atgtacaaga ttgctgttaa gaacctcctg      660
cctcaattgg tttcagttat catgactatg ttgtcacaaa tgctaccagt ttatgtatct      720
tctgaggcct tcttatcctt ctttgggatt ggtttaccaa ccaccactcc aagtttagga      780
cgttttattg ctaattattc aagcaactta acaacaaaatg cctacctctt ttggattccc      840
ttagtaacat tgattttagt atcgttacca ctatacattg tcggacaaaa cttggctgat      900
gccagtgacc cacgttcaca tagatag                                     927

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<210> SEQ ID NO 540
<211> LENGTH: 308
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 540
Met Glu Ser Ile Asp Lys Ser Lys Phe Arg Phe Val Glu Arg Asp Ser
1          5          10          15
Glu Ala Ser Glu Val Ile Asp Thr Pro Ala Tyr Ser Tyr Trp Lys Ser
20        25        30
Val Phe Arg Gln Phe Phe Ser Lys Lys Ser Thr Val Phe Met Leu Val
35        40        45
Ile Leu Val Thr Val Leu Met Met Ser Phe Ile Tyr Pro Met Phe Ala
50        55        60
Asn Tyr Asp Phe Asn Asp Val Ser Asn Ile Asn Asp Phe Ser Lys Arg
65        70        75        80
Tyr Ile Trp Pro Asn Ala Glu Tyr Trp Phe Gly Thr Asp Lys Asn Gly
85        90        95
Gln Ser Leu Phe Asp Gly Val Trp Tyr Gly Ala Arg Asn Ser Ile Leu
100       105       110
Ile Ser Val Ile Ala Thr Leu Ile Asn Ile Thr Ile Gly Val Val Leu
115       120       125
Gly Ala Ile Trp Gly Val Ser Lys Ala Phe Asp Lys Val Met Ile Glu
130       135       140
Ile Tyr Asn Ile Ile Ser Asn Ile Pro Ser Met Leu Ile Ile Ile Val
145       150       155       160
Leu Thr Tyr Ser Leu Gly Ala Gly Phe Trp Asn Leu Ile Leu Ala Phe
165       170       175
Cys Ile Thr Gly Trp Ile Gly Val Ala Tyr Ser Ile Arg Val Gln Ile
180       185       190

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Leu	Arg	Tyr	Arg	Asp	Leu	Glu	Tyr	Asn	Leu	Ala	Ser	Gln	Thr	Leu	Gly
	195						200					205			
Thr	Pro	Met	Tyr	Lys	Ile	Ala	Val	Lys	Asn	Leu	Leu	Pro	Gln	Leu	Val
	210					215					220				
Ser	Val	Ile	Met	Thr	Met	Leu	Ser	Gln	Met	Leu	Pro	Val	Tyr	Val	Ser
225					230					235					240
Ser	Glu	Ala	Phe	Leu	Ser	Phe	Phe	Gly	Ile	Gly	Leu	Pro	Thr	Thr	Thr
			245					250						255	
Pro	Ser	Leu	Gly	Arg	Phe	Ile	Ala	Asn	Tyr	Ser	Ser	Asn	Leu	Thr	Thr
		260						265					270		
Asn	Ala	Tyr	Leu	Phe	Trp	Ile	Pro	Leu	Val	Thr	Leu	Ile	Leu	Val	Ser
	275						280					285			
Leu	Pro	Leu	Tyr	Ile	Val	Gly	Gln	Asn	Leu	Ala	Asp	Ala	Ser	Asp	Pro
	290					295					300				
Arg	Ser	His	Arg												
305															

<210> SEQ ID NO 541
 <211> LENGTH: 1182
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 541

ttgaccaaaa	gaattatact	aactatTTTT	acctttatTTT	gcttttcggt	gatgcctctt	60
gtccacgccg	aagatgtcat	ggatattaca	aggcaagcag	gctacacagt	tagtgagggt	120
aatcgaccaa	aatcttctat	tgctgttgat	gcaaatagtt	cagatattct	ttggcaagat	180
aatattgata	ttcctaggga	tcttgctagt	atgtctaaga	tgtttacgct	ttacatttta	240
tttgaagagc	tcgctaaggg	aaaaattacg	atggacacta	ctattacggc	aactccaacc	300
gatcaagcta	tcgctaacat	ttatgagatt	agcaataata	atatcgtcgc	tggagtagct	360
tatcctattc	gtgatcttat	tactatgaca	gctgtgcctt	catcaaagtc	agcaactggt	420
atgattgcca	attatTTTatc	aaacaatgat	gcttctgcgt	ttatcgatcg	tgtaaatgcc	480
acagccaaac	aattaggcat	gactaacact	catttttcaa	acgctagtgg	tgcagcagca	540
caagcttttc	aagggtatta	taatcctact	aaatatgatt	tatctgcttc	aaatattacg	600
accgctcgag	atttgtccaa	gttactctat	gccttcttaa	aaaaatacc	tgaaattatc	660
tcctttacaa	ataaatctgt	tgtgcacact	atggtaggaa	cgccatatga	agaagaattt	720
cacacctata	accactctct	cccagataat	caatttggt	tgaaaggagt	tgatggatta	780
aaaacagggt	ctagtcccag	tgctgctttt	aacgccatga	taactgccaa	aagaggcaaa	840
actcgactca	ttactattgt	catgggggtc	ggagattggt	cagatcaaaa	cggggagttt	900
tatagacatc	ctttcgtaaa	tgcttggact	gagaaagggt	ttaaagatag	taagacctta	960
tccaaaaaag	cacgccaaaa	actcgaaaaa	ttagtgccac	aaacaaaaaa	agaaacatca	1020
tctaaacagc	agcacttcaa	agccactaaa	aagcaatcgt	acttggaag	agtcgaagat	1080
tttatgaatc	acaaccacac	tttcttgctt	atttgcttag	ctatctttat	aattactatc	1140
cttttactaa	gcctcgttgt	ctttgcaatg	ggacgccaat	aa		1182

<210> SEQ ID NO 542
 <211> LENGTH: 393
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 542

Met	Thr	Lys	Arg	Ile	Ile	Leu	Thr	Ile	Phe	Thr	Phe	Ile	Cys	Phe	Ser
1			5						10				15		
Val	Met	Pro	Leu	Val	His	Ala	Glu	Asp	Val	Met	Asp	Ile	Thr	Arg	Gln
		20						25				30			
Ala	Gly	Tyr	Thr	Val	Ser	Glu	Val	Asn	Arg	Pro	Lys	Ser	Ser	Ile	Val
	35						40				45				
Val	Asp	Ala	Asn	Ser	Ser	Asp	Ile	Leu	Trp	Gln	Asp	Asn	Ile	Asp	Ile
	50					55				60					
Pro	Arg	Asp	Pro	Ala	Ser	Met	Ser	Lys	Met	Phe	Thr	Leu	Tyr	Ile	Leu

65					70					75					80
Phe	Glu	Glu	Leu	Ala	Lys	Gly	Lys	Ile	Thr	Met	Asp	Thr	Thr	Ile	Thr
				85					90					95	
Ala	Thr	Pro	Thr	Asp	Gln	Ala	Ile	Ala	Asn	Ile	Tyr	Glu	Ile	Ser	Asn
			100					105					110		
Asn	Asn	Ile	Val	Ala	Gly	Val	Ala	Tyr	Pro	Ile	Arg	Asp	Leu	Ile	Thr
		115					120					125			
Met	Thr	Ala	Val	Pro	Ser	Ser	Asn	Ala	Ala	Thr	Val	Met	Ile	Ala	Asn
	130					135					140				
Tyr	Leu	Ser	Asn	Asn	Asp	Ala	Ser	Ala	Phe	Ile	Asp	Arg	Val	Asn	Ala
145					150					155					160
Thr	Ala	Lys	Gln	Leu	Gly	Met	Thr	Asn	Thr	His	Phe	Ser	Asn	Ala	Ser
				165					170					175	
Gly	Ala	Ala	Ala	Gln	Ala	Phe	Gln	Gly	Tyr	Tyr	Asn	Pro	Thr	Lys	Tyr
			180					185					190		
Asp	Leu	Ser	Ala	Ser	Asn	Ile	Thr	Thr	Ala	Arg	Asp	Leu	Ser	Lys	Leu
	195						200				205				
Leu	Tyr	Ala	Phe	Leu	Lys	Lys	Tyr	Pro	Glu	Ile	Ile	Ser	Phe	Thr	Asn
	210					215					220				
Lys	Ser	Val	Val	His	Thr	Met	Val	Gly	Thr	Pro	Tyr	Glu	Glu	Glu	Phe
225					230					235					240
His	Thr	Tyr	Asn	His	Ser	Leu	Pro	Asp	Asn	Gln	Phe	Gly	Met	Lys	Gly
			245						250					255	
Val	Asp	Gly	Leu	Lys	Thr	Gly	Ser	Ser	Pro	Ser	Ala	Ala	Phe	Asn	Ala
			260					265					270		
Met	Ile	Thr	Ala	Lys	Arg	Gly	Lys	Thr	Arg	Leu	Ile	Thr	Ile	Val	Met
	275						280					285			
Gly	Val	Gly	Asp	Trp	Ser	Asp	Gln	Asn	Gly	Glu	Phe	Tyr	Arg	His	Pro
	290					295					300				
Phe	Val	Asn	Ala	Leu	Thr	Glu	Lys	Gly	Phe	Lys	Asp	Ser	Lys	Thr	Leu
305					310					315					320
Ser	Lys	Lys	Ala	Arg	Gln	Lys	Leu	Glu	Lys	Leu	Val	Pro	Gln	Thr	Lys
			325						330					335	
Lys	Glu	Thr	Ser	Ser	Lys	Gln	Gln	His	Phe	Lys	Ala	Thr	Lys	Lys	Gln
			340					345					350		
Ser	Tyr	Leu	Glu	Arg	Val	Glu	Asp	Phe	Met	Asn	His	Asn	His	Thr	Phe
	355						360				365				
Leu	Leu	Ile	Cys	Leu	Ala	Ile	Phe	Ile	Ile	Thr	Ile	Leu	Leu	Leu	Ser
	370					375					380				
Leu	Val	Val	Phe	Ala	Met	Gly	Arg	Gln							
385						390									

<210> SEQ ID NO 543

<211> LENGTH: 1170

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 543

atgttttcat	tcacaataga	ttatgtcctt	gttctgatag	gggctttgtt	aatgtcctta	60
ttcttaaccc	ctcttggtcg	cttttttagcc	tttcgtgtgg	gtgcagtaga	caatcccaat	120
gccagacggg	tcaataaggt	tccgatgccca	accagtgggtg	gattagctat	ttttatgtct	180
tttttagtag	caagtttggg	acttattccg	attgcttcta	aaggcgccat	gttttttggt	240
cagacctact	tcagttatat	ttacctgtc	gtgattgggtg	ctacagtaat	tacccttact	300
ggtttttttag	atgatttgta	tgagttaagt	cctaaattaa	agatgtttgg	tattctaatt	360
ggtgcagtga	ttgtctgggc	ttttaccgac	tttaaatttg	atagcttcaa	aattcctttt	420
ggaggggcgt	tgtagttttt	tggtcctttc	ttaaccttat	tcttaacagt	cctgtggatt	480
gtttccatca	ctaagtctat	taacttgatt	gacggtttgg	atggtttggg	tagtggggtc	540
tctattatta	gttttagtgac	catggctatt	gtatcttatt	tctttttacc	tcaaaaggat	600

ttctttttga	cgtaaccat	tttggctcttg	atttctgcta	ttgcaggatt	ttttccttat	660
aattaccatc	cagctatgat	ttatttgggt	gacacaggag	ccctctttat	tggctttatg	720
ataggggttt	tgtctcttca	aggattgaaa	aattcaacgg	ctgtggctgt	ggtgacacct	780
gttattattc	ttgggtgtacc	cattatggat	accatcgtgg	ctattattcg	acgtagttta	840
tcagggtcaaa	aattctacga	gccggataag	atgcacctgc	atcatcgact	cttatcaatg	900
ggctttactc	atcgaggagc	tgtcttagta	gtttatggta	ttaccatgct	tttttcctt	960
atttctttac	ttttaaatgt	ttctagtcga	attgggtggcg	tcctcttgat	gcttggactt	1020
ttatttgggt	tagaagtttt	tattgaagga	ttggagatct	ggggtgaaaa	gcgaacgcct	1080
ttgtttaact	tgttaaagtt	tattggtaat	agtgattatc	gtcaagcaat	gcttctgaaa	1140
tggaaagaaa	agaaggattt	gaaacactaa				1170

<210> SEQ ID NO 544
 <211> LENGTH: 389
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 544

Met	Phe	Ser	Phe	Thr	Ile	Asp	Tyr	Val	Leu	Val	Leu	Ile	Gly	Ala	Leu
1				5					10					15	
Leu	Met	Ser	Leu	Phe	Leu	Thr	Pro	Leu	Val	Arg	Phe	Leu	Ala	Phe	Arg
			20					25					30		
Val	Gly	Ala	Val	Asp	Asn	Pro	Asn	Ala	Arg	Arg	Val	Asn	Lys	Val	Pro
		35				40					45				
Met	Pro	Thr	Ser	Gly	Gly	Leu	Ala	Ile	Phe	Met	Ser	Phe	Leu	Val	Ala
	50					55				60					
Ser	Leu	Gly	Leu	Ile	Pro	Ile	Ala	Ser	Lys	Gly	Ala	Met	Phe	Phe	Gly
65				70					75					80	
Gln	Thr	Tyr	Phe	Ser	Tyr	Ile	Leu	Pro	Val	Val	Ile	Gly	Ala	Thr	Val
			85					90					95		
Ile	Thr	Leu	Thr	Gly	Phe	Leu	Asp	Asp	Leu	Tyr	Glu	Leu	Ser	Pro	Lys
			100				105						110		
Leu	Lys	Met	Phe	Gly	Ile	Leu	Ile	Gly	Ala	Val	Ile	Val	Trp	Ala	Phe
		115				120					125				
Thr	Asp	Phe	Lys	Phe	Asp	Ser	Phe	Lys	Ile	Pro	Phe	Gly	Gly	Pro	Leu
	130					135				140					
Leu	Val	Phe	Gly	Pro	Phe	Leu	Thr	Leu	Phe	Leu	Thr	Val	Leu	Trp	Ile
145				150					155					160	
Val	Ser	Ile	Thr	Asn	Ala	Ile	Asn	Leu	Ile	Asp	Gly	Leu	Asp	Gly	Leu
			165					170					175		
Val	Ser	Gly	Val	Ser	Ile	Ile	Ser	Leu	Val	Thr	Met	Ala	Ile	Val	Ser
		180					185					190			
Tyr	Phe	Phe	Leu	Pro	Gln	Lys	Asp	Phe	Phe	Leu	Thr	Leu	Thr	Ile	Leu
	195					200					205				
Val	Leu	Ile	Ser	Ala	Ile	Ala	Gly	Phe	Phe	Pro	Tyr	Asn	Tyr	His	Pro
	210					215				220					
Ala	Met	Ile	Tyr	Leu	Gly	Asp	Thr	Gly	Ala	Leu	Phe	Ile	Gly	Phe	Met
225				230					235					240	
Ile	Gly	Val	Leu	Ser	Leu	Gln	Gly	Leu	Lys	Asn	Ser	Thr	Ala	Val	Ala
			245					250					255		
Val	Val	Thr	Pro	Val	Ile	Ile	Leu	Gly	Val	Pro	Ile	Met	Asp	Thr	Ile
		260					265					270			
Val	Ala	Ile	Ile	Arg	Arg	Ser	Leu	Ser	Gly	Gln	Lys	Phe	Tyr	Glu	Pro
	275					280					285				
Asp	Lys	Met	His	Leu	His	His	Arg	Leu	Leu	Ser	Met	Gly	Phe	Thr	His
	290					295				300					
Arg	Gly	Ala	Val	Leu	Val	Val	Tyr	Gly	Ile	Thr	Met	Leu	Phe	Ser	Leu
305				310					315					320	
Ile	Ser	Leu	Leu	Leu	Asn	Val	Ser	Ser	Arg	Ile	Gly	Gly	Val	Leu	Leu

				325						330					335				
Met	Leu	Gly	Leu	Leu	Phe	Gly	Leu	Glu	Val	Phe	Ile	Glu	Gly	Leu	Glu				
			340					345					350						
Ile	Trp	Gly	Glu	Lys	Arg	Thr	Pro	Leu	Phe	Asn	Leu	Leu	Lys	Phe	Ile				
		355					360					365							
Gly	Asn	Ser	Asp	Tyr	Arg	Gln	Ala	Met	Leu	Leu	Lys	Trp	Lys	Glu	Lys				
	370					375					380								
Lys	Asp	Leu	Lys	His															
385																			

<210> SEQ ID NO 545
 <211> LENGTH: 1899
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 545

atgaaaaaaaa	ttttgatgac	gcttgtgctc	tgcttcagtc	ttttagggat	acgaataaaa	60
gcagctgatg	tagactatag	catcaccaac	tatgaaggtc	agttactgtt	atcaaaaagaa	120
aatactgctc	ggtttgagca	aaaagtaacc	tatcaatttg	acacttctta	taacggccag	180
tatatttcgc	tgggccggac	aggtcatttg	ccagcgggct	ttgctattga	ccaaaagcct	240
aaagttgagg	tatatcagaa	tggtcaacag	gtacctgtta	gtcaagagtt	tagtgacctt	300
ggagatggct	atcgtttaaa	actttataat	gctggccaag	ctggtgataa	ggttgacgtc	360
aaggttatct	ggcaactgca	ccacctttta	acagcttatc	aagacgtggc	agagctgaat	420
tggacaccga	ttagtgattg	ggacaaaaca	ttagaaaagg	tgagtttgac	cgtcactacc	480
ccaactgata	ttcaggattc	taatctatgg	gctcacagag	gatattacca	aaagaaacct	540
caagtgttaa	aagaaggtaa	cagtcgctat	cagattaatg	ccaagaatgt	ctcagggcaa	600
ctggaattgc	atgcttattg	ggataaaaaa	gcattattgg	gaaaagagcc	agttgatgtt	660
tcaacgagta	aaaagaataa	aattgtagcg	ttagaaacta	agatttccag	acgaaggacc	720
ttgttacagc	tgctatttgg	caaagtcatt	cctctggtag	aggtaggttt	tcttctttgg	780
cagttaatac	agtttacaa	attaaagaaa	caattcaatc	gttatcattt	ggctaaccat	840
acagatcaca	gttacgaagt	ccctgaagat	ctttcgctc	ttgtgttgac	acaagcgatt	900
tatggacaga	gttttgccta	tttatccctt	acagcatcag	aaagccagaa	attattgatc	960
cctaaaggag	tgacctttga	ggcccttggt	caagctacct	tggtggatct	gatcgaccaa	1020
aagggtgcttt	tattaacgaa	agaagaaggg	aaagcttatc	ttgaaatcag	tcagttagat	1080
cgtgtgacag	atgaggaagc	tgcttctcta	gatatggctt	ttggaaacaa	ggtgacattg	1140
ccggtgggac	aattgtttag	tcaataccat	tatgatgctg	ataccattaa	acaattaaag	1200
aaaacgtaca	aaggtaaaaa	gctcgagcaa	gaagtccgtc	aatcgtctga	gcagggtgatt	1260
aaggcgatga	aaaaagcgtc	ggcagctatt	acaaacaatg	tcctagaaac	tatcaaaaag	1320
ttaaacttac	cagatactta	tcgtcaaagt	acccggcgag	agaaacgaaa	aagcaatagt	1380
gtccagggat	taggttggtt	gttgcttatt	ctaaatagtg	gtttattgat	ttacttggct	1440
attaaagaaa	gtgggttagc	cctcatttac	cttgctttaa	tggtgctaac	gatgtgcctt	1500
ggctttttaca	ttagcctgaa	gtagatcaa	tacaagaaat	tggttattga	aacacctgag	1560
gggggtgttc	ggttacatca	atggcagagc	tttaaaaaaca	tgatacgaga	cattgacaaa	1620
tttgaggatg	ttgctattga	aggtttggtt	gtttggaacc	gtgttttggt	ttatgccacc	1680
ttatttggtt	acgctaagaa	agtggaacgc	tatttgaaag	tccatcgtat	tgctttacct	1740
gagggtttacc	aagctgttcg	accaggtgaa	ttatcaatgg	taatgtatgc	tacgacacca	1800
acctttgtgt	ctagcttgct	ttcagctaca	acttcctcaa	atttctcagt	ctcttcgga	1860
ggcgggatta	gtggtggtgg	cggcggcggt	gccttttaa			1899

<210> SEQ ID NO 546
 <211> LENGTH: 632
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 546

Met	Lys	Lys	Ile	Leu	Met	Thr	Leu	Val	Leu	Cys	Phe	Ser	Leu	Leu	Gly
1			5					10						15	
Ile	Arg	Ile	Lys	Ala	Ala	Asp	Val	Asp	Tyr	Ser	Ile	Thr	Asn	Tyr	Glu
			20					25						30	

Gly	Gln	Leu	Leu	Leu	Ser	Lys	Glu	Asn	Thr	Ala	Arg	Phe	Glu	Gln	Lys	
		35					40					45				
Val	Thr	Tyr	Gln	Phe	Asp	Thr	Ser	Tyr	Asn	Gly	Gln	Tyr	Ile	Ser	Leu	
	50					55				60						
Gly	Arg	Thr	Gly	His	Leu	Pro	Ala	Gly	Phe	Ala	Ile	Asp	Gln	Lys	Pro	
65					70					75					80	
Lys	Val	Glu	Val	Tyr	Gln	Asn	Gly	Gln	Gln	Val	Pro	Val	Ser	Gln	Glu	
				85					90					95		
Phe	Ser	Asp	Leu	Gly	Asp	Gly	Tyr	Arg	Leu	Lys	Leu	Tyr	Asn	Ala	Gly	
			100					105					110			
Gln	Ala	Gly	Asp	Lys	Val	Asp	Val	Lys	Val	Ile	Trp	Gln	Leu	His	His	
		115					120					125				
Leu	Leu	Thr	Ala	Tyr	Gln	Asp	Val	Ala	Glu	Leu	Asn	Trp	Thr	Pro	Ile	
	130					135					140					
Ser	Asp	Trp	Asp	Lys	Thr	Leu	Glu	Lys	Val	Ser	Leu	Thr	Val	Thr	Thr	
145				150						155					160	
Pro	Thr	Asp	Ile	Gln	Asp	Ser	Asn	Leu	Trp	Ala	His	Arg	Gly	Tyr	Tyr	
			165						170					175		
Gln	Lys	Lys	Pro	Gln	Val	Leu	Lys	Glu	Gly	Asn	Ser	Arg	Tyr	Gln	Ile	
			180					185					190			
Asn	Ala	Lys	Asn	Val	Ser	Gly	Gln	Leu	Glu	Leu	His	Ala	Tyr	Trp	Asp	
		195					200				205					
Lys	Lys	Ala	Leu	Leu	Gly	Lys	Glu	Pro	Val	Asp	Val	Ser	Thr	Ser	Lys	
	210					215				220						
Lys	Asn	Lys	Ile	Val	Ala	Leu	Glu	Thr	Lys	Ile	Ser	Arg	Arg	Arg	Thr	
225				230						235					240	
Leu	Leu	Gln	Leu	Leu	Phe	Gly	Lys	Val	Ile	Pro	Leu	Val	Glu	Val	Gly	
			245						250					255		
Phe	Leu	Leu	Trp	Gln	Leu	Ile	Gln	Phe	Thr	Arg	Leu	Lys	Lys	Gln	Phe	
		260						265					270			
Asn	Arg	Tyr	His	Leu	Ala	Asn	His	Thr	Asp	His	Ser	Tyr	Glu	Val	Pro	
	275						280					285				
Glu	Asp	Leu	Ser	Pro	Leu	Val	Leu	Thr	Gln	Ala	Ile	Tyr	Gly	Gln	Ser	
	290					295					300					
Phe	Ala	Tyr	Leu	Ser	Pro	Thr	Ala	Ser	Glu	Ser	Gln	Lys	Leu	Leu	Ile	
305				310						315					320	
Pro	Lys	Gly	Val	Thr	Phe	Glu	Ala	Leu	Val	Gln	Ala	Thr	Leu	Leu	Asp	
			325						330					335		
Leu	Ile	Asp	Gln	Lys	Val	Leu	Leu	Leu	Thr	Lys	Glu	Glu	Gly	Lys	Ala	
		340					345					350				
Tyr	Leu	Glu	Ile	Ser	Gln	Leu	Asp	Arg	Val	Thr	Asp	Glu	Glu	Ala	Ala	
	355						360				365					
Phe	Leu	Asp	Met	Ala	Phe	Gly	Asn	Lys	Val	Thr	Leu	Pro	Val	Asp	Gln	
	370					375					380					
Leu	Phe	Ser	Gln	Tyr	His	Tyr	Asp	Ala	Asp	Thr	Ile	Lys	Gln	Leu	Lys	
385				390						395					400	
Lys	Thr	Tyr	Lys	Gly	Lys	Lys	Leu	Glu	Gln	Glu	Val	Arg	Gln	Ser	Ser	
			405						410					415		
Glu	Gln	Val	Ile	Lys	Ala	Met	Lys	Lys	Ala	Ser	Ala	Ala	Ile	Thr	Asn	
		420						425					430			
Asn	Val	Leu	Glu	Thr	Ile	Lys	Lys	Leu	Asn	Leu	Pro	Asp	Thr	Tyr	Arg	
	435						440					445				
Gln	Met	Thr	Pro	Ala	Glu	Lys	Arg	Lys	Ser	Asn	Ser	Val	Gln	Gly	Leu	
	450					455					460					
Gly	Cys	Leu	Leu	Leu	Ile	Leu	Asn	Ser	Gly	Leu	Leu	Ile	Tyr	Leu	Ala	
465				470						475					480	
Ile	Lys	Glu	Ser	Gly	Leu	Ala	Leu	Ile	Tyr	Leu	Ala	Leu	Met	Val	Leu	

				485					490					495			
Thr	Met	Cys	Leu	Gly	Phe	Tyr	Ile	Ser	Leu	Lys	Leu	Asp	Gln	Tyr	Lys		
			500					505					510				
Lys	Leu	Gly	Ile	Glu	Thr	Pro	Glu	Gly	Gly	Val	Arg	Leu	His	Gln	Trp		
		515					520					525					
Gln	Ser	Phe	Lys	Asn	Met	Ile	Arg	Asp	Ile	Asp	Lys	Phe	Glu	Asp	Val		
	530					535					540						
Ala	Ile	Glu	Gly	Leu	Val	Val	Trp	Asn	Arg	Val	Leu	Val	Tyr	Ala	Thr		
545						550				555					560		
Leu	Phe	Gly	Tyr	Ala	Lys	Lys	Val	Glu	Arg	Tyr	Leu	Lys	Val	His	Arg		
			565					570						575			
Ile	Ala	Leu	Pro	Glu	Val	Tyr	Gln	Ala	Val	Arg	Pro	Gly	Glu	Leu	Ser		
		580						585					590				
Met	Val	Met	Tyr	Ala	Thr	Thr	Pro	Thr	Phe	Val	Ser	Ser	Leu	Ser	Ser		
		595					600					605					
Ala	Thr	Thr	Ser	Ser	Asn	Phe	Ser	Val	Ser	Ser	Gly	Gly	Gly	Ile	Ser		
	610					615					620						
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Phe									
625						630											

<210> SEQ ID NO 547

<211> LENGTH: 1587

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 547

ttgaaacagg	agacctatat	gaaaaagcta	atccttagct	gtttggtcgc	cttggccctt	60
ctgtttggag	gaatgagccg	ggctcaagca	aaccaatatt	taagagtcgg	aatggaagca	120
gcctatgctc	cttttaactg	gactcaagat	gacgcttcaa	acggggctgt	tccaattgaa	180
ggaactagcc	aatacgccaa	cggttacgat	gtccaagtcg	ctaaaaaagt	cgctaaagct	240
atgaacaaaag	aacttttagt	cgttaagacc	tcttggtaccg	gtttaattcc	agcattaact	300
tctggaaaaa	tcatatgat	cgctgctggt	atgagtccta	ccaaagagcg	tagaaacgaa	360
attagcttct	caaacagcta	ctacactagc	caccatgttc	tagtcgtaac	tgccaatggc	420
aaatatgctg	atgcaacaag	cctcaaggat	ttttctggag	ctaaagtaac	tgcccagcaa	480
ggcgtttggc	atgtcaatct	cttaactcaa	ctaaaagggtg	ctaagttaca	aacaccaatg	540
ggagatttct	ctcaaatgcg	acaagccctt	acttcgggtg	ttatcgatgc	ctatatttct	600
gaacgacctg	aagccatgac	tgctgaagct	gctgatagcc	gtttgaaaat	gatcactctt	660
aaaaaagggg	ttgctgtgtg	tgaatcagat	gctgctatcg	ctgtcggaat	gaaaaaaaaat	720
gacgatcgta	tggcaactgt	caaccaagtg	cttgaaggat	tttctcaaac	agatcgtag	780
gccctgatgg	atgatatggt	taccaaacia	cccgtggaaa	agaaagccga	agatgctaaa	840
gcatcatttc	taggccaaat	gtgggctatt	tttaaaggta	actggaagca	attcttacgt	900
ggaactggaa	tgacccttct	gatttccatg	gtcggaacca	ttacaggtct	ctttattgga	960
ttattaatcg	gtattttccg	tacagctcct	aaagctaagc	ataaagtagc	tgctttggga	1020
caaaaactct	ttggttggtt	actcactatt	tatatcgaaa	tcttcctggtg	gacacctatg	1080
attgttcaat	ctatggttat	ctactacgga	acagcgcaag	cctttggtat	ttcgatcgac	1140
cgtaccctag	cggctatatt	tatcgatatc	atcaatacgg	gggcctatat	gagtgaat	1200
gttcgcgggg	gtattttcgc	tgctgacaaa	ggtcaattca	aagcagcaac	tgctcttggc	1260
tttactcacg	gacaaacat	gcgtaaaatc	gtgctaccac	aagttgttcg	aaacatttta	1320
ccagcaacag	gtaatgagtt	tgtcatcaat	atcaaagata	cttctgtctt	gaatgttatc	1380
tctgttgtgg	aactttactt	ctcaggtaat	accgtagcca	cacaaacctt	ccaatatttc	1440
caaaccttta	cgattatcgc	cattatctac	ttgtttctta	ccttcacggg	gacacgtatc	1500
cttcgttata	ttgaacgccg	tttcgatgcc	gatacttaca	ccactggagc	aaaccaaatg	1560
cagattgcgg	aggtctcaaa	tgtcttaa				1587

<210> SEQ ID NO 548

<211> LENGTH: 528

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 548

Met	Lys	Gln	Glu	Thr	Tyr	Met	Lys	Lys	Leu	Ile	Leu	Ser	Cys	Leu	Val
1				5					10					15	
Ala	Leu	Ala	Leu	Leu	Phe	Gly	Gly	Met	Ser	Arg	Ala	Gln	Ala	Asn	Gln
			20					25					30		
Tyr	Leu	Arg	Val	Gly	Met	Glu	Ala	Ala	Tyr	Ala	Pro	Phe	Asn	Trp	Thr
		35				40						45			
Gln	Asp	Asp	Ala	Ser	Asn	Gly	Ala	Val	Pro	Ile	Glu	Gly	Thr	Ser	Gln
	50					55					60				
Tyr	Ala	Asn	Gly	Tyr	Asp	Val	Gln	Val	Ala	Lys	Lys	Val	Ala	Lys	Ala
65					70					75					80
Met	Asn	Lys	Glu	Leu	Leu	Val	Val	Lys	Thr	Ser	Trp	Thr	Gly	Leu	Ile
			85						90					95	
Pro	Ala	Leu	Thr	Ser	Gly	Lys	Ile	Asp	Met	Ile	Ala	Ala	Gly	Met	Ser
			100					105						110	
Pro	Thr	Lys	Glu	Arg	Arg	Asn	Glu	Ile	Ser	Phe	Ser	Asn	Ser	Tyr	Tyr
		115					120						125		
Thr	Ser	His	His	Val	Leu	Val	Val	Thr	Ala	Asn	Gly	Lys	Tyr	Ala	Asp
	130					135						140			
Ala	Thr	Ser	Leu	Lys	Asp	Phe	Ser	Gly	Ala	Lys	Val	Thr	Ala	Gln	Gln
145					150					155					160
Gly	Val	Trp	His	Val	Asn	Leu	Leu	Thr	Gln	Leu	Lys	Gly	Ala	Lys	Leu
			165						170					175	
Gln	Thr	Pro	Met	Gly	Asp	Phe	Ser	Gln	Met	Arg	Gln	Ala	Leu	Thr	Ser
			180					185					190		
Gly	Val	Ile	Asp	Ala	Tyr	Ile	Ser	Glu	Arg	Pro	Glu	Ala	Met	Thr	Ala
	195						200					205			
Glu	Ala	Ala	Asp	Ser	Arg	Leu	Lys	Met	Ile	Thr	Leu	Lys	Lys	Gly	Phe
	210					215					220				
Ala	Val	Ala	Glu	Ser	Asp	Ala	Ala	Ile	Ala	Val	Gly	Met	Lys	Lys	Asn
225					230					235					240
Asp	Asp	Arg	Met	Ala	Thr	Val	Asn	Gln	Val	Leu	Glu	Gly	Phe	Ser	Gln
			245						250					255	
Thr	Asp	Arg	Met	Ala	Leu	Met	Asp	Asp	Met	Val	Thr	Lys	Gln	Pro	Val
			260					265					270		
Glu	Lys	Lys	Ala	Glu	Asp	Ala	Lys	Ala	Ser	Phe	Leu	Gly	Gln	Met	Trp
		275					280						285		
Ala	Ile	Phe	Lys	Gly	Asn	Trp	Lys	Gln	Phe	Leu	Arg	Gly	Thr	Gly	Met
	290					295					300				
Thr	Leu	Leu	Ile	Ser	Met	Val	Gly	Thr	Ile	Thr	Gly	Leu	Phe	Ile	Gly
305					310					315					320
Leu	Leu	Ile	Gly	Ile	Phe	Arg	Thr	Ala	Pro	Lys	Ala	Lys	His	Lys	Val
			325						330					335	
Ala	Ala	Leu	Gly	Gln	Lys	Leu	Phe	Gly	Trp	Leu	Leu	Thr	Ile	Tyr	Ile
			340					345					350		
Glu	Ile	Phe	Arg	Gly	Thr	Pro	Met	Ile	Val	Gln	Ser	Met	Val	Ile	Tyr
		355					360					365			
Tyr	Gly	Thr	Ala	Gln	Ala	Phe	Gly	Ile	Ser	Ile	Asp	Arg	Thr	Leu	Ala
	370					375					380				
Ala	Ile	Phe	Ile	Val	Ser	Ile	Asn	Thr	Gly	Ala	Tyr	Met	Ser	Glu	Ile
385					390					395					400
Val	Arg	Gly	Gly	Ile	Phe	Ala	Val	Asp	Lys	Gly	Gln	Phe	Lys	Ala	Ala
			405						410					415	
Thr	Ala	Leu	Gly	Phe	Thr	His	Gly	Gln	Thr	Met	Arg	Lys	Ile	Val	Leu
			420					425					430		
Pro	Gln	Val	Val	Arg	Asn	Ile	Leu	Pro	Ala	Thr	Gly	Asn	Glu	Phe	Val
		435					440						445		

Ile	Asn	Ile	Lys	Asp	Thr	Ser	Val	Leu	Asn	Val	Ile	Ser	Val	Val	Glu
	450					455				460					
Leu	Tyr	Phe	Ser	Gly	Asn	Thr	Val	Ala	Thr	Gln	Thr	Tyr	Gln	Tyr	Phe
465				470					475						480
Gln	Thr	Phe	Thr	Ile	Ile	Ala	Ile	Ile	Tyr	Phe	Val	Leu	Thr	Phe	Thr
			485					490						495	
Val	Thr	Arg	Ile	Leu	Arg	Tyr	Ile	Glu	Arg	Arg	Phe	Asp	Ala	Asp	Thr
		500						505					510		
Tyr	Thr	Thr	Gly	Ala	Asn	Gln	Met	Gln	Ile	Ala	Glu	Val	Ser	Asn	Val
	515					520						525			

<210> SEQ ID NO 549

<211> LENGTH: 1038

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 549

ttgattttca	taaggaggaa	atcactaatg	gtagttaaaag	ttggtattaa	cggtttcggt	60
cgtatcggac	gtcttgcatt	ccgccgtatt	caaaacatcg	aaggtgttga	agtaactcgt	120
atcaatgacc	ttacagatcc	aaatatgctt	gcacacttgt	tgaaatacga	tacaactcaa	180
ggtcgttttg	atggaacagt	tgaagttaaa	gaaggtggat	ttgaagtaaa	cggaaacttc	240
atcaaagttt	ctgctgaacg	tgatccagaa	aacatcgact	gggcaactga	tggggttgaa	300
atcgttcttg	aagcaactgg	tttctttgct	aaaaaagaag	cagctgaaaa	acacttacat	360
gctaacgggtg	ctaaaaaagt	tgttatcaca	gctcctgggtg	gaaacgatgt	taaaacagtt	420
gttttcaaca	ctaaccacga	cattcttgac	ggtactgaaa	cagttatctc	aggtgcttca	480
tgtactacaa	actgttttagc	tcctatggct	aaagctcttc	acgatgcatt	cggatttcaa	540
aaagggtctta	tgactacaat	ccacgccttac	actggtgacc	aaatgatcct	tgacggacca	600
caccgtgggtg	gtgaccttcg	tcgtgcacgc	gctggtgctg	caaatatcgt	tcctaactca	660
actggtgctg	ctaaagctat	cggctcttgt	atcccagaac	ttaacggtaa	acttgacggg	720
gctgcacaac	gtgttcctgt	tccaactgga	tcagtaactg	agttgggtgt	aactcttgac	780
aaaaacgttt	ctgttgacga	aatcaacgct	gctatgaaag	ctgcttcaaa	cgatagcttc	840
ggttacactg	aagatccaat	cgtttcttca	gatatcgtag	gcgtatcata	cgggttcattg	900
tttgacgcaa	ctcaaaactaa	agtaatggaa	gttgacggat	cacaattggt	taaagtgtga	960
tcatgggtatg	acaacgaaat	gtcttacact	gctcaacttg	tacgtactct	tgagtacttc	1020
gcaaaaattg	ctaaataa					1038

<210> SEQ ID NO 550

<211> LENGTH: 345

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 550

Met	Ile	Phe	Ile	Arg	Arg	Lys	Ser	Leu	Met	Val	Val	Lys	Val	Gly	Ile
1			5					10						15	
Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Leu	Ala	Phe	Arg	Arg	Ile	Gln	Asn
		20						25					30		
Ile	Glu	Gly	Val	Glu	Val	Thr	Arg	Ile	Asn	Asp	Leu	Thr	Asp	Pro	Asn
		35				40					45				
Met	Leu	Ala	His	Leu	Leu	Lys	Tyr	Asp	Thr	Thr	Gln	Gly	Arg	Phe	Asp
	50					55					60				
Gly	Thr	Val	Glu	Val	Lys	Glu	Gly	Gly	Phe	Glu	Val	Asn	Gly	Asn	Phe
65				70					75					80	
Ile	Lys	Val	Ser	Ala	Glu	Arg	Asp	Pro	Glu	Asn	Ile	Asp	Trp	Ala	Thr
			85					90						95	
Asp	Gly	Val	Glu	Ile	Val	Leu	Glu	Ala	Thr	Gly	Phe	Phe	Ala	Lys	Lys
		100						105					110		
Glu	Ala	Ala	Glu	Lys	His	Leu	His	Ala	Asn	Gly	Ala	Lys	Lys	Val	Val
	115					120						125			
Ile	Thr	Ala	Pro	Gly	Gly	Asn	Asp	Val	Lys	Thr	Val	Val	Phe	Asn	Thr

130	135	140
Asn His Asp Ile Leu Asp Gly Thr Glu Thr Val Ile Ser Gly Ala Ser		
145	150	155
Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys Ala Leu His Asp Ala		160
	165	170
Phe Gly Ile Gln Lys Gly Leu Met Thr Thr Ile His Ala Tyr Thr Gly		175
	180	185
Asp Gln Met Ile Leu Asp Gly Pro His Arg Gly Gly Asp Leu Arg Arg		190
	195	200
Ala Arg Ala Gly Ala Ala Asn Ile Val Pro Asn Ser Thr Gly Ala Ala		205
	210	215
Lys Ala Ile Gly Leu Val Ile Pro Glu Leu Asn Gly Lys Leu Asp Gly		220
225	230	235
Ala Ala Gln Arg Val Pro Val Pro Thr Gly Ser Val Thr Glu Leu Val		240
	245	250
Val Thr Leu Asp Lys Asn Val Ser Val Asp Glu Ile Asn Ala Ala Met		255
	260	265
Lys Ala Ala Ser Asn Asp Ser Phe Gly Tyr Thr Glu Asp Pro Ile Val		270
	275	280
Ser Ser Asp Ile Val Gly Val Ser Tyr Gly Ser Leu Phe Asp Ala Thr		285
	290	295
Gln Thr Lys Val Met Glu Val Asp Gly Ser Gln Leu Val Lys Val Val		300
305	310	315
Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr Ala Gln Leu Val Arg Thr		320
	325	330
Leu Glu Tyr Phe Ala Lys Ile Ala Lys		335
	340	345

<210> SEQ ID NO 551

<211> LENGTH: 663

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 551

ttgacatcga	aaaaacaggg	actttttacac	tctctcttca	agcttgatag	taaattggatg	60
agggctagcg	cagcactggt	tgatttgctc	gtgtttaatc	tcttatttgt	cttgctcctgc	120
cttcccccttc	taacgattgg	ggttgctaaa	atggctttgt	atgcgagttt	gttggattgg	180
cgagaaggtc	aagttagtca	gcttgttact	acttatagct	ctcattttta	atattacttt	240
aaaagtgggc	tacgccttgg	ccttattgag	cttgggataa	tgactatttg	tctcttagat	300
cttttcttaa	ttcgaaacca	atcaggccta	gtttttcaag	ggtttaaagt	actttgcgtt	360
gctgttttat	ttttggtggt	tatactcttt	ttgtacgctt	atcctcaggc	cgtcaaaaga	420
gacctttccc	tatctacgct	gtttaagcga	agctttttat	tagcaggact	cttttttcca	480
tggagttttg	ctttcttggc	ttttatttgt	ctcacgatat	ttagcctaca	attgtctctg	540
ttaacgttat	ttggaggcgt	gtctttgcta	gctatcatcg	gcatcagtag	tctaacttat	600
ctctacttga	ttatcatgga	atctcttctt	aggcgattcc	cacttaataa	tgacattgaa	660
taa						663

<210> SEQ ID NO 552

<211> LENGTH: 220

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 552

Met Thr Ser Lys Lys Gln Gly Leu Leu His Ser Leu Phe Lys Leu Asp		
1	5	10
Ser Lys Trp Met Arg Ala Ser Ala Ala Leu Phe Asp Leu Leu Val Phe		
	20	25
Asn Leu Leu Phe Val Leu Ser Cys Leu Pro Leu Leu Thr Ile Gly Val		
	35	40
		45

Ala	Lys	Met	Ala	Leu	Tyr	Ala	Ser	Leu	Leu	Asp	Trp	Arg	Glu	Gly	Gln
50						55					60				
Val	Ser	Gln	Leu	Val	Thr	Thr	Tyr	Ser	Ser	His	Phe	Lys	Tyr	Tyr	Phe
65					70					75					80
Lys	Ser	Gly	Leu	Arg	Leu	Gly	Leu	Ile	Glu	Leu	Gly	Ile	Met	Thr	Ile
				85					90					95	
Cys	Leu	Leu	Asp	Leu	Phe	Leu	Ile	Arg	Asn	Gln	Ser	Gly	Leu	Val	Phe
			100					105					110		
Gln	Gly	Phe	Lys	Val	Leu	Cys	Val	Ala	Val	Leu	Phe	Leu	Val	Val	Ile
		115					120					125			
Leu	Phe	Leu	Tyr	Ala	Tyr	Pro	Gln	Ala	Val	Lys	Arg	Asp	Leu	Ser	Leu
	130					135					140				
Ser	Thr	Leu	Phe	Lys	Arg	Ser	Phe	Leu	Leu	Ala	Gly	Leu	Phe	Phe	Pro
145				150						155					160
Trp	Ser	Phe	Ala	Phe	Leu	Ala	Phe	Ile	Cys	Leu	Thr	Ile	Phe	Ser	Leu
				165					170					175	
Gln	Leu	Ser	Leu	Leu	Thr	Leu	Phe	Gly	Gly	Val	Ser	Leu	Leu	Ala	Ile
			180					185					190		
Ile	Gly	Ile	Ser	Ser	Leu	Thr	Tyr	Leu	Tyr	Leu	Ile	Ile	Met	Glu	Ser
	195						200					205			
Leu	Leu	Arg	Arg	Phe	Pro	Leu	Asn	Asn	Asp	Ile	Glu				
	210					215					220				

<210> SEQ ID NO 553

<211> LENGTH: 831

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 553

atgacgaaaa	agaaactaac	cgcatacagat	atcttaacca	ctgtgatgct	atgtgttttg	60
accatttttg	ttatttttcc	attttattgg	attatgacag	gagcatttaa	ggctcaagcc	120
gataaccatta	tgattccacc	gcaatggtgg	ccaaaggcgc	ctactattga	aaattttaag	180
gccttggtag	tgcaaaatcc	agccttaaaa	tggttgtgga	atagtgtcct	tatttcggtg	240
gcgaccatgt	tcttggtttg	tggaaacctcc	tcgttggctg	gctatgcttt	ggccaaaaag	300
cggttttatg	gacagcggct	tttgttttcg	atttttattg	ctgctatggc	cttgccaaaa	360
cagggtgttc	tagtgcctct	tgtgcggatt	gttaatttta	tgggaatcca	tgacactttg	420
gcggctgtta	ttttgcctct	tgtgggctgg	ccatttggtg	ttttccttat	gaaacagttc	480
tcagaaaaata	ttccaaccga	gttattggaa	tccgccaaga	ttgatggatg	tggcgaaatt	540
cgtacctttt	tcaatgtggc	tttccctatt	gtcaaaccag	gctttgcagc	gctagcgatt	600
tttaccttta	tcaatacttg	gaatgattat	tttatgcagt	tagtgatgtt	aacctctcga	660
gaaaatttaa	cgatttcact	tggggttgcc	actatgcaag	ctgaaatggc	tactaattat	720
ggcttgatta	tggcaggggc	tgccatggct	gcagtgccta	ttgtaacagt	ctttcttgtc	780
ttccaaaaat	catttaccca	aggcattact	atgggtgctg	tgaaagggtta	g	831

<210> SEQ ID NO 554

<211> LENGTH: 276

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 554

Met	Thr	Lys	Lys	Lys	Leu	Thr	Ala	Ser	Asp	Ile	Leu	Thr	Thr	Val	Met
1				5					10					15	
Leu	Cys	Val	Leu	Thr	Ile	Leu	Phe	Ile	Phe	Pro	Phe	Tyr	Trp	Ile	Met
			20					25					30		
Thr	Gly	Ala	Phe	Lys	Ala	Gln	Ala	Asp	Thr	Ile	Met	Ile	Pro	Pro	Gln
		35					40					45			
Trp	Trp	Pro	Lys	Ala	Pro	Thr	Ile	Glu	Asn	Phe	Lys	Ala	Leu	Val	Val
	50					55					60				
Gln	Asn	Pro	Ala	Leu	Lys	Trp	Leu	Trp	Asn	Ser	Val	Phe	Ile	Ser	Val

65		70		75		80									
Ala	Thr	Met	Phe	Leu	Val	Cys	Gly	Thr	Ser	Ser	Leu	Ala	Gly	Tyr	Ala
			85						90					95	
Leu	Ala	Lys	Lys	Arg	Phe	Tyr	Gly	Gln	Arg	Leu	Leu	Phe	Ser	Ile	Phe
		100						105					110		
Ile	Ala	Ala	Met	Ala	Leu	Pro	Lys	Gln	Val	Val	Leu	Val	Pro	Leu	Val
		115					120					125			
Arg	Ile	Val	Asn	Phe	Met	Gly	Ile	His	Asp	Thr	Leu	Ala	Ala	Val	Ile
	130					135					140				
Leu	Pro	Leu	Val	Gly	Trp	Pro	Phe	Gly	Val	Phe	Leu	Met	Lys	Gln	Phe
	145			150						155				160	
Ser	Glu	Asn	Ile	Pro	Thr	Glu	Leu	Leu	Glu	Ser	Ala	Lys	Ile	Asp	Gly
		165						170					175		
Cys	Gly	Glu	Ile	Arg	Thr	Phe	Phe	Asn	Val	Ala	Phe	Pro	Ile	Val	Lys
		180					185						190		
Pro	Gly	Phe	Ala	Ala	Leu	Ala	Ile	Phe	Thr	Phe	Ile	Asn	Thr	Trp	Asn
	195					200						205			
Asp	Tyr	Phe	Met	Gln	Leu	Val	Met	Leu	Thr	Ser	Arg	Glu	Asn	Leu	Thr
	210				215						220				
Ile	Ser	Leu	Gly	Val	Ala	Thr	Met	Gln	Ala	Glu	Met	Ala	Thr	Asn	Tyr
	225			230					235					240	
Gly	Leu	Ile	Met	Ala	Gly	Ala	Ala	Met	Ala	Ala	Val	Pro	Ile	Val	Thr
		245				250							255		
Val	Phe	Leu	Val	Phe	Gln	Lys	Ser	Phe	Thr	Gln	Gly	Ile	Thr	Met	Gly
		260					265						270		
Ala	Val	Lys	Gly												
		275													

<210> SEQ ID NO 555

<211> LENGTH: 990

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 555

gtgttcctaa	caagtggcctt	cttttcaatg	cacatgtcaa	atggtcactg	gaaagaagct	60
tttcttttta	gaaaagttga	acagaaaaaa	gaggtatttc	aagtgaacgt	caataaatta	120
aaaatgagag	agacgctcat	ctcatacgct	ttcttagctc	cggctcttgg	tttctttgtg	180
atttttgtct	tgataccgat	gattatgggc	tttgtgacga	gctttttcaa	ttattccatg	240
acagagttta	cctttgttgg	ttttgcta	tatgctagga	tgtttcaaga	tcccattttc	300
atgaagtctc	ttattaacac	cttgattatt	gttattgggt	cggtagcctg	tgtagttttc	360
ttttccctct	ttgtggcggc	taaaacctac	gacaaaaatg	tagtggcgcg	ttcgttttac	420
cgggcagttt	tctttctgcc	tgttggtacc	ggaagtgttg	cggtgacggg	ggtttggaaa	480
tggatctatg	atccaatgtc	agggattttg	aattatgtct	taaaatatgc	tcatgtgatt	540
gaacaaaata	ttagttggct	gggagataag	cactgggctt	tgttggctat	tattgttatt	600
ttattaacca	catctgttgg	gcagcctatt	attctatata	ttgctgctat	gggaaatatt	660
gataactcct	tggtagaagc	tgcgcggtg	gacggcgcca	cagaatttca	ggtgttttgg	720
aatatcaagt	ggccaagtct	gctgccaaca	accttatata	ttgctgtcat	aacaaccatt	780
aattccttcc	aatgttttgc	tttgattcaa	cttttgacgt	ctggaggggc	aaattattca	840
accagtaccc	tcatgtacta	tttgatgaa	aaggccttta	agctctctga	atacggctat	900
gccaacacaa	tgggtgtatt	cttggcagtc	atgattgcaa	tcacagctt	tgctcaattt	960
aaaattttag	gtaatgatgt	ggaatattag				990

<210> SEQ ID NO 556

<211> LENGTH: 329

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 556

Met Phe Leu Thr Ser Gly Phe Phe Ser Met His Met Ser Asn Gly His

1				5					10					15			
Trp	Lys	Glu	Ala	Phe	Leu	Phe	Arg	Lys	Val	Glu	Gln	Lys	Lys	Glu	Val		
			20					25					30				
Phe	Gln	Val	Asn	Val	Asn	Lys	Leu	Lys	Met	Arg	Glu	Thr	Leu	Ile	Ser		
		35					40					45					
Tyr	Ala	Phe	Leu	Ala	Pro	Val	Leu	Val	Phe	Phe	Val	Ile	Phe	Val	Leu		
	50					55					60						
Ile	Pro	Met	Ile	Met	Gly	Phe	Val	Thr	Ser	Phe	Phe	Asn	Tyr	Ser	Met		
65					70					75					80		
Thr	Glu	Phe	Thr	Phe	Val	Gly	Phe	Ala	Asn	Tyr	Ala	Arg	Met	Phe	Gln		
				85					90					95			
Asp	Pro	Ile	Phe	Met	Lys	Ser	Leu	Ile	Asn	Thr	Leu	Ile	Ile	Val	Ile		
			100					105					110				
Gly	Ser	Val	Pro	Val	Val	Val	Phe	Phe	Ser	Leu	Phe	Val	Ala	Ala	Lys		
		115					120					125					
Thr	Tyr	Asp	Lys	Asn	Val	Val	Ala	Arg	Ser	Phe	Tyr	Arg	Ala	Val	Phe		
	130					135					140						
Phe	Leu	Pro	Val	Val	Thr	Gly	Ser	Val	Ala	Val	Thr	Val	Val	Trp	Lys		
145					150				155						160		
Trp	Ile	Tyr	Asp	Pro	Met	Ser	Gly	Ile	Leu	Asn	Tyr	Val	Leu	Lys	Tyr		
				165				170						175			
Ala	His	Val	Ile	Glu	Gln	Asn	Ile	Ser	Trp	Leu	Gly	Asp	Lys	His	Trp		
			180					185					190				
Ala	Leu	Leu	Ala	Ile	Ile	Val	Ile	Leu	Leu	Thr	Thr	Ser	Val	Gly	Gln		
		195					200					205					
Pro	Ile	Ile	Leu	Tyr	Ile	Ala	Ala	Met	Gly	Asn	Ile	Asp	Asn	Ser	Leu		
	210					215					220						
Val	Glu	Ala	Ala	Arg	Val	Asp	Gly	Ala	Thr	Glu	Phe	Gln	Val	Phe	Trp		
225					230				235						240		
Asn	Ile	Lys	Trp	Pro	Ser	Leu	Leu	Pro	Thr	Thr	Leu	Tyr	Ile	Ala	Val		
				245					250					255			
Ile	Thr	Thr	Ile	Asn	Ser	Phe	Gln	Cys	Phe	Ala	Leu	Ile	Gln	Leu	Leu		
			260					265					270				
Thr	Ser	Gly	Gly	Pro	Asn	Tyr	Ser	Thr	Ser	Thr	Leu	Met	Tyr	Tyr	Leu		
		275					280					285					
Tyr	Glu	Lys	Ala	Phe	Lys	Leu	Ser	Glu	Tyr	Gly	Tyr	Ala	Asn	Thr	Met		
	290					295					300						
Gly	Val	Phe	Leu	Ala	Val	Met	Ile	Ala	Ile	Ile	Ser	Phe	Ala	Gln	Phe		
305					310					315					320		
Lys	Ile	Leu	Gly	Asn	Asp	Val	Glu	Tyr									
				325													

<210> SEQ ID NO 557

<211> LENGTH: 1347

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 557

atggctaata	gcgaatatat	gtttttatta	ttatcaatta	ttgtctatta	tatgacaaaa	60
atztatattt	tttcctttct	atctgatatc	acattaccag	tttgaaaca	actaacgatt	120
ttggcttttag	ccctattttt	caatcagttc	ccgtatttgt	cgccattgct	aattgatcct	180
ctattatttt	tagttgtttt	aaggcaagaa	accaagcaat	tattttcttt	gaaagctctt	240
tttttggtctg	ttgcacctag	tgttttggtg	gatttgctat	ctcgatttat	gggtacaatc	300
gttatcccct	atcttttttt	gtcgagtggg	atttatctgg	gtcatattat	ctttgacttg	360
cttgcttatc	tgctgatttt	tccaagtttt	gctattatta	attatatgat	tggaaaagat	420
tacaagatga	tatgccaatc	cggatatctg	aaacgatcgc	ataatttcta	tcaaacattg	480
ctgatgtttg	ttttggttta	ttatgtggac	atttttgtca	ttttaggatt	tacggacccc	540
tttttacatt	ttcatcattc	tctttttgtt	cccacacctt	ataagttatt	gtttttgatg	600

tttatacttc	ttttagttta	tcttctatct	tatttttaatc	atagttctaa	agaatacctt	660
aaaaatgagt	tgagaagaga	acaacaagct	tatatgacta	acttagagat	ttatgggaaa	720
catcttgaga	aactctatcg	agatgtaaga	gctttttcaaa	gtgattacct	gagccgtata	780
gagcgttttag	gtcaagccat	taagagtga	tccattactc	agattcaaga	tattttatgcc	840
caaacggttc	atgaagctaa	cgactactgg	gatgataaac	actataatat	ctcgaagctt	900
aggaaaatta	atatctcatc	gattaagagc	ttattgtcag	ctaaaattat	cagtgcggaa	960
aaatcaggta	ttgatttgaa	tgtggaagt	ccagataata	taaaagaaac	ttacattcct	1020
gagttggact	tactattggt	gatgtctatt	ttttgtgata	acgccattga	ggcagctctt	1080
gaagcacaac	aacctcatat	gtcaattgct	tactttttgt	taggtgacta	tcagatgttt	1140
gttgtgacaa	atacgactaa	aaaaaaggta	gacattaaca	agatccttga	agaaggctat	1200
tcttcaaaag	gttcagaacg	tggtatcggc	cttttctaag	cgcagcgtat	tctcaaaaag	1260
tatccttatt	tatccttgcg	gactaaaagt	tttgataagg	aatttagcca	aaccttgacc	1320
atgccaaagg	aggaggtgga	tagatga				1347

<210> SEQ ID NO 558

<211> LENGTH: 448

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 558

Met	Ala	Asn	Ser	Glu	Tyr	Met	Phe	Leu	Leu	Leu	Ser	Ile	Ile	Val	Tyr
1				5				10						15	
Tyr	Met	Thr	Lys	Ile	Tyr	Ile	Phe	Ser	Phe	Leu	Ser	Asp	Ile	Thr	Leu
			20					25					30		
Pro	Val	Trp	Lys	Gln	Leu	Thr	Ile	Leu	Ala	Leu	Ala	Leu	Phe	Phe	Asn
			35					40					45		
Gln	Phe	Pro	Tyr	Leu	Ser	Pro	Leu	Leu	Ile	Asp	Pro	Leu	Leu	Phe	Leu
			50					55				60			
Val	Val	Leu	Arg	Gln	Glu	Thr	Lys	Gln	Leu	Phe	Ser	Leu	Lys	Ala	Leu
65								70				75			80
Phe	Leu	Ala	Val	Ala	Pro	Ser	Val	Leu	Val	Asp	Leu	Leu	Ser	Arg	Phe
				85				90						95	
Met	Gly	Thr	Ile	Val	Ile	Pro	Tyr	Leu	Phe	Leu	Ser	Ser	Gly	Ile	Tyr
				100				105						110	
Leu	Gly	His	Ile	Ile	Phe	Asp	Leu	Leu	Ala	Tyr	Leu	Leu	Ile	Phe	Pro
				115				120					125		
Ser	Phe	Ala	Ile	Ile	Asn	Tyr	Met	Ile	Gly	Lys	Asp	Tyr	Lys	Met	Ile
								135				140			
Cys	Gln	Ser	Gly	Tyr	Ser	Lys	Arg	Ser	His	Asn	Phe	Tyr	Gln	Thr	Leu
145						150				155					160
Leu	Met	Phe	Val	Leu	Val	Tyr	Tyr	Val	Asp	Ile	Phe	Val	Ile	Leu	Gly
				165				170						175	
Phe	Thr	Asp	Pro	Phe	Leu	His	Phe	His	His	Ser	Leu	Phe	Val	Pro	Thr
				180				185					190		
Pro	Tyr	Lys	Leu	Leu	Phe	Leu	Met	Phe	Ile	Leu	Leu	Leu	Val	Tyr	Leu
								200					205		
Leu	Ser	Tyr	Phe	Asn	His	Ser	Ser	Lys	Glu	Tyr	Leu	Lys	Asn	Glu	Leu
								215					220		
Arg	Arg	Glu	Gln	Gln	Ala	Tyr	Met	Thr	Asn	Leu	Glu	Ile	Tyr	Gly	Lys
225						230				235					240
His	Leu	Glu	Lys	Leu	Tyr	Arg	Asp	Val	Arg	Ala	Phe	Gln	Ser	Asp	Tyr
				245				250						255	
Leu	Ser	Arg	Ile	Glu	Arg	Leu	Gly	Gln	Ala	Ile	Lys	Ser	Glu	Ser	Ile
				260				265					270		
Thr	Gln	Ile	Gln	Asp	Ile	Tyr	Ala	Gln	Thr	Val	His	Glu	Ala	Asn	Asp
				275				280					285		
Tyr	Trp	Asp	Asp	Lys	His	Tyr	Asn	Ile	Ser	Lys	Leu	Arg	Lys	Ile	Asn
				290				295					300		

Ile	Ser	Ser	Ile	Lys	Ser	Leu	Leu	Ser	Ala	Lys	Ile	Ile	Ser	Ala	Glu
305				310					315						320
Lys	Ser	Gly	Ile	Asp	Leu	Asn	Val	Glu	Val	Pro	Asp	Asn	Ile	Lys	Glu
				325				330						335	
Thr	Tyr	Ile	Pro	Glu	Leu	Asp	Leu	Leu	Leu	Leu	Met	Ser	Ile	Phe	Cys
			340				345						350		
Asp	Asn	Ala	Ile	Glu	Ala	Ala	Leu	Glu	Ala	Gln	Gln	Pro	His	Met	Ser
		355					360					365			
Ile	Ala	Tyr	Phe	Leu	Leu	Gly	Asp	Tyr	Gln	Met	Phe	Val	Val	Thr	Asn
	370					375					380				
Thr	Thr	Lys	Lys	Lys	Val	Asp	Ile	Asn	Lys	Ile	Phe	Glu	Glu	Gly	Tyr
385					390					395					400
Ser	Ser	Lys	Gly	Ser	Glu	Arg	Gly	Ile	Gly	Leu	Ser	Asn	Ala	Gln	Arg
			405					410						415	
Ile	Leu	Lys	Lys	Tyr	Pro	Tyr	Leu	Ser	Leu	Arg	Thr	Lys	Ser	Phe	Asp
			420				425					430			
Lys	Glu	Phe	Ser	Gln	Thr	Leu	Thr	Met	Pro	Lys	Glu	Glu	Val	Asp	Arg
		435				440						445			

<210> SEQ ID NO 559

<211> LENGTH: 906

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 559

gtgctgatga	ccaaagtcag	aaaagctatt	attcccgcag	caggtttagg	cacacgtttt	60
ttacctgcaa	ccaaggccct	tgccaaggag	atgctaccta	ttgttgataa	accaactatt	120
caatttatcg	ttgaagaagc	tctaaaatca	ggtatcgaag	aaattccttat	cgttactgga	180
aaatccaaac	gctccataga	agatcatttt	gattcctaatt	ttgaattaga	atataattta	240
caggctaaag	gaaaaatcga	acttctaaag	ttagtagacg	agaccacttc	tattaatcct	300
cactttattc	gacagagtca	tccaagagga	ttaggagacg	cagttcttca	agcaaagacc	360
tttgttggca	atgaaccttt	tgttgtcatg	ctagggtgatg	atctgatgga	tattacaaat	420
ccaaatgtaa	aaccattaac	caaacaattg	atcgatgact	atgaagaaac	tcatgctgca	480
actattgccg	tcatgagggg	tcctcacgag	gatgtctcta	actacggtat	cattgctcct	540
caagcaaaag	cagtaaaagg	actctatagt	gtggatactt	ttgttgaaaa	accacaacct	600
caagatgcac	ctagtgattt	ggcaattatt	ggacgttact	tgctcacacc	agaaattttt	660
agtattttag	aaaaacaaga	acctgggtgca	ggcaatgaag	ttcaactgac	tgatgctatt	720
gataccctca	ataagacaca	gcgtgtcctt	gctcgtgagt	ttaaagggaa	acgctatgat	780
gttggcgata	aatttgggtt	tatgaaaaact	tctttggatt	atgccctgaa	acaccctcaa	840
gtcaaagatg	acttgaaaagc	ctacatcatc	caactgggca	aagcactaga	gaagacaaaa	900
ccataa						906

<210> SEQ ID NO 560

<211> LENGTH: 301

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 560

Met	Leu	Met	Thr	Lys	Val	Arg	Lys	Ala	Ile	Ile	Pro	Ala	Ala	Gly	Leu
1				5				10						15	
Gly	Thr	Arg	Phe	Leu	Pro	Ala	Thr	Lys	Ala	Leu	Ala	Lys	Glu	Met	Leu
			20				25					30			
Pro	Ile	Val	Asp	Lys	Pro	Thr	Ile	Gln	Phe	Ile	Val	Glu	Glu	Ala	Leu
		35				40					45				
Lys	Ser	Gly	Ile	Glu	Glu	Ile	Leu	Ile	Val	Thr	Gly	Lys	Ser	Lys	Arg
	50					55				60					
Ser	Ile	Glu	Asp	His	Phe	Asp	Ser	Asn	Phe	Glu	Leu	Glu	Tyr	Asn	Leu
65				70					75					80	
Gln	Ala	Lys	Gly	Lys	Ile	Glu	Leu	Leu	Lys	Leu	Val	Asp	Glu	Thr	Thr

				85					90					95			
Ser	Ile	Asn	Leu	His	Phe	Ile	Arg	Gln	Ser	His	Pro	Arg	Gly	Leu	Gly		
			100					105					110				
Asp	Ala	Val	Leu	Gln	Ala	Lys	Thr	Phe	Val	Gly	Asn	Glu	Pro	Phe	Val		
		115					120					125					
Val	Met	Leu	Gly	Asp	Asp	Leu	Met	Asp	Ile	Thr	Asn	Pro	Asn	Val	Lys		
	130					135					140						
Pro	Leu	Thr	Lys	Gln	Leu	Ile	Asp	Asp	Tyr	Glu	Glu	Thr	His	Ala	Ala		
145				150					155					160			
Thr	Ile	Ala	Val	Met	Arg	Val	Pro	His	Glu	Asp	Val	Ser	Asn	Tyr	Gly		
			165						170					175			
Ile	Ile	Ala	Pro	Gln	Ala	Lys	Ala	Val	Lys	Gly	Leu	Tyr	Ser	Val	Asp		
		180					185						190				
Thr	Phe	Val	Glu	Lys	Pro	Gln	Pro	Gln	Asp	Ala	Pro	Ser	Asp	Leu	Ala		
	195					200						205					
Ile	Ile	Gly	Arg	Tyr	Leu	Leu	Thr	Pro	Glu	Ile	Phe	Ser	Ile	Leu	Glu		
210				215					220								
Lys	Gln	Glu	Pro	Gly	Ala	Gly	Asn	Glu	Val	Gln	Leu	Thr	Asp	Ala	Ile		
225				230					235					240			
Asp	Thr	Leu	Asn	Lys	Thr	Gln	Arg	Val	Phe	Ala	Arg	Glu	Phe	Lys	Gly		
			245					250					255				
Lys	Arg	Tyr	Asp	Val	Gly	Asp	Lys	Phe	Gly	Phe	Met	Lys	Thr	Ser	Leu		
		260					265						270				
Asp	Tyr	Ala	Leu	Lys	His	Pro	Gln	Val	Lys	Asp	Asp	Leu	Lys	Ala	Tyr		
	275					280						285					
Ile	Ile	Gln	Leu	Gly	Lys	Ala	Leu	Glu	Lys	Thr	Lys	Pro					
	290					295						300					

<210> SEQ ID NO 561

<211> LENGTH: 705

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 561

atgaaaaacaa	acatttttgac	aattatcata	ttatcatgtg	tttttagcta	tggaagtcaa	60
ttagcttatg	cagatgaaaa	tttaaaagat	ttaaaaagaa	gtttaagatt	tgccataaat	120
attaccccat	gcgattatga	aaatgtagaa	attgcatttg	ttactacaaa	tagcatacat	180
attaatacta	aacaaaaaag	atcggaatgt	attcttttat	ttgattctat	tgtatcttta	240
ggcattactg	atcagtttat	aaaaggggat	aaggtcgatg	tttttggtct	cccttataat	300
ttttcccccac	cttatgtaga	taatatttat	ggtggtattg	taaaacattc	gaatcaagga	360
aataaatcat	tacagtttgt	aggaatttta	aatcaagatg	ggaaagaaac	ttatttgccc	420
tctgaggctg	ttcgcataaa	aaagaaacag	tttactttac	aggaatttga	ttttaaaata	480
agaaaatttc	taatggaaaa	atacaatatc	tatgattcgg	aatcgcggtta	tacatcgggg	540
agccttttcc	ttgctactaa	agatagtaaa	cattatgaag	ttgatttatt	taataaggat	600
gataagcttt	taagtcgaga	cagtttcttt	aaaaggtata	aagataataa	gatttttaat	660
agtgaagaaa	ttagtcattt	tgatatctac	ttaaaaacgc	actag		705

<210> SEQ ID NO 562

<211> LENGTH: 234

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 562

Met	Lys	Thr	Asn	Ile	Leu	Thr	Ile	Ile	Ile	Leu	Ser	Cys	Val	Phe	Ser
1			5					10					15		
Tyr	Gly	Ser	Gln	Leu	Ala	Tyr	Ala	Asp	Glu	Asn	Leu	Lys	Asp	Leu	Lys
		20					25					30			
Arg	Ser	Leu	Arg	Phe	Ala	Tyr	Asn	Ile	Thr	Pro	Cys	Asp	Tyr	Glu	Asn
	35					40						45			

Val	Glu	Ile	Ala	Phe	Val	Thr	Thr	Asn	Ser	Ile	His	Ile	Asn	Thr	Lys
50						55					60				
Gln	Lys	Arg	Ser	Glu	Cys	Ile	Leu	Tyr	Val	Asp	Ser	Ile	Val	Ser	Leu
65					70					75					80
Gly	Ile	Thr	Asp	Gln	Phe	Ile	Lys	Gly	Asp	Lys	Val	Asp	Val	Phe	Gly
				85					90					95	
Leu	Pro	Tyr	Asn	Phe	Ser	Pro	Pro	Tyr	Val	Asp	Asn	Ile	Tyr	Gly	Gly
			100					105					110		
Ile	Val	Lys	His	Ser	Asn	Gln	Gly	Asn	Lys	Ser	Leu	Gln	Phe	Val	Gly
		115					120					125			
Ile	Leu	Asn	Gln	Asp	Gly	Lys	Glu	Thr	Tyr	Leu	Pro	Ser	Glu	Ala	Val
	130					135					140				
Arg	Ile	Lys	Lys	Lys	Gln	Phe	Thr	Leu	Gln	Glu	Phe	Asp	Phe	Lys	Ile
145					150					155					160
Arg	Lys	Phe	Leu	Met	Glu	Lys	Tyr	Asn	Ile	Tyr	Asp	Ser	Glu	Ser	Arg
			165					170						175	
Tyr	Thr	Ser	Gly	Ser	Leu	Phe	Leu	Ala	Thr	Lys	Asp	Ser	Lys	His	Tyr
		180					185						190		
Glu	Val	Asp	Leu	Phe	Asn	Lys	Asp	Asp	Lys	Leu	Leu	Ser	Arg	Asp	Ser
	195						200					205			
Phe	Phe	Lys	Arg	Tyr	Lys	Asp	Asn	Lys	Ile	Phe	Asn	Ser	Glu	Glu	Ile
	210					215					220				
Ser	His	Phe	Asp	Ile	Tyr	Leu	Lys	Thr	His						
225						230									

<210> SEQ ID NO 563

<211> LENGTH: 1311

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 563

atgattcatt	taataataat	tagcgccatt	gctctagcca	ttggaattgg	ttaccgcacc	60
aaaatcaata	ttggcctgct	ggctattgct	ttttcttacc	tcatcgcaac	cactctcatg	120
ggattaagcc	ccaaagaact	tcttcatttt	tggccaacct	cactcttttt	taccattttt	180
agcgtctctc	tcttttataa	cgttgcaaca	actaacggca	ctcttgatgt	tttggctcaa	240
cacattctct	accgcacacg	caccaccct	aacgccctct	acatgatttt	atacctgata	300
gcaacccttt	tgtctgcttt	aggtgctgga	tttttacta	ctatggccgt	ttgctgtcct	360
ctagcgatta	ccctctgtca	aaaagcggac	aaacaccctt	tgattggagc	tcaagccgtc	420
aattggggag	cttcaggagg	ggctaatttg	ataaccagtg	gctcaggcat	tgtctttcaa	480
ggcctgttta	agcaaatggg	atgggaagag	caagcttttt	cacttggcaa	tcatatcttt	540
atcgtcagca	ttatctaccc	actcatcgtc	ttgcttttat	tatcttgta	catccgtac	600
agtaagggaa	gaacaaactc	atccttgact	attgaccaac	caccagtcct	cagcaaggctc	660
caaagacaaa	ccaccttgct	catgatcagc	agcatgggtt	tggtttggct	ttttcccttg	720
ttgcttctca	ttttcccaaa	catcgcatgg	atagctactt	atcgacaaaac	atttgatatt	780
ggctttgtct	caatactcat	ggtctgcctc	gccttaaggc	tcaaattagg	gaagcaagaa	840
gccatttttg	ctaaggttcc	ctgggctata	attatcatgc	tctgcggtat	gagcttacta	900
atgtctctag	cgggtcaagtc	aggtttagtt	acactgatag	ggcacctcat	aacaacaacc	960
attcctcatt	tctggttacc	tctgttcttt	tgtgtgatag	cggagtgat	gtcactcttt	1020
agttccaccc	tatccgtcgt	agccccaact	ctctttccca	tcattgctac	catcagtgtc	1080
caaagtcctc	acattgatat	tcgcttactc	acaacagcca	ctattattgg	cgctctatct	1140
actaatatct	ctcctttttc	atcagctggg	tccctcattc	aactctccct	tccccatata	1200
gaggaacgca	gtcttgcttt	caaaaaacaa	attcttctgg	gtgtgcccat	cagcttaagt	1260
ttggcactct	tgaccatctg	gattctcatg	ctgctagctt	ccttaagtta	g	1311

<210> SEQ ID NO 564

<211> LENGTH: 436

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 564

[illegible]

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<210> SEQ ID NO 565
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 565
gtgaaaaaca aattatTTTT agttgccctt gcgaccgtaa ctgtcctagg gccgtcttta      60
gcaacccttc atcaccagac cgtgcatgct agtgatgtaa cattaactga gacatgtgat      120
aaaaacggaa cagtatgttt tggctacgaa aacgtagatg gtgaagtatg taaattaaca      180
gctgacggaa agggaaccat ttgtgtgggt tacgaaaata gagacataaa agagagtgaa      240
acttctagca ccaaaaatga ttgttcta attggtttgggt gctttttaaa ttatctttgg      300
actacaataa aaagctgggt ttcgtaa                                     327

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<210> SEQ ID NO 566
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 566
Met Lys Asn Lys Leu Phe Leu Val Ala Leu Ala Thr Val Thr Val Leu
 1           5           10          15
Gly Pro Ser Leu Ala Thr Pro His His Gln Thr Val His Ala Ser Asp
          20          25          30
Val Thr Leu Thr Glu Thr Cys Asp Lys Asn Gly Thr Val Cys Phe Gly
          35          40          45
Tyr Glu Asn Val Asp Gly Glu Val Cys Lys Leu Thr Ala Asp Gly Lys
          50          55          60
Gly Thr Ile Cys Val Gly Tyr Glu Asn Arg Asp Ile Lys Glu Ser Glu
65          70          75          80
Thr Ser Ser Thr Lys Asn Asp Cys Ser Asn Trp Phe Trp Cys Phe Leu
          85          90          95
Asn Tyr Leu Trp Thr Thr Ile Lys Ser Trp Val Ser
          100         105

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<210> SEQ ID NO 567
<211> LENGTH: 429
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 567
atgaaacaac aatcttacca gcctctacgc ttcgtctacc tcttggtggc tctatttgct      60
gctctggtgc ttatagcaag acctgttatg gcagatgagg gaacaaatag tgctgatgcg      120
gcgtattata aagggaagag tgctggagaa gaagcagggg aaaaagctgg aaaagaagct      180
acttggactg atttgacccc aactgtccca actaatccag aaacacctag tgacatcgga      240
gagactacta ataaacagct ctataaagaa gggataaaag atgggtacaa agagggttat      300
aatgaaggct ggaaatctca gtatcccgtt ttgactccgg tcaagggttat atgggatttg      360
atctcttatt ggctacagcg attattcccc aataatcagt caagtaccgc agcacaaagc      420
atgtcataa                                     429

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<210> SEQ ID NO 568
<211> LENGTH: 142
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 568
Met Lys Gln Gln Ser Tyr Gln Pro Leu Arg Phe Val Tyr Leu Leu Val
 1           5           10          15
Ala Leu Phe Ala Ala Leu Leu Leu Ile Ala Arg Pro Val Met Ala Asp
          20          25          30
Glu Gly Thr Asn Ser Ala Asp Ala Ala Tyr Tyr Lys Gly Gln Ser Ala

```

		35					40					45					
Gly	Glu	Glu	Ala	Gly	Lys	Lys	Ala	Gly	Lys	Glu	Ala	Thr	Trp	Thr	Asp		
	50					55					60						
Leu	Thr	Pro	Thr	Val	Pro	Thr	Asn	Pro	Glu	Thr	Pro	Ser	Asp	Ile	Gly		
65					70					75					80		
Glu	Thr	Thr	Asn	Lys	Gln	Leu	Tyr	Lys	Glu	Gly	Tyr	Lys	Asp	Gly	Tyr		
			85						90					95			
Lys	Glu	Gly	Tyr	Asn	Glu	Gly	Trp	Lys	Ser	Gln	Tyr	Pro	Val	Leu	Thr		
		100						105					110				
Pro	Val	Lys	Val	Ile	Trp	Asp	Leu	Ile	Ser	Tyr	Trp	Leu	Gln	Arg	Leu		
	115					120						125					
Phe	Pro	Asn	Asn	Gln	Ser	Ser	Thr	Ala	Ala	Gln	Ser	Met	Ser				
	130					135					140						

<210> SEQ ID NO 569
 <211> LENGTH: 1353
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 569

gtggtttaca	tgagaaacaa	aaaagtaaca	ttagctcata	ttgtcgcaaa	gacaagtgtt	60
gctattgctt	tggctggagc	aatgggtagc	agttttattag	ctaatagcac	aacgtacgct	120
gtagtgga	aagaaaataa	aaaaagcgat	gtcaaataatg	aaacgaccaa	agttatggaa	180
gctaacgcaa	cttcctctaa	agaagacaat	catgtcatgc	acacattaga	cggctcaatg	240
agtactgtct	gggaggaaaa	ttcacctggg	ggtggtgttg	gtgaagtact	ttcctacaag	300
tttgcgctccc	cgatgcatat	tgggagaatt	ttaattgtta	atggagatac	atctagcaag	360
gagaattact	acaagaaaaa	tagaattgca	aaggctgatg	ttaaatacta	taacaggaat	420
aaattggtcc	tctttcaaaa	aattgaatta	ggcgacacct	acactaaaaa	accgcatcac	480
attgagattg	ataaaaaaatt	agatgttgat	cgtattgata	ttgaggtaac	agaggtccat	540
cagggacaaa	acaaggatat	tttagccttg	tcagaggtca	cttttgcaa	tatagaacgc	600
gatatttttg	aaaaaaaagt	taaagaaatt	aaagataaat	gggtaacaga	taaacaagca	660
gatgagttta	ttgaaactgc	cgacaagtat	gctgataaag	ctgttcagat	gtctgtgtgt	720
gcgtcacgtg	ctgagtatta	tcggatgtac	gttagccgca	aataccacta	caaaaaagaa	780
tttggtgaaa	aactaaaaca	agtctacaaa	gaaagcggag	cttcccacgt	tacaagcaaa	840
aaagatgtga	tgttagcttt	tgacgatgct	aaaaaaaaagt	caacgattgg	tcgacaagaa	900
aacggtcttt	ttgtgacaag	ttttgctgag	gatatggcct	tgctctttac	tgatcaaggt	960
aagttaaaat	cagctgacca	aattgaaaat	ataaaaagatg	tcgatagcgg	aaaatatagc	1020
gatgggggtt	atcaatatga	gtacgattct	gaactaacia	aaaacattga	taagctaggc	1080
tatatccgaa	cagctagcgg	agatactcct	ggagcaaatt	cgctcaacgt	tcctgggtgc	1140
caaacgtggt	caggaaaaca	cattgaaaat	tcagaaagtg	aattaatttt	cccatcgatt	1200
agtgttaaag	atctaaaatc	taaagctgtc	ttagcagaga	ttgatgccaa	aggctatttt	1260
gaaattattg	atcctaccat	cattgctcca	aatggtgacc	ataaaaaagt	aactggtcgc	1320
ttcaaaatta	agaaaatgca	agataggaag	taa			1353

<210> SEQ ID NO 570
 <211> LENGTH: 450
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 570

Met	Val	Tyr	Met	Arg	Asn	Lys	Lys	Val	Thr	Leu	Ala	His	Ile	Val	Ala
1			5					10					15		
Lys	Thr	Ser	Val	Ala	Ile	Ala	Leu	Ala	Gly	Ala	Met	Gly	Ser	Ser	Leu
		20					25				30				
Leu	Ala	Asn	Ser	Thr	Thr	Tyr	Ala	Val	Ser	Gly	Lys	Glu	Asn	Lys	Lys
	35					40				45					
Ser	Asp	Val	Lys	Tyr	Glu	Thr	Thr	Lys	Val	Met	Glu	Ala	Asn	Ala	Thr
	50				55					60					
Ser	Ser	Lys	Glu	Asp	Asn	His	Val	Met	His	Thr	Leu	Asp	Gly	Ser	Met

65					70					75				80	
Ser	Thr	Val	Trp	Glu	Glu	Asn	Ser	Pro	Gly	Gly	Gly	Val	Gly	Glu	Val
				85					90					95	
Leu	Ser	Tyr	Lys	Phe	Ala	Ser	Pro	Met	His	Ile	Gly	Arg	Ile	Leu	Ile
			100					105					110		
Val	Asn	Gly	Asp	Thr	Ser	Ser	Lys	Glu	Asn	Tyr	Tyr	Lys	Lys	Asn	Arg
		115					120					125			
Ile	Ala	Lys	Ala	Asp	Val	Lys	Tyr	Tyr	Asn	Arg	Asn	Lys	Leu	Val	Leu
	130					135					140				
Phe	Gln	Lys	Ile	Glu	Leu	Gly	Asp	Thr	Tyr	Thr	Lys	Lys	Pro	His	His
145					150					155				160	
Ile	Glu	Ile	Asp	Lys	Lys	Leu	Asp	Val	Asp	Arg	Ile	Asp	Ile	Glu	Val
			165						170					175	
Thr	Glu	Val	His	Gln	Gly	Gln	Asn	Lys	Asp	Ile	Leu	Ala	Leu	Ser	Glu
			180					185					190		
Val	Thr	Phe	Gly	Asn	Ile	Glu	Arg	Asp	Ile	Phe	Glu	Lys	Lys	Phe	Lys
	195						200					205			
Glu	Ile	Lys	Asp	Lys	Trp	Val	Thr	Asp	Lys	Gln	Ala	Asp	Glu	Phe	Ile
	210					215					220				
Glu	Thr	Ala	Asp	Lys	Tyr	Ala	Asp	Lys	Ala	Val	Gln	Met	Ser	Ala	Val
225					230					235				240	
Ala	Ser	Arg	Ala	Glu	Tyr	Tyr	Arg	Met	Tyr	Val	Ser	Arg	Lys	Tyr	His
			245					250					255		
Tyr	Lys	Lys	Glu	Phe	Val	Glu	Lys	Leu	Lys	Gln	Val	Tyr	Lys	Glu	Ser
			260					265					270		
Gly	Ala	Ser	His	Val	Thr	Ser	Lys	Lys	Asp	Val	Met	Leu	Ala	Phe	Asp
	275						280					285			
Asp	Ala	Lys	Lys	Lys	Ser	Thr	Ile	Gly	Arg	Gln	Glu	Asn	Gly	Leu	Phe
	290					295					300				
Val	Thr	Ser	Phe	Ala	Glu	Asp	Met	Ala	Leu	Leu	Phe	Thr	Asp	Gln	Gly
305					310					315				320	
Lys	Leu	Lys	Ser	Ala	Asp	Gln	Ile	Glu	Asn	Ile	Lys	Asp	Val	Asp	Ser
			325					330					335		
Gly	Lys	Tyr	Ser	Asp	Gly	Val	Tyr	Gln	Tyr	Glu	Tyr	Asp	Ser	Glu	Leu
			340				345					350			
Thr	Lys	Asn	Ile	Asp	Lys	Leu	Gly	Tyr	Ile	Arg	Thr	Ala	Ser	Gly	Asp
	355						360					365			
Thr	Pro	Gly	Ala	Asn	Ser	Leu	Asn	Val	Pro	Gly	Cys	Gln	Thr	Trp	Ser
	370					375					380				
Gly	Lys	His	Ile	Glu	Asn	Ser	Glu	Ser	Glu	Leu	Ile	Phe	Pro	Ser	Ile
385					390					395				400	
Ser	Val	Lys	Asp	Leu	Lys	Ser	Lys	Ala	Val	Leu	Ala	Glu	Ile	Asp	Ala
			405					410					415		
Lys	Gly	Tyr	Phe	Glu	Ile	Ile	Asp	Pro	Thr	Ile	Ile	Ala	Pro	Asn	Gly
			420				425					430			
Asp	His	Lys	Lys	Val	Thr	Gly	Arg	Phe	Lys	Ile	Lys	Lys	Met	Gln	Asp
		435					440					445			
Arg	Lys														
	450														

<210> SEQ ID NO 571

<211> LENGTH: 879

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 571

atgattagaa	agtatgaccg	cacgagcaca	aaaaagaaat	cactaaactg	gatttggcta	60
atcattgctt	tttttatgat	ttcaagcttt	ataggtggct	cttcttttac	tgagtcactt	120

ctagacattt	tgcctgccat	agccattgggt	ggtacagggt	atgctatttt	tcggtttaga	180
tctcatcaaa	agcggctagc	aaaggccaag	attgccaaac	aattagaaga	tctaaaagca	240
aaaattcagc	tagctgatcg	taaagttcgg	ctggttagaca	cttatctggc	agaccatgat	300
gacttccaat	ataacgtact	agctcagcaa	ttattaccac	aacttagtga	catcaaagca	360
aaagctatta	cgttaaaaga	ccagtttagat	ccccaaattt	atcgctcgat	cacccaaaaa	420
gccaatgacg	ttgaaagtga	tattaccctt	caactcgaaa	cactgcagat	tgccacaact	480
cttaaccctc	agcctttgaa	aaccccatct	cctaattctta	ttaacaaagc	acctgagctc	540
aaaccgtatt	atgataatat	tcagacagat	catcaagcta	tccttgctaa	aatccaagga	600
gccgacaatc	aagaagaatt	gcttgcgctg	catgatgcta	acatgaggag	gtttgaggat	660
atcttaacag	gctacttaaa	aatcaaagaa	gagcctaaaa	attactataa	cgctgctgct	720
cgtttagaac	aggccaaaca	agctattccaa	caatttgatg	aagatcttga	cgaaccctt	780
gctcgactca	atgaaagtga	tcttaaagat	tttgatatta	gccttcgaat	catgcaaggt	840
gctactcaaa	gacgaacaac	gcatacccaa	aaagactaa			879

[illegible]


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<210> SEQ ID NO 573
<211> LENGTH: 1416
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 573
  atgagcgttc tcaaagaata tcggacgggtt agcgaagtgg ttggcccttt gatgattggt      60
  gatcaagttg caggagtgc ctacaacgaa ttggtagata ttactttgca taatggagaa      120
  aggcgtaaag gtcaagtctt agaagtccaa ggtgacaagg ctatggtaca gctatttgaa      180
  ggatcaactg gcatcaacct agccaaaacc aaggttcgat ttacagggca tcctttggaa      240
  ttagccgtat cagaagatat ggtagggcgc atctttgatg gaatggggca gcccatagac      300
  ggcggtccag aacttattcc cgaaaaatac cttgatattg atggtcaagc gatcaatcct      360
  gtcgctcgtg attaccacga cgaatttatc cagacaggta tctcagctat tgatcacctc      420
  aataccctcg ttcgtgggtc aaagttacca gttttttcgg gctcagggtt acctcataat      480
  gaattggccg cacagattgc tcgtcaggca actgttctaa actctgatga taactttgcg      540
  gttgtgtttg cagctatggg tattactttt gaagaggcag aattctttat gaatgacttg      600
  cgtgaaacgg gtgccattga tcgatctggt ttatttatca atttagctaa tgaccctgct      660
  attgaacgca ttgcaacacc acgtatagct ctgacaacag ccgaataactt ggcttatgaa      720
  aaaggatatg atgttttagt catcatgaca gatatgacaa attattgtga agccttacga      780
  gaagtatcag ccgctcgcag agaagttcca ggcagacgag gttatcctgg ctatctctat      840
  actaatctct ccaccttata tgaacgggct ggtcgcttga tcgggaaaaa agggtcagtg      900
  actcaaattc ctattttaac catgccagaa gatgacatta cccaccctat ccccgatttg      960
  acaggttata ttaccgaagg tcagattatt ttgtcgcaag aactatataa aaatggtttt      1020
  agaccgccta ttaatgtctt gccatcgcta tctcgcttaa aagataaagg ctcaggtgaa      1080
  ggtaagactc gacaagacca tgctgttaca atgaatcagc tctttgcagc ctatgcccaa      1140
  ggaaaacaag ctaaggaatt ggctgttggtg ctcggtgaat cagccctttc tgaaacggat      1200
  aaactatatg tggcctttac caaccgggtt gaagaagaat acattaacca aggattttac      1260
  accaaccgta gcattgaaga aagtcttgac ttgggttggg aattgttgtc gattttgccca      1320
  cgtaccgaat taaaacgcat taaagatgat atgtagatc gttatttgcc taaagcagat      1380
  accacgatga caaagggttt tgttgcaaat gattga      1416

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<210> SEQ ID NO 574
<211> LENGTH: 471
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 574
  Met Ser Val Leu Lys Glu Tyr Arg Thr Val Ser Glu Val Val Gly Pro
  1          5          10          15
  Leu Met Ile Val Asp Gln Val Ala Gly Val His Tyr Asn Glu Leu Val
  20          25          30
  Asp Ile Thr Leu His Asn Gly Glu Arg Arg Lys Gly Gln Val Leu Glu
  35          40          45
  Val Gln Gly Asp Lys Ala Met Val Gln Leu Phe Glu Gly Ser Thr Gly
  50          55          60
  Ile Asn Leu Ala Lys Thr Lys Val Arg Phe Thr Gly His Pro Leu Glu
  65          70          75          80
  Leu Ala Val Ser Glu Asp Met Val Gly Arg Ile Phe Asp Gly Met Gly
  85          90          95
  Gln Pro Ile Asp Gly Gly Pro Glu Leu Ile Pro Glu Lys Tyr Leu Asp
  100         105         110
  Ile Asp Gly Gln Ala Ile Asn Pro Val Ala Arg Asp Tyr Pro Asp Glu
  115         120         125
  Phe Ile Gln Thr Gly Ile Ser Ala Ile Asp His Leu Asn Thr Leu Val
  130         135         140
  Arg Gly Gln Lys Leu Pro Val Phe Ser Gly Ser Gly Leu Pro His Asn
  145         150         155         160
  Glu Leu Ala Ala Gln Ile Ala Arg Gln Ala Thr Val Leu Asn Ser Asp

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				165					170				175				
Asp	Asn	Phe	Ala	Val	Val	Phe	Ala	Ala	Met	Gly	Ile	Thr	Phe	Glu	Glu		
			180					185					190				
Ala	Glu	Phe	Phe	Met	Asn	Asp	Leu	Arg	Glu	Thr	Gly	Ala	Ile	Asp	Arg		
		195					200					205					
Ser	Val	Leu	Phe	Ile	Asn	Leu	Ala	Asn	Asp	Pro	Ala	Ile	Glu	Arg	Ile		
	210					215					220						
Ala	Thr	Pro	Arg	Ile	Ala	Leu	Thr	Thr	Ala	Glu	Tyr	Leu	Ala	Tyr	Glu		
225					230					235					240		
Lys	Gly	Met	His	Val	Leu	Val	Ile	Met	Thr	Asp	Met	Thr	Asn	Tyr	Cys		
				245					250					255			
Glu	Ala	Leu	Arg	Glu	Val	Ser	Ala	Ala	Arg	Arg	Glu	Val	Pro	Gly	Arg		
		260						265					270				
Arg	Gly	Tyr	Pro	Gly	Tyr	Leu	Tyr	Thr	Asn	Leu	Ser	Thr	Leu	Tyr	Glu		
	275						280					285					
Arg	Ala	Gly	Arg	Leu	Ile	Gly	Lys	Lys	Gly	Ser	Val	Thr	Gln	Ile	Pro		
	290					295					300						
Ile	Leu	Thr	Met	Pro	Glu	Asp	Asp	Ile	Thr	His	Pro	Ile	Pro	Asp	Leu		
305					310					315					320		
Thr	Gly	Tyr	Ile	Thr	Glu	Gly	Gln	Ile	Ile	Leu	Ser	Gln	Glu	Leu	Tyr		
				325					330					335			
Lys	Asn	Gly	Phe	Arg	Pro	Pro	Ile	Asn	Val	Leu	Pro	Ser	Leu	Ser	Arg		
			340					345					350				
Leu	Lys	Asp	Lys	Gly	Ser	Gly	Glu	Gly	Lys	Thr	Arg	Gln	Asp	His	Ala		
	355					360						365					
Ala	Thr	Met	Asn	Gln	Leu	Phe	Ala	Ala	Tyr	Ala	Gln	Gly	Lys	Gln	Ala		
	370					375						380					
Lys	Glu	Leu	Ala	Val	Val	Leu	Gly	Glu	Ser	Ala	Leu	Ser	Glu	Thr	Asp		
385					390					395					400		
Lys	Leu	Tyr	Val	Ala	Phe	Thr	Asn	Arg	Phe	Glu	Glu	Glu	Tyr	Ile	Asn		
			405						410					415			
Gln	Gly	Phe	Tyr	Thr	Asn	Arg	Ser	Ile	Glu	Glu	Ser	Leu	Asp	Leu	Gly		
			420					425					430				
Trp	Glu	Leu	Leu	Ser	Ile	Leu	Pro	Arg	Thr	Glu	Leu	Lys	Arg	Ile	Lys		
	435						440					445					
Asp	Asp	Met	Leu	Asp	Arg	Tyr	Leu	Pro	Lys	Ala	Asp	Thr	Thr	Met	Thr		
	450					455					460						
Lys	Val	Phe	Val	Ala	Asn	Asp											
465					470												

<210> SEQ ID NO 575

<211> LENGTH: 1440

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 575

gtgcttttgg	acaatgtgaa	aggaattgac	aacatgaata	acatcaaaac	caaaaaaagg	60
tttatggatc	gctatattga	tggctttatg	aaatggatgc	cagaatcgct	ttttatctgt	120
tttattttaa	cctttttagt	cgttactatg	tctgtgttga	tgacggatag	tccctttatt	180
ggtagcgaaa	agacgggcgg	gattatctat	ggctgggtaa	atggtttttg	ggggctgttg	240
tcctttgcca	tgcatatgac	tattttactt	gcgacaggga	atgctgtagc	gagttctcca	300
cctgctcata	agatgtttaa	gtcccttgcc	aaactgcctc	aaaccaggac	tcagattttt	360
atctttttcca	ctgtagtagg	ctctatcttt	ggctttttac	actgggggtct	tggtatgatg	420
gttgctattg	tgtttgggaa	agagttgctt	gttcaggcta	ggcaaaaagg	gattaagggtg	480
catacgccct	tgtttgttgc	tactttatct	tttacctttt	taccagctac	ttctggtcta	540
tctggtgctg	cggtgcttta	ttcggtactt	ccagattatt	tgcgaaatag	tgtcgcagat	600
gcttataaac	aggttggttc	tgaaagtgtt	cctctgacag	aatcagtttt	gaatcttcca	660
tttatcagtc	ttttagtggg	gtgtatgctg	gtaccgcttt	gcttttgcttt	attggcgcac	720

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ccaaaagatg aaactaaaat catggaactt gatgatgaga tctatcacca tagtcttgat      780
accgcttcac atgttggtat tgcaagaaac acacctgctg aaaagatgaa cgcctctcgc      840
ttagtgatgt atcttggttg tggggccatt gttagctata gcctttatca ttttccgggtg      900
gtgggcttgt ctggtctaga tctcaattgt ttttaactttt tatttttagg cttaggcttg      960
cttctttgtg gtcaacaagg accagaatat tatggttcct tattcaaaga tggggtcattg     1020
tcatcttggg gcttggtgct tcagtttcca ttttacgctg gtatttttgg aatcattcaa     1080
agtacagggtt taggattaga gatttcccat ttctttgtcg ctatttcaaa tgggacaaca     1140
tggccgggtct ttgcttatct ttactcggct ttgctgaata ttgcggtacc atcaggaggc     1200
tcaaaatttg tgattgaagc tccctatatc gtccctgcaa ctatcgaagt tggtaatgac     1260
ttaggtaaga ttttgcaggc ttatcaatta ggagatgccca caacaaactt gatagttcct     1320
ttttgggcct tatcttacct ctcaaacttc aaactaaaat tcaatcaaat tgtggccttat     1380
actatttcctt gtgtcttggt ggtcacagggt attgccatca tttacctatt tgtatttttag     1440

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<210> SEQ ID NO 576
<211> LENGTH: 479
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 576

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Met Leu Leu Asp Asn Val Lys Gly Ile Asp Asn Met Asn Asn Ile Lys
 1             5             10             15
Thr Lys Lys Arg Phe Met Asp Arg Tyr Ile Asp Gly Phe Met Lys Trp
      20             25             30
Met Pro Glu Ser Leu Phe Ile Cys Phe Ile Leu Thr Phe Leu Val Val
      35             40             45
Thr Met Ser Val Leu Met Thr Asp Ser Pro Phe Ile Gly Thr Glu Lys
 50             55             60
Thr Gly Gly Ile Ile Tyr Gly Trp Val Asn Gly Phe Trp Gly Leu Leu
65             70             75             80
Ser Phe Ala Met Gln Met Thr Ile Leu Leu Ala Thr Gly Asn Ala Val
      85             90             95
Ala Ser Ser Pro Pro Ala His Lys Met Phe Lys Ser Leu Ala Lys Leu
      100            105            110
Pro Gln Thr Arg Thr Gln Ile Phe Ile Phe Ser Ile Val Val Gly Ser
      115            120            125
Ile Phe Gly Phe Leu His Trp Gly Leu Gly Met Met Val Ala Ile Val
      130            135            140
Phe Gly Lys Glu Leu Leu Val Gln Ala Arg Gln Lys Gly Ile Lys Val
      145            150            155            160
His Thr Pro Leu Phe Val Ala Thr Leu Phe Phe Thr Phe Leu Pro Ala
      165            170            175
Thr Ser Gly Leu Ser Gly Ala Ala Val Leu Tyr Ser Ala Thr Pro Asp
      180            185            190
Tyr Leu Arg Asn Ser Val Ala Asp Ala Tyr Lys Gln Val Val Pro Glu
      195            200            205
Ser Val Pro Leu Thr Glu Ser Val Leu Asn Leu Pro Phe Ile Ser Leu
      210            215            220
Leu Val Val Cys Met Leu Val Pro Leu Cys Phe Ala Leu Leu Ala His
      225            230            235            240
Pro Lys Asp Glu Thr Lys Ile Met Glu Leu Asp Asp Glu Ile Tyr His
      245            250            255
His Ser Leu Asp Thr Ala Ser His Val Val Ile Ala Arg Asn Thr Pro
      260            265            270
Ala Glu Lys Met Asn Ala Ser Arg Leu Val Met Tyr Leu Val Gly Gly
      275            280            285
Ala Ile Val Ser Tyr Ser Leu Tyr His Phe Ser Val Val Gly Leu Ser
      290            295            300
Gly Leu Asp Leu Asn Cys Phe Asn Phe Leu Phe Leu Gly Leu Gly Leu

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305		310		315		320									
Leu	Leu	Cys	Gly	Gln	Gln	Gly	Pro	Glu	Tyr	Tyr	Gly	Ser	Leu	Phe	Lys
		325		330		335									
Asp	Gly	Val	Met	Ser	Ser	Trp	Gly	Leu	Val	Leu	Gln	Phe	Pro	Phe	Tyr
		340		345		350									
Ala	Gly	Ile	Phe	Gly	Ile	Ile	Gln	Ser	Thr	Gly	Leu	Gly	Leu	Glu	Ile
		355		360		365									
Ser	His	Phe	Phe	Val	Ala	Ile	Ser	Asn	Gly	Thr	Thr	Trp	Pro	Val	Phe
	370			375		380									
Ala	Tyr	Leu	Tyr	Ser	Ala	Leu	Leu	Asn	Ile	Ala	Val	Pro	Ser	Gly	Gly
385				390		395									400
Ser	Lys	Phe	Val	Ile	Glu	Ala	Pro	Tyr	Ile	Val	Pro	Ala	Thr	Ile	Glu
			405		410									415	
Val	Gly	Asn	Asp	Leu	Gly	Lys	Ile	Leu	Gln	Ala	Tyr	Gln	Leu	Gly	Asp
		420		425		430									
Ala	Thr	Thr	Asn	Leu	Ile	Val	Pro	Phe	Trp	Ala	Leu	Ser	Tyr	Leu	Ser
		435		440		445									
Asn	Phe	Lys	Leu	Lys	Phe	Asn	Gln	Ile	Val	Ala	Tyr	Thr	Ile	Pro	Cys
	450			455		460									
Val	Leu	Val	Val	Thr	Gly	Ile	Ala	Ile	Ile	Tyr	Leu	Phe	Val	Phe	
465				470		475									

<210> SEQ ID NO 577

<211> LENGTH: 666

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 577

atgaaacgat	gtaataaata	tctcttcact	tcactactag	cagcttcgat	gctgttttagt	60
tcgtataaat	cagtacatgc	ccatgataac	attgatgaga	aaggtaaagt	gcacctttac	120
tggcagggaa	attactatgt	tgataactat	gtcgactata	ctaaaaaatt	ggtcgatagc	180
gataaaaaata	ttgaatggac	tgtaaccttt	aattcagcta	aagaacaatg	ggtttaccct	240
gattttctcag	tttttcttcc	taagggtgta	aaagctccta	cagagataac	ttatgagcat	300
cattattggg	acggtacagt	tcgttctgaa	acacgcaata	atacacaatg	gcattatgat	360
tggaaaagcc	aacaaacaaa	ttttaatcaa	gaatttgata	aattccctgg	tttactgggt	420
tggagtcctt	ctctagataa	attttacaaa	ctaaaaaacg	acggaaaatt	ttctcacggt	480
ttagtagata	cctatggccg	tcaatcacac	acttattttt	ctcataaaat	ggtttggaag	540
tttaaaactg	agcttgaaga	taattacaaa	aataaatggg	ataaattacc	gtttatagca	600
ggtattaaac	aaaacaaccc	attagcagca	tcattcccaa	gttataaagg	ggaattcggt	660
gagtaa						666

<210> SEQ ID NO 578

<211> LENGTH: 221

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 578

Met	Lys	Arg	Cys	Asn	Lys	Tyr	Leu	Phe	Thr	Ser	Leu	Leu	Ala	Ala	Ser
1				5					10					15	
Met	Leu	Phe	Ser	Ser	Tyr	Lys	Ser	Val	His	Ala	His	Asp	Asn	Ile	Asp
			20					25					30		
Glu	Lys	Gly	Lys	Val	His	Leu	Tyr	Trp	Gln	Gly	Asn	Tyr	Tyr	Val	Asp
		35				40					45				
Asn	Tyr	Val	Asp	Tyr	Thr	Lys	Lys	Leu	Val	Asp	Ser	Asp	Lys	Asn	Ile
	50					55				60					
Glu	Trp	Thr	Val	Thr	Phe	Asn	Ser	Ala	Lys	Glu	Gln	Trp	Val	Tyr	Pro
65				70					75					80	
Asp	Phe	Ser	Val	Phe	Leu	Pro	Lys	Gly	Val	Lys	Ala	Pro	Thr	Glu	Ile
				85					90					95	

Thr	Tyr	Glu	His	His	Tyr	Trp	Asp	Gly	Thr	Val	Arg	Ser	Glu	Thr	Arg
			100					105					110		
Asn	Asn	Thr	Gln	Trp	His	Tyr	Asp	Trp	Lys	Ser	Gln	Gln	Thr	Asn	Phe
		115					120				125				
Asn	Gln	Glu	Phe	Asp	Lys	Phe	Pro	Gly	Tyr	Thr	Gly	Trp	Ser	Pro	Ser
	130				135						140				
Leu	Asp	Lys	Phe	Tyr	Lys	Leu	Lys	Asn	Asp	Gly	Lys	Phe	Ser	His	Val
145					150					155				160	
Leu	Val	Asp	Thr	Tyr	Gly	Arg	Gln	Ser	His	Thr	Tyr	Phe	Ser	His	Lys
			165						170					175	
Met	Val	Trp	Lys	Phe	Lys	Thr	Glu	Leu	Glu	Asp	Asn	Tyr	Lys	Asn	Lys
		180						185					190		
Trp	Asp	Lys	Leu	Pro	Phe	Ile	Ala	Gly	Ile	Lys	Gln	Asn	Asn	Pro	Leu
	195						200				205				
Ala	Ala	Ser	Phe	Pro	Ser	Tyr	Lys	Gly	Glu	Phe	Gly	Glu			
	210					215					220				

<210> SEQ ID NO 579

<211> LENGTH: 756

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 579

gtggaatgct	atcgtgatcg	tcaattgtta	tcaacttadc	acaaacaagt	gactcaaaag	60
aagccctcag	aatggagga	ggtgtggcaa	aaggctaagg	cgtataacgc	taggcttggg	120
attcagcctg	ttccagatgc	tttttcattt	agggatggca	ttcatgataa	aaactacgaa	180
agcctacttc	aaattgaaaa	caatgatatt	atgggatatg	ttgaagtgcc	ctctattaaa	240
gtgacgttac	ccatatacca	ctatacgaca	gacgagggtc	taactaaagg	agcaggtcac	300
ttatttggaa	gtgccttacc	agttggtggt	gacgggactc	acacgggttat	ttctgctcat	360
agaggccttc	catcggcaga	aatgtttact	aatttgaatt	tagtgaaaaa	gggagatact	420
ttttactttc	gtgtgttaaa	taaagtattg	gcttataaaag	ttgatcagat	actaactggt	480
gaaccagatc	aagtcacatc	actttctgga	gtcatgggga	aagattatgc	tactttgggt	540
acctgcacac	catatgggtg	taacaccaag	cgtctattgg	tccgagggtca	tagaattgca	600
tatcattata	aaaagtatca	acaggctaaa	aaagcaatga	aactcgtgga	taaatcaaga	660
atgtgggcag	aagtagtggtg	tgctgctttc	ggggtgggta	tagctattat	tttagtggtt	720
atgtattcgc	gagtaagtgc	taagaaaagc	aagtga			756

<210> SEQ ID NO 580

<211> LENGTH: 251

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 580

Met	Glu	Cys	Tyr	Arg	Asp	Arg	Gln	Leu	Leu	Ser	Thr	Tyr	His	Lys	Gln
1			5					10					15		
Val	Thr	Gln	Lys	Lys	Pro	Ser	Glu	Met	Glu	Glu	Val	Trp	Gln	Lys	Ala
		20					25					30			
Lys	Ala	Tyr	Asn	Ala	Arg	Leu	Gly	Ile	Gln	Pro	Val	Pro	Asp	Ala	Phe
	35				40					45					
Ser	Phe	Arg	Asp	Gly	Ile	His	Asp	Lys	Asn	Tyr	Glu	Ser	Leu	Leu	Gln
	50				55					60					
Ile	Glu	Asn	Asn	Asp	Ile	Met	Gly	Tyr	Val	Glu	Val	Pro	Ser	Ile	Lys
65			70						75				80		
Val	Thr	Leu	Pro	Ile	Tyr	His	Tyr	Thr	Thr	Asp	Glu	Val	Leu	Thr	Lys
			85					90					95		
Gly	Ala	Gly	His	Leu	Phe	Gly	Ser	Ala	Leu	Pro	Val	Gly	Gly	Asp	Gly
		100					105					110			
Thr	His	Thr	Val	Ile	Ser	Ala	His	Arg	Gly	Leu	Pro	Ser	Ala	Glu	Met
	115					120						125			

Phe	Thr	Asn	Leu	Asn	Leu	Val	Lys	Lys	Gly	Asp	Thr	Phe	Tyr	Phe	Arg
130						135					140				
Val	Leu	Asn	Lys	Val	Leu	Ala	Tyr	Lys	Val	Asp	Gln	Ile	Leu	Thr	Val
145					150					155					160
Glu	Pro	Asp	Gln	Val	Thr	Ser	Leu	Ser	Gly	Val	Met	Gly	Lys	Asp	Tyr
			165						170					175	
Ala	Thr	Leu	Val	Thr	Cys	Thr	Pro	Tyr	Gly	Val	Asn	Thr	Lys	Arg	Leu
			180					185					190		
Leu	Val	Arg	Gly	His	Arg	Ile	Ala	Tyr	His	Tyr	Lys	Lys	Tyr	Gln	Gln
		195					200					205			
Ala	Lys	Lys	Ala	Met	Lys	Leu	Val	Asp	Lys	Ser	Arg	Met	Trp	Ala	Glu
	210					215					220				
Val	Val	Cys	Ala	Ala	Phe	Gly	Val	Val	Ile	Ala	Ile	Ile	Leu	Val	Phe
225					230					235					240
Met	Tyr	Ser	Arg	Val	Ser	Ala	Lys	Lys	Ser	Lys					
				245					250						

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<210> SEQ ID NO 581
<211> LENGTH: 714
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 581
atgatagtaa gactgattaa gctccttgac aagttgataa acgtcattgt tctttgtttc      60
ttctttcttt gtttattgat tgcggcactt ggaatctacg atgctttaac agtttatcaa      120
ggagctaata ctactaacta tcaacaatat aagaaaaagg gtgttcagtt tgacgattta      180
ttagctatta attctgatgt tatggcatgg ctgactgtta aaggaacgca tattgattat      240
ccaattgtac agggagagaa taatttagaa tatatcaaca aatcagtaga aggagagtac      300
tccttatcag gaagtgtttt tctagattat cgtaataaag taacttttga agataaatac      360
tcattaatct atgcacatca tatggctgga aatgttatgt ttggcgaatt acctaacttt      420
aggaaaaaat cattttttta taaacacaaa gaatttagta ttgaaaccaa aacaaagcaa      480
aaactgaaaa tcaatatatt tgcatgtatc caaacagatg cttttgacag tttactgttt      540
aatccaattg atgttgatat ttctagtaaa aatgaatttt taaaccatat caagcaaaaa      600
tcggtacagt atcgtgaaat attgacaaca aatgaaagtc gttttgttgc cttatcaacc      660
tgtgaggata tgacaacaga tggtaggatt atcgttattg gacaaattga ataa          714

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<210> SEQ ID NO 582
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 582
Met Ile Val Arg Leu Ile Lys Leu Leu Asp Lys Leu Ile Asn Val Ile
1      5      10      15
Val Leu Cys Phe Phe Phe Leu Cys Leu Leu Ile Ala Ala Leu Gly Ile
20     25     30
Tyr Asp Ala Leu Thr Val Tyr Gln Gly Ala Asn Ala Thr Asn Tyr Gln
35     40     45
Gln Tyr Lys Lys Lys Gly Val Gln Phe Asp Asp Leu Leu Ala Ile Asn
50     55     60
Ser Asp Val Met Ala Trp Leu Thr Val Lys Gly Thr His Ile Asp Tyr
65     70     75     80
Pro Ile Val Gln Gly Glu Asn Asn Leu Glu Tyr Ile Asn Lys Ser Val
85     90     95
Glu Gly Glu Tyr Ser Leu Ser Gly Ser Val Phe Leu Asp Tyr Arg Asn
100    105    110
Lys Val Thr Phe Glu Asp Lys Tyr Ser Leu Ile Tyr Ala His His Met
115    120    125
Ala Gly Asn Val Met Phe Gly Glu Leu Pro Asn Phe Arg Lys Lys Ser

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130		135		140
Phe Phe Asn Lys His Lys Glu Phe Ser Ile Glu Thr Lys Thr Lys Gln				
145		150		155
Lys Leu Lys Ile Asn Ile Phe Ala Cys Ile Gln Thr Asp Ala Phe Asp				
	165		170	175
Ser Leu Leu Phe Asn Pro Ile Asp Val Asp Ile Ser Ser Lys Asn Glu				
	180		185	190
Phe Leu Asn His Ile Lys Gln Lys Ser Val Gln Tyr Arg Glu Ile Leu				
	195		200	205
Thr Thr Asn Glu Ser Arg Phe Val Ala Leu Ser Thr Cys Glu Asp Met				
	210		215	220
Thr Thr Asp Gly Arg Ile Ile Val Ile Gly Gln Ile Glu				
225		230		235

<210> SEQ ID NO 583

<211> LENGTH: 2289

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 583

ttgagaggag	agaaaaatgaa	aaaaacaagg	tttccaaata	agcttaatac	tcttaatact	60
caaagggat	taagtaaaaa	ctcaaaacga	tttactgtca	ctttagtggg	agtcttttta	120
atgatcttcg	cttttgtaac	ttccatgggt	gggtgctaaga	ctgttttttg	tttagtagaa	180
tctcgcacgc	caaacgcaat	aaatccagat	tcaagttcgg	aatacacatg	gtatggatat	240
gaatcttatg	taagagggca	tccatattat	aaacagttta	gagtagcaca	cgatttaagg	300
gttaacttag	aaggaagtag	aagttatcaa	gtttattgct	ttaattttaa	gaaagcattt	360
cctctcggat	cagatagtag	tgtaaaaaag	tggtataaaa	aacatgatgg	aatctctaca	420
aaatttgaag	attatgcgat	gagccctaga	attacgggag	atgagctaaa	tcagaagtta	480
cgagctgtta	tgtataatgg	acatccacaa	aatgccaatg	gtattatgga	aggcttggaa	540
cccttgaatg	ctatcagagt	tacacaagag	gcggtatggt	actattctga	taatgctcct	600
atttctaata	cagatgaaag	ttttaaaagg	gagtcagaaa	gtaacttggg	tagtacttct	660
caattatctt	tgatgcgta	agctttgaag	caactgattg	atccgaattt	ggcaactaaa	720
atgccaaaac	aagttccgga	tgattttcag	ctaagtattt	ttgagctctg	ggacaaggga	780
gataaatata	ataaaaggata	ccaaaatctt	ttgagtgggt	gtttagtccc	tactaaacca	840
ccaactccag	gagaccacc	aatgcctcca	aatcaacctc	aaacgacttc	agtacttatt	900
agaaagtatg	ctataggtga	ttactctaaa	ttgcttgaag	gtgcaacatt	acagttgaca	960
gggggataacg	tgaatagttt	tcaagcgaga	gtgtttagca	gtaatgatat	tgagaaaaga	1020
attgaactat	cagatggaac	ttatacttta	actgaattga	attctccagc	tggttatagt	1080
atcgagagagc	caatcacttt	taagggtgaa	gctggcgaag	tgtatactat	tattgatgga	1140
aaacagattg	aaaatcccaa	taaagagata	gtagagcctt	actcagtaga	agcatataat	1200
gattttgaag	aatttagcgt	tttaactaca	caaaactatg	caaaatttta	ttatgcaaaa	1260
aataaaaaatg	gaagttcaca	ggttgtctat	tgctttaatg	cagatctaaa	atctccacca	1320
gactctgaag	atggtgggaa	aacaatgact	ccagacttta	caacaggaga	agtaaaatac	1380
actcatattg	caggtcgtga	cctctttaa	tatactgtga	aaccaagaga	taccgatcct	1440
gacactttct	taaaacatat	caaaaaagta	attgagaagg	gttacaggga	aaaaggacaa	1500
gctattgagt	atagtgggtc	aactgagaca	caattgctgt	cggctactca	gtagcaata	1560
tattatttca	ctgatagtgc	tgaattagat	aaggataaac	taaaagacta	tcattggttt	1620
ggagacatga	atgatagtac	tttagcagtt	gctaaaatcc	ttgtagaata	cgctcaagat	1680
agtaatcctc	cacagctaac	tgaccttgat	ttctttattc	cgaataacaa	taaatatcaa	1740
tctcttattg	gaactcagtg	gcattccagaa	gatttagttg	atattattcg	tatggaagat	1800
aaaaaagaag	ttataacctgt	aactcataat	ttaacattga	gaaaaacggg	gactggttta	1860
gctggtgaca	gaactaaaaga	tttccatttt	gaaattgaat	taaaaaataa	taagcaagaa	1920
ttgctttctc	aaactgttaa	aacagataaa	acaaacctcg	aatttaaaga	tggtaaagca	1980
accattaatt	taaaacatgg	ggaaagttaa	acacttcaag	gtttaccaga	aggttattct	2040
taccttgta	aagaaacaga	ttctgaaggc	tataaggtta	aagttaatag	ccaagaagta	2100
gcaaatgcta	cagtttcaaa	aacaggaata	acaagtgatg	agacacttgc	ttttgaaaat	2160
aataaagagc	ctgttggtcc	tacaggagtt	gatcaaaaga	tcaatggcta	tctagctttg	2220
atagttatcg	ctggtatcag	tttggggatc	tggggaattc	acacgataag	gataagaaaa	2280

<210> SEQ ID NO 584

<211> LENGTH: 762

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 584

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Met Arg Gly Glu Lys Met Lys Lys Thr Arg Phe Pro Asn Lys Leu Asn
1      5      10      15
Thr Leu Asn Thr Gln Arg Val Leu Ser Lys Asn Ser Lys Arg Phe Thr
20      25      30
Val Thr Leu Val Gly Val Phe Leu Met Ile Phe Ala Leu Val Thr Ser
35      40      45
Met Val Gly Ala Lys Thr Val Phe Gly Leu Val Glu Ser Ser Thr Pro
50      55      60
Asn Ala Ile Asn Pro Asp Ser Ser Ser Glu Tyr Arg Trp Tyr Gly Tyr
65      70      75      80
Glu Ser Tyr Val Arg Gly His Pro Tyr Tyr Lys Gln Phe Arg Val Ala
85      90      95
His Asp Leu Arg Val Asn Leu Glu Gly Ser Arg Ser Tyr Gln Val Tyr
100      105      110
Cys Phe Asn Leu Lys Lys Ala Phe Pro Leu Gly Ser Asp Ser Ser Val
115      120      125
Lys Lys Trp Tyr Lys Lys His Asp Gly Ile Ser Thr Lys Phe Glu Asp
130      135      140
Tyr Ala Met Ser Pro Arg Ile Thr Gly Asp Glu Leu Asn Gln Lys Leu
145      150      155      160
Arg Ala Val Met Tyr Asn Gly His Pro Gln Asn Ala Asn Gly Ile Met
165      170      175
Glu Gly Leu Glu Pro Leu Asn Ala Ile Arg Val Thr Gln Glu Ala Val
180      185      190
Trp Tyr Tyr Ser Asp Asn Ala Pro Ile Ser Asn Pro Asp Glu Ser Phe
195      200      205
Lys Arg Glu Ser Glu Ser Asn Leu Val Ser Thr Ser Gln Leu Ser Leu
210      215      220
Met Arg Gln Ala Leu Lys Gln Leu Ile Asp Pro Asn Leu Ala Thr Lys
225      230      235      240
Met Pro Lys Gln Val Pro Asp Asp Phe Gln Leu Ser Ile Phe Glu Ser
245      250      255
Glu Asp Lys Gly Asp Lys Tyr Asn Lys Gly Tyr Gln Asn Leu Leu Ser
260      265      270
Gly Gly Leu Val Pro Thr Lys Pro Pro Thr Pro Gly Asp Pro Pro Met
275      280      285
Pro Pro Asn Gln Pro Gln Thr Thr Ser Val Leu Ile Arg Lys Tyr Ala
290      295      300
Ile Gly Asp Tyr Ser Lys Leu Leu Glu Gly Ala Thr Leu Gln Leu Thr
305      310      315      320
Gly Asp Asn Val Asn Ser Phe Gln Ala Arg Val Phe Ser Ser Asn Asp
325      330      335
Ile Gly Glu Arg Ile Glu Leu Ser Asp Gly Thr Tyr Thr Leu Thr Glu
340      345      350
Leu Asn Ser Pro Ala Gly Tyr Ser Ile Ala Glu Pro Ile Thr Phe Lys
355      360      365
Val Glu Ala Gly Lys Val Tyr Thr Ile Ile Asp Gly Lys Gln Ile Glu
370      375      380
Asn Pro Asn Lys Glu Ile Val Glu Pro Tyr Ser Val Glu Ala Tyr Asn
385      390      395      400

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<210> SEQ ID NO 585
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 585
      gtgggaatta tcaaaaaaca agtcaaagct tacatagccc ttgaaagtat gatcgcaaca      60
      ggcatcctct ttagtattgt cattctcgtc ttaagcagtt tacagcagag tcaggctgct      120
      ctaacgtact atcgaaagca gcaagaaaag cttaatctag ccttgatggc agtacaaact      180
      agaactaaag agatgacatt gaatggttgt catattacta ttttacgtac ggatagatac      240
      attagtattc acgatgacga aggagaagtg atgaagattg agtaa                        285
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<210> SEQ ID NO 586
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 586
Met Gly Ile Ile Lys Lys Gln Val Lys Ala Tyr Ile Ala Leu Glu Ser
1           5           10           15
Met Ile Ala Thr Gly Ile Leu Phe Ser Ile Val Ile Leu Val Leu Ser
20           25           30
Ser Leu Gln Gln Ser Gln Ala Ala Leu Thr Tyr Tyr Arg Lys Gln Gln
35           40           45
Glu Lys Leu Asn Leu Ala Leu Met Ala Val Gln Thr Arg Thr Lys Glu
50           55           60
Met Thr Leu Asn Gly Cys His Ile Thr Ile Leu Arg Thr Asp Arg Tyr
65           70           75           80
Ile Ser Ile His Asp Asp Glu Gly Glu Val Met Lys Ile Glu
85           90

<210> SEQ ID NO 587
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 587
atgcggcaat cctattacca atttaccaaa atatgggagg tatttttttaa gatgattaat      60
caatggaaca acttacgaca caagaagcta aaaggattta ctcttctaga aatgttattg      120
gtgattcttg tcatcagtg tttgatgcta ttatttgtgc ctaatttaag caagcaaaaa      180
gacagggtta cagaaacagg taatgccgct gttgttaa at tagtggagaa tcaagcagaa      240
ctatatgaat tatctcaagg ctcaaaaacca agtttgagcc agttaaaggc agatggtagt      300
atcactgaga aacaagaaaa agcttatcaa gactattatg acaaacataa aaatgaaaaa      360
gcccgctctta gcaattaa
378

<210> SEQ ID NO 588
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 588
Met Arg Gln Ser Tyr Tyr Gln Phe Thr Lys Ile Trp Glu Val Phe Phe
1           5           10           15
Lys Met Ile Asn Gln Trp Asn Asn Leu Arg His Lys Lys Leu Lys Gly
20           25           30
Phe Thr Leu Leu Glu Met Leu Leu Val Ile Leu Val Ile Ser Val Leu
35           40           45
Met Leu Leu Phe Val Pro Asn Leu Ser Lys Gln Lys Asp Arg Val Thr
50           55           60
Glu Thr Gly Asn Ala Ala Val Val Lys Leu Val Glu Asn Gln Ala Glu
65           70           75           80
Leu Tyr Glu Leu Ser Gln Gly Ser Lys Pro Ser Leu Ser Gln Leu Lys
85           90           95
Ala Asp Gly Ser Ile Thr Glu Lys Gln Glu Lys Ala Tyr Gln Asp Tyr
100          105          110
Tyr Asp Lys His Lys Asn Glu Lys Ala Arg Leu Ser Asn
115          120          125

<210> SEQ ID NO 589
<211> LENGTH: 939
<212> TYPE: DNA

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<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 589

```
atggtacaag cattagcaaa agctattcta gcaaaagctg aacaggttca tgcacaagat      60
atttatattt tgccaagagc agatcaatat gatctttttt tacgaatagg agatgaaagg      120
agattagttg atgtttatca gagcgatcgg atggctcctc ttattagtca ctttaaattc      180
gttgcaggaa tgatagttgg tgaaaagaga cgttgtcagg tgggttcattg tgattataag      240
cttagtaaaag ataagcagtt atctttgctc ttatctagcg tgggtgatta tcgcggggcaa      300
gaaagcttag tgattcgtct gcttcatcat caaaataaaa gtgtacatta ttggtttgat      360
ggattgacaa aagtagccaa tcagggtggc ggtagagggt tgtatttatt tgcaggacca      420
gttgggtctg ggaagacaac cttgatgtac cagctgattt cgaattatca tcaagaagca      480
caggttatta gtatagaaga tcctgtagaa attaaaaatc accaaatttt acaattacaa      540
gtgaatgatg atattgggtat gacttatgac aatttgatca aactgtcttt acgcatcga      600
ccagatattt tagttattgg tgagattcga gatagtcaaa cagcaagagc cgttattagg      660
gctagtctaa caggtgccat gggttttttca acggttcacg ctaaaagtat ctcggtgtgt      720
tatgcaagat tgtagaact tgggtgtaacg aaagcagaac tgtctaattg ctagcatta      780
attgcttacc aaaggttact taatggagga gcattgattg actctactca aaacgaattt      840
gaatattatt cctcatcgaa ctggaatcaa caaattgatc agcttcttga ggcaggacat      900
ctcaatccca agcaagctaa gcttgaaaaa attatctag      939
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<210> SEQ ID NO 590

<211> LENGTH: 312

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 590

```
Met Val Gln Ala Leu Ala Lys Ala Ile Leu Ala Lys Ala Glu Gln Val
1      5      10      15
His Ala Gln Asp Ile Tyr Ile Leu Pro Arg Ala Asp Gln Tyr Asp Leu
20     25     30
Phe Leu Arg Ile Gly Asp Glu Arg Arg Leu Val Asp Val Tyr Gln Ser
35     40     45
Asp Arg Met Ala Pro Leu Ile Ser His Phe Lys Phe Val Ala Gly Met
50     55     60
Ile Val Gly Glu Lys Arg Arg Cys Gln Val Gly Ser Cys Asp Tyr Lys
65     70     75     80
Leu Ser Lys Asp Lys Gln Leu Ser Leu Arg Leu Ser Ser Val Gly Asp
85     90     95
Tyr Arg Gly Gln Glu Ser Leu Val Ile Arg Leu Leu His His Gln Asn
100    105    110
Lys Ser Val His Tyr Trp Phe Asp Gly Leu Thr Lys Val Ala Asn Gln
115    120    125
Val Gly Gly Arg Gly Leu Tyr Leu Phe Ala Gly Pro Val Gly Ser Gly
130    135    140
Lys Thr Thr Leu Met Tyr Gln Leu Ile Ser Asn Tyr His Gln Glu Ala
145    150    155    160
Gln Val Ile Ser Ile Glu Asp Pro Val Glu Ile Lys Asn His Gln Ile
165    170    175
Leu Gln Leu Gln Val Asn Asp Asp Ile Gly Met Thr Tyr Asp Asn Leu
180    185    190
Ile Lys Leu Ser Leu Arg His Arg Pro Asp Ile Leu Val Ile Gly Glu
195    200    205
Ile Arg Asp Ser Gln Thr Ala Arg Ala Val Ile Arg Ala Ser Leu Thr
210    215    220
Gly Ala Met Val Phe Ser Thr Val His Ala Lys Ser Ile Ser Gly Val
225    230    235    240
Tyr Ala Arg Leu Leu Glu Leu Gly Val Thr Lys Ala Glu Leu Ser Asn
245    250    255
Cys Leu Ala Leu Ile Ala Tyr Gln Arg Leu Leu Asn Gly Gly Ala Leu
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			260					265					270						
Ile	Asp	Ser	Thr	Gln	Asn	Glu	Phe	Glu	Tyr	Tyr	Ser	Ser	Ser	Asn	Trp				
		275					280						285						
Asn	Gln	Gln	Ile	Asp	Gln	Leu	Leu	Glu	Ala	Gly	His	Leu	Asn	Pro	Lys				
	290					295					300								
Gln	Ala	Lys	Leu	Glu	Lys	Ile	Ile												
305						310													

<210> SEQ ID NO 591

<211> LENGTH: 855

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 591

atgaagctga	aacagatgac	gaaaaaggag	gtcatgggtca	tgcttgatat	tttattctat	60
gatttcatgc	aacggggcgg	aatggcggtta	gttgccatta	gtatttttgc	tccgatttta	120
gggtattttcc	ttatttttacg	tcgtcaaaagt	ttgatgagcg	atacccttag	tcatgtttct	180
ttggctgggg	tagcgcttgg	ggtagtcctt	ggtagttcac	caaccatcac	tactattatt	240
gttggtggtt	tagctgctat	tttgttagaa	tacctgcgtg	tagtttacia	acactacatg	300
gagatttcaa	cggcgatttt	gatgtcactt	ggcttggccc	tatctctgat	tattatgagt	360
aagtcgcata	gttcatcaag	catgagttta	gaacaatacc	tttttggatc	gatcatcacg	420
attagtagtg	aacaagttgt	cgccttggtt	gctattgctg	cgattatttt	aatcttgacc	480
gttctcttca	ttagaccgat	gtacattctg	acctttgatg	aagatactgc	ttttgtagat	540
ggtttgcccg	ttcgcttgat	gtctgttcta	ttcaatatcg	tcactggggg	tgctattgct	600
ttgaccattc	cagcagcagg	agcacttttg	gtttctacca	ttatggtcct	gccagcaagt	660
atcgcaatga	gattgggtaa	aaactttaaa	acagttatct	tactgggaat	tgatcatcgt	720
tttagcggta	tgttatctgg	tattttctta	tcttatttct	ttgaaacgcc	agctagtggc	780
actattacca	tgattttcat	tagtattttc	ctcttagtta	gtctaggtgg	aatgcttaaa	840
aaacggttat	tttaa					855

<210> SEQ ID NO 592

<211> LENGTH: 284

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 592

Met	Lys	Leu	Lys	Gln	Met	Thr	Lys	Lys	Glu	Val	Met	Val	Met	Leu	Asp
1				5					10					15	
Ile	Leu	Phe	Tyr	Asp	Phe	Met	Gln	Arg	Ala	Val	Met	Ala	Val	Val	Ala
			20					25					30		
Ile	Ser	Ile	Phe	Ala	Pro	Ile	Leu	Gly	Ile	Phe	Leu	Ile	Leu	Arg	Arg
			35				40					45			
Gln	Ser	Leu	Met	Ser	Asp	Thr	Leu	Ser	His	Val	Ser	Leu	Ala	Gly	Val
			50			55				60					
Ala	Leu	Gly	Val	Val	Leu	Gly	Ile	Ser	Pro	Thr	Ile	Thr	Thr	Ile	Ile
65					70				75					80	
Val	Val	Val	Leu	Ala	Ala	Ile	Leu	Leu	Glu	Tyr	Leu	Arg	Val	Val	Tyr
				85				90						95	
Lys	His	Tyr	Met	Glu	Ile	Ser	Thr	Ala	Ile	Leu	Met	Ser	Leu	Gly	Leu
			100					105					110		
Ala	Leu	Ser	Leu	Ile	Ile	Met	Ser	Lys	Ser	His	Ser	Ser	Ser	Ser	Met
			115			120						125			
Ser	Leu	Glu	Gln	Tyr	Leu	Phe	Gly	Ser	Ile	Ile	Thr	Ile	Ser	Met	Glu
			130			135					140				
Gln	Val	Val	Ala	Leu	Phe	Ala	Ile	Ala	Ala	Ile	Ile	Leu	Ile	Leu	Thr
145				150						155				160	
Val	Leu	Phe	Ile	Arg	Pro	Met	Tyr	Ile	Leu	Thr	Phe	Asp	Glu	Asp	Thr
				165				170					175		
Ala	Phe	Val	Asp	Gly	Leu	Pro	Val	Arg	Leu	Met	Ser	Val	Leu	Phe	Asn

			180					185				190					
Ile	Val	Thr	Gly	Val	Ala	Ile	Ala	Leu	Thr	Ile	Pro	Ala	Ala	Gly	Ala		
			195				200					205					
Leu	Leu	Val	Ser	Thr	Ile	Met	Val	Leu	Pro	Ala	Ser	Ile	Ala	Met	Arg		
		210				215					220						
Leu	Gly	Lys	Asn	Phe	Lys	Thr	Val	Ile	Leu	Leu	Gly	Ile	Val	Ile	Gly		
225					230				235					240			
Phe	Ser	Gly	Met	Leu	Ser	Gly	Ile	Phe	Leu	Ser	Tyr	Phe	Phe	Glu	Thr		
			245					250					255				
Pro	Ala	Ser	Ala	Thr	Ile	Thr	Met	Ile	Phe	Ile	Ser	Ile	Phe	Leu	Leu		
		260					265					270					
Val	Ser	Leu	Gly	Gly	Met	Leu	Lys	Lys	Arg	Leu	Phe						
		275				280											

<210> SEQ ID NO 593

<211> LENGTH: 720

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 593

atgagataca	tatcagtga	aaatctctcc	tttcaatatg	aaagtgagcc	agtttttagaa	60
gggatcactt	atcatttaga	tagtggagaa	tttgtcacca	tgaccggtga	aaatggtgct	120
gcaaagtcaa	ccttaataaa	agcaacctta	ggaattttac	aaccaaaggc	tggaacgagtt	180
actattgcta	aaaaaaataa	agacggtaaa	caattaagaa	ttgcttactt	gccgcagcaa	240
gtagctagct	ttaacgctgg	ttttccatcc	accgtttacg	agtttgtcaa	atcaggtcgc	300
tacccacgta	gtggttggtt	tagacatttg	aacaaacacg	atgaagagca	tgtgcaagca	360
agcttagaag	cagtcggcat	gtgggaaaac	cgtcataaga	gaattggtag	tttatcaggt	420
ggtcaaaaac	aacgtgtggt	tattgcccg	atgtttgctt	ctgaccctga	tatttttgtg	480
ctagacgagc	caacaacggg	aatggatagc	ggtactactg	atacctttta	tgaactgatg	540
caccacagtg	cacatcaaca	tgggaaatcc	gttctgatga	ttacccatga	cccagaagaa	600
gtgaaggctt	atgctgatcg	gaacattcat	ttagtcagaa	accaaaaact	tccttggcgt	660
tgtttcaaca	ttcatgaagc	tgaaacagat	gacgaaaaag	gaggtcatgg	tcatgcttga	720

<210> SEQ ID NO 594

<211> LENGTH: 239

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 594

Met	Arg	Tyr	Ile	Ser	Val	Lys	Asn	Leu	Ser	Phe	Gln	Tyr	Glu	Ser	Glu
1				5				10					15		
Pro	Val	Leu	Glu	Gly	Ile	Thr	Tyr	His	Leu	Asp	Ser	Gly	Glu	Phe	Val
		20				25					30				
Thr	Met	Thr	Gly	Glu	Asn	Gly	Ala	Ala	Lys	Ser	Thr	Leu	Ile	Lys	Ala
		35				40					45				
Thr	Leu	Gly	Ile	Leu	Gln	Pro	Lys	Ala	Gly	Arg	Val	Thr	Ile	Ala	Lys
	50				55				60						
Lys	Asn	Lys	Asp	Gly	Lys	Gln	Leu	Arg	Ile	Ala	Tyr	Leu	Pro	Gln	Gln
65			70			75				80					
Val	Ala	Ser	Phe	Asn	Ala	Gly	Phe	Pro	Ser	Thr	Val	Tyr	Glu	Phe	Val
		85				90				95					
Lys	Ser	Gly	Arg	Tyr	Pro	Arg	Ser	Gly	Trp	Phe	Arg	His	Leu	Asn	Lys
		100				105				110					
His	Asp	Glu	Glu	His	Val	Gln	Ala	Ser	Leu	Glu	Ala	Val	Gly	Met	Trp
	115				120				125						
Glu	Asn	Arg	His	Lys	Arg	Ile	Gly	Ser	Leu	Ser	Gly	Gly	Gln	Lys	Gln
	130				135				140						
Arg	Val	Val	Ile	Ala	Arg	Met	Phe	Ala	Ser	Asp	Pro	Asp	Ile	Phe	Val
145				150					155					160	

Leu	Asp	Glu	Pro	Thr	Thr	Gly	Met	Asp	Ser	Gly	Thr	Thr	Asp	Thr	Phe
				165					170					175	
Tyr	Glu	Leu	Met	His	His	Ser	Ala	His	Gln	His	Gly	Lys	Ser	Val	Leu
			180					185					190		
Met	Ile	Thr	His	Asp	Pro	Glu	Glu	Val	Lys	Ala	Tyr	Ala	Asp	Arg	Asn
		195					200					205			
Ile	His	Leu	Val	Arg	Asn	Gln	Lys	Leu	Pro	Trp	Arg	Cys	Phe	Asn	Ile
	210					215					220				
His	Glu	Ala	Glu	Thr	Asp	Asp	Glu	Lys	Gly	Gly	His	Gly	His	Ala	
225					230					235					

<210> SEQ ID NO 595
 <211> LENGTH: 1353
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 595

ttgctaaagg	tggttcaatc	gaagtcac	aatgagggga	tactcattat	gttcttaaaa	60
atactaaaag	acgcgttaaa	gataaagact	gtacggaata	aaattttctt	tactatattt	120
atcattcttg	tattccgaat	tgggacacat	attaccgtac	ctgggtgtaa	tgccaagagc	180
ttagagcaat	taagtgaact	ccctttctta	aatatgtaa	acttagttag	tggtaatgcg	240
atgagaaatt	tctcagtatt	ttcaatgggg	gttagcccat	atattactgc	ttctatcggt	300
gttcagttat	tgcagatgga	tattttac	aagtttggtg	agtggggcaa	acaaggtgag	360
gttggacgtc	gtaaattaaa	tcaagcgacg	cgctatattt	cacttgtttt	ggcttttgcc	420
caatccattg	gtatcactgc	agggtttaat	actttgtcga	acgttgca	tgtaagaca	480
ccagacatca	aaacatattt	actgatcggg	gcattactga	caacaggtag	cgttattggt	540
acctggcttg	gagaacaaat	cacagataaa	ggatttggtg	atggcgatc	aatgattatc	600
tttgcgggta	ttatttcgtc	tattccaagt	gcaattgcaa	caattcgtga	agactatttt	660
gtaaatgtta	aggcaagtga	tttacctcg	tcttatctca	ttgttgggat	tttaatcata	720
gctgttcttg	ctattgtttt	ctttacaaca	tatgtccaac	aagcggaata	taaaattcca	780
atccaataca	caaagcta	gcaaggtgca	cctacaagtt	catatcttcc	attaaaagta	840
aatccagccg	gcgttattcc	cggtatcttt	gctagctcga	ttacaactat	ccaagtacg	900
attattcctt	ttgttcaaaa	tggtagagat	ttaccgtggt	taaaccgttt	gcaagaaatt	960
tttaattatc	aaactccagt	cggaatgata	gtttacgcct	tgttgattat	attgttctca	1020
ttcttctata	cctttgtaca	agttaatcct	gagaagacag	cagaaaatct	tcagaagaat	1080
tcctcatata	taccaagtgt	tcgccctgga	cgtgagacag	aacaatttat	gtccgcattg	1140
ctaaaaaac	tagcaaccgt	aggagctatc	ttcttagcat	ttatctcttt	agcgccaata	1200
gcagcacaac	aagctctcaa	cctttcttct	agtattgctt	taggtggaac	tagtttgctc	1260
attttgattt	caactgggat	cgaaggtatg	aaacagcttg	agggatatct	tctaaagaga	1320
aaatatgtcg	gatttatgaa	tacagcagaa	tag			1353

<210> SEQ ID NO 596
 <211> LENGTH: 450
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 596

Met	Leu	Lys	Val	Val	Gln	Ser	Lys	Ser	Ser	Asn	Glu	Gly	Ile	Leu	Ile
1			5					10					15		
Met	Phe	Leu	Lys	Ile	Leu	Lys	Asp	Ala	Leu	Lys	Ile	Lys	Thr	Val	Arg
		20					25					30			
Asn	Lys	Ile	Phe	Phe	Thr	Ile	Phe	Ile	Ile	Leu	Val	Phe	Arg	Ile	Gly
	35					40					45				
Thr	His	Ile	Thr	Val	Pro	Gly	Val	Asn	Ala	Lys	Ser	Leu	Glu	Gln	Leu
	50					55					60				
Ser	Glu	Leu	Pro	Phe	Leu	Asn	Met	Leu	Asn	Leu	Val	Ser	Gly	Asn	Ala
65					70					75				80	
Met	Arg	Asn	Phe	Ser	Val	Phe	Ser	Met	Gly	Val	Ser	Pro	Tyr	Ile	Thr
			85						90					95	

cctgtgaata	agacaccaag	cataggggct	atcgcttggg	ttgataaaaa	cgcttatcag	360
tcaaatgctg	cttacgggtca	tgtagcatgg	gtagctgata	tccgtggaga	cactgtcact	420
atcgaagagt	ataattacaa	cgctggacaa	ggccctgaaa	gataccataa	gcgtcaaatt	480
ccaaaatctc	aggtaagtgg	ttatatccat	tttaaagact	tatcatctca	gacaagtcac	540
tcctacccaa	gacaactaaa	acacatttct	caagcttcat	ttgacccttc	tggaacttat	600
cactttacaa	ccagattacc	agtcaaagga	caaaccagta	tcgatagccc	tgatcttgct	660
tactatgaag	caggtcaatc	tgtttattac	gataaagtcg	tgactgctgg	aggttataca	720
tggttagct	acctcagttt	ttctggaaac	cgacgctata	ttcccattaa	agagcccgcg	780
cagtctgtgg	ttcaaaatga	caatacaaaa	ccttccatta	aggtcggtga	tactgttacc	840
ttccctggcg	tttttcgtgt	agatcagctt	gttaataaatt	tgatcggtta	taaagaatta	900
gccggaggag	acccaactcc	actaaactgg	attgatccca	caccattaga	tgaaacagat	960
aaccaaggaa	aagtttttagg	agatcaaatt	ctccgtgtgg	gtgaatattt	tatcgtcact	1020
ggtagttata	aagtattaaa	aattgatcaa	ccaagtaatg	gtattttatgt	tcaaacgga	1080
tctcgtggaa	catgggtaaa	tgctgataaa	gctaacaaat	tatag		1125

<210> SEQ ID NO 598

<211> LENGTH: 374

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 598

Met	Lys	Lys	Phe	His	Arg	Phe	Leu	Val	Ser	Gly	Val	Ile	Leu	Leu	Gly
1				5					10					15	
Phe	Asn	Gly	Leu	Val	Pro	Thr	Met	Pro	Ser	Thr	Leu	Ile	Ser	Gln	Gln
			20					25					30		
Glu	Asn	Leu	Val	His	Ala	Ala	Val	Leu	Gly	Asp	Asn	Tyr	Pro	Ser	Lys
			35				40					45			
Trp	Lys	Lys	Gly	Asn	Gly	Ile	Asp	Ser	Trp	Asn	Met	Tyr	Ile	Arg	Gln
	50				55					60					
Cys	Thr	Ser	Phe	Ala	Ala	Phe	Arg	Leu	Ser	Ser	Ala	Asn	Gly	Phe	Gln
65				70					75					80	
Leu	Pro	Lys	Gly	Tyr	Gly	Asn	Ala	Cys	Thr	Trp	Gly	His	Ile	Ala	Lys
			85					90					95		
Asn	Gln	Gly	Tyr	Pro	Val	Asn	Lys	Thr	Pro	Ser	Ile	Gly	Ala	Ile	Ala
			100					105					110		
Trp	Phe	Asp	Lys	Asn	Ala	Tyr	Gln	Ser	Asn	Ala	Ala	Tyr	Gly	His	Val
		115					120					125			
Ala	Trp	Val	Ala	Asp	Ile	Arg	Gly	Asp	Thr	Val	Thr	Ile	Glu	Glu	Tyr
		130				135						140			
Asn	Tyr	Asn	Ala	Gly	Gln	Gly	Pro	Glu	Arg	Tyr	His	Lys	Arg	Gln	Ile
145				150					155					160	
Pro	Lys	Ser	Gln	Val	Ser	Gly	Tyr	Ile	His	Phe	Lys	Asp	Leu	Ser	Ser
			165					170					175		
Gln	Thr	Ser	His	Ser	Tyr	Pro	Arg	Gln	Leu	Lys	His	Ile	Ser	Gln	Ala
			180					185					190		
Ser	Phe	Asp	Pro	Ser	Gly	Thr	Tyr	His	Phe	Thr	Thr	Arg	Leu	Pro	Val
		195					200					205			
Lys	Gly	Gln	Thr	Ser	Ile	Asp	Ser	Pro	Asp	Leu	Ala	Tyr	Tyr	Glu	Ala
	210					215					220				
Gly	Gln	Ser	Val	Tyr	Tyr	Asp	Lys	Val	Val	Thr	Ala	Gly	Gly	Tyr	Thr
225				230					235					240	
Trp	Leu	Ser	Tyr	Leu	Ser	Phe	Ser	Gly	Asn	Arg	Arg	Tyr	Ile	Pro	Ile
			245					250					255		
Lys	Glu	Pro	Ala	Gln	Ser	Val	Val	Gln	Asn	Asp	Asn	Thr	Lys	Pro	Ser
			260					265					270		
Ile	Lys	Val	Gly	Asp	Thr	Val	Thr	Phe	Pro	Gly	Val	Phe	Arg	Val	Asp
		275				280						285			
Gln	Leu	Val	Asn	Asn	Leu	Ile	Val	Asn	Lys	Glu	Leu	Ala	Gly	Gly	Asp

290	295	300
Pro Thr Pro Leu Asn Trp	Ile Asp Pro Thr Pro	Leu Asp Glu Thr Asp
305	310	315
Asn Gln Gly Lys Val Leu	Gly Asp Gln Ile Leu	Arg Val Gly Glu Tyr
325	330	335
Phe Ile Val Thr Gly Ser Tyr Lys	Val Leu Lys Ile Asp	Gln Pro Ser
340	345	350
Asn Gly Ile Tyr Val Gln Ile	Gly Ser Arg Gly Thr	Trp Val Asn Ala
355	360	365
Asp Lys Ala Asn Lys Leu		
370		

<210> SEQ ID NO 599

<211> LENGTH: 1197

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 599

atgaaaaaaa	gaattttatc	agcagttctt	gtaagtgggtg	ttaccctcgg	agcagctaca	60
actgtaggag	cggaggattt	aagtactaag	attgctaagc	aagattctat	tatctcaa	120
ctgactacag	agcaaaaagc	tgacagaa	caagtttcag	cggtacaggc	tcaagtaagt	180
tcactacaat	ctgaacaaga	taaactgacc	gcaagaaata	cagaacttga	ggcgctttca	240
aagcgatttg	agcaagaaat	taaggctcta	acaagtcaaa	ttgttgctcg	taatgaaaaa	300
ttaaaaaatc	aagctcgtag	tgcttataaa	aacaatgaaa	cttctgggta	tattaatgca	360
cttttggaatt	ctaaatcaat	ttctgatggt	gtaaaccggt	tagtagcaat	taatagagct	420
gtctctgcta	acgctaaaatt	gtagaacia	caaaaagctg	ataaagtttc	ccttgaagaa	480
aagcaagctg	ctaaccaaaac	agctattaat	accattgccg	ctaatatggc	aatggctgaa	540
gaaaacaaaa	atacattacg	tactcaacia	gctaatttgg	tagctgcaac	tgcaaattta	600
gctctccaat	tagcatctgc	tactgaagat	aaagctaatt	tggtagctca	aaaagaagct	660
gcagaaaaag	ctgctgctga	agccttagca	caagaacagg	ctgctaaagt	taaggcacaa	720
gaacaggctg	cacaacaagc	agcatctggt	gaagcagcaa	aatctgctat	tactccagca	780
ccacaagcta	ctccggcagc	gcaaagtagt	aatgctattg	aaccagctgc	actcacggct	840
ccggcagctc	cttctgcagg	accacaaaca	tcatatgatt	cttctaatac	ttatccagtt	900
ggacaatgca	catggggagc	taaattctta	gctccttggg	caggaaataa	ttggggaaat	960
gggtggtcaat	gggcttatag	tgctcaagca	gctgggtatc	gtactgggtc	aacgccgatg	1020
gtagggtgcga	ttgccgtttg	gaacgatggg	ggttatggac	atgtcgccgt	tgtagttgag	1080
gttcaaaagt	cctcaagtat	tcgtgtgatg	gagtctaact	acagtggtag	acagtacatt	1140
gctgaccacc	gtggctgggt	taatccaaca	ggtgttacat	ttatttatcc	acactaa	1197

<210> SEQ ID NO 600

<211> LENGTH: 398

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 600

Met Lys Lys Arg Ile Leu Ser Ala Val Leu Val Ser Gly Val Thr Leu	
1	15
Gly Ala Ala Thr Thr Val Gly Ala Glu Asp Leu Ser Thr Lys Ile Ala	
20	30
Lys Gln Asp Ser Ile Ile Ser Asn Leu Thr Thr Glu Gln Lys Ala Ala	
35	45
Gln Asn Gln Val Ser Ala Leu Gln Ala Gln Val Ser Ser Leu Gln Ser	
50	60
Glu Gln Asp Lys Leu Thr Ala Arg Asn Thr Glu Leu Glu Ala Leu Ser	
65	80
Lys Arg Phe Glu Gln Glu Ile Lys Ala Leu Thr Ser Gln Ile Val Ala	
85	95
Arg Asn Glu Lys Leu Lys Asn Gln Ala Arg Ser Ala Tyr Lys Asn Asn	
100	110

Glu	Thr	Ser	Gly	Tyr	Ile	Asn	Ala	Leu	Leu	Asn	Ser	Lys	Ser	Ile	Ser	
		115					120					125				
Asp	Val	Val	Asn	Arg	Leu	Val	Ala	Ile	Asn	Arg	Ala	Val	Ser	Ala	Asn	
		130					135					140				
Ala	Lys	Leu	Leu	Glu	Gln	Gln	Lys	Ala	Asp	Lys	Val	Ser	Leu	Glu	Glu	
				150						155					160	
Lys	Gln	Ala	Ala	Asn	Gln	Thr	Ala	Ile	Asn	Thr	Ile	Ala	Ala	Asn	Met	
				165						170					175	
Ala	Met	Ala	Glu	Glu	Asn	Gln	Asn	Thr	Leu	Arg	Thr	Gln	Gln	Ala	Asn	
			180					185					190			
Leu	Val	Ala	Ala	Thr	Ala	Asn	Leu	Ala	Leu	Gln	Leu	Ala	Ser	Ala	Thr	
		195					200					205				
Glu	Asp	Lys	Ala	Asn	Leu	Val	Ala	Gln	Lys	Glu	Ala	Ala	Glu	Lys	Ala	
	210					215					220					
Ala	Ala	Glu	Ala	Leu	Ala	Gln	Glu	Gln	Ala	Ala	Lys	Val	Lys	Ala	Gln	
	225				230					235					240	
Glu	Gln	Ala	Ala	Gln	Gln	Ala	Ala	Ser	Val	Glu	Ala	Ala	Lys	Ser	Ala	
				245					250						255	
Ile	Thr	Pro	Ala	Pro	Gln	Ala	Thr	Pro	Ala	Ala	Gln	Ser	Ser	Asn	Ala	
			260					265						270		
Ile	Glu	Pro	Ala	Ala	Leu	Thr	Ala	Pro	Ala	Ala	Pro	Ser	Ala	Gly	Pro	
		275					280					285				
Gln	Thr	Ser	Tyr	Asp	Ser	Ser	Asn	Thr	Tyr	Pro	Val	Gly	Gln	Cys	Thr	
	290					295					300					
Trp	Gly	Ala	Lys	Ser	Leu	Ala	Pro	Trp	Ala	Gly	Asn	Asn	Trp	Gly	Asn	
	305				310					315					320	
Gly	Gly	Gln	Trp	Ala	Tyr	Ser	Ala	Gln	Ala	Ala	Gly	Tyr	Arg	Thr	Gly	
			325					330						335		
Ser	Thr	Pro	Met	Val	Gly	Ala	Ile	Ala	Val	Trp	Asn	Asp	Gly	Gly	Tyr	
			340					345					350			
Gly	His	Val	Ala	Val	Val	Val	Glu	Val	Gln	Ser	Ala	Ser	Ser	Ile	Arg	
		355					360					365				
Val	Met	Glu	Ser	Asn	Tyr	Ser	Gly	Arg	Gln	Tyr	Ile	Ala	Asp	His	Arg	
	370					375					380					
Gly	Trp	Phe	Asn	Pro	Thr	Gly	Val	Thr	Phe	Ile	Tyr	Pro	His			
	385				390					395						

<210> SEQ ID NO 601

<211> LENGTH: 1287

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 601

atgagaaaat	tattagcggc	tatgttaatg	actttttttc	tgactccttt	accagtgatt	60
agtacagaaa	aaaaacttat	attttcaaaa	aatgctgttt	atcaattgaa	acaagatgtc	120
gttcaatcaa	cacaattcta	taatcaaata	ccctctaata	caaatactta	tcaagaaacg	180
tgtgcctata	aagacagtga	tttaactcta	ccagcaggaa	gattaggtgt	aaatcaacca	240
ttacttatta	aatcgcttgt	gcttaacaaa	gaatctttac	cggtttttga	gttagctgat	300
ggtacctatg	ttgaggctaa	tcgacaattg	atztatgacg	atattgtact	taatcaagta	360
gatatagata	gctatttttg	gacacaaaag	aaacttaggc	tttattcagc	cccttatggt	420
ttaggtagcg	aaacaattcc	ttcttctttt	ttatttgctc	aaaaagttca	tgccactcaa	480
atggcacaaa	caaaccatgg	aacttattat	cttattgatg	ataagggctg	ggcatcacaa	540
gaagatctag	ttcaatttga	taaccgcatg	ttaaaagtcc	aggaaatgct	cttacaaaaa	600
tataataacc	caaattattc	aatttttgta	aagcaactca	acacacaaac	aagtgtctggt	660
attaatgctg	ataaaaaaat	gtatgctgca	agtatctcga	agttagcacc	actttatatt	720
gttcaaaaaa	aattacaaaa	aaagaaatta	gcagagaata	aaactttgac	ttatactaaa	780
gatgttaatc	attttttatg	agactatgat	ccattgggaa	gtggtaaaat	tagtaaaaata	840
gctgataata	aagattatcg	tgttgaagac	ctactgaaag	ctgtagcaca	acaatcggat	900

aatgtagcaa	ctaataat	tttt	aggttatt	at	ctatgtcatc	agtatgataa	agctttccgc	960
tcagagataa	aagctttatc	aggatatcgat	tgggatatgg	agcagcgctt	attaacttct			1020
cgttcagctg	caaatatgat	ggaagctatt	tatcatcaaa	aaggccaaat	tatttcttac			1080
ctttcaaata	cgaatttga	tcaacaacgt	atcacaaaaa	atattactgt	tccagttgca			1140
cataaaattg	gtgatgctta	tgattataaaa	catgacgttg	ctattgttta	cggtaatact			1200
ccatttat	tttt	tgtctat	tttt	tacaaataaa	tcaacctatg	aagatattac	ggctattgca	1260
gatgacgt	ttt	atgg	tatttt	aaaatga				1287

<210> SEQ ID NO 602

<211> LENGTH: 428

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 602

Met	Arg	Lys	Leu	Leu	Ala	Ala	Met	Leu	Met	Thr	Phe	Phe	Leu	Thr	Pro
1			5					10					15		
Leu	Pro	Val	Ile	Ser	Thr	Glu	Lys	Lys	Leu	Ile	Phe	Ser	Lys	Asn	Ala
			20					25					30		
Val	Tyr	Gln	Leu	Lys	Gln	Asp	Val	Val	Gln	Ser	Thr	Gln	Phe	Tyr	Asn
		35					40					45			
Gln	Ile	Pro	Ser	Asn	Pro	Asn	Leu	Tyr	Gln	Glu	Thr	Cys	Ala	Tyr	Lys
	50					55					60				
Asp	Ser	Asp	Leu	Thr	Leu	Pro	Ala	Gly	Arg	Leu	Gly	Val	Asn	Gln	Pro
65					70				75					80	
Leu	Leu	Ile	Lys	Ser	Leu	Val	Leu	Asn	Lys	Glu	Ser	Leu	Pro	Val	Phe
			85					90					95		
Glu	Leu	Ala	Asp	Gly	Thr	Tyr	Val	Glu	Ala	Asn	Arg	Gln	Leu	Ile	Tyr
		100					105					110			
Asp	Asp	Ile	Val	Leu	Asn	Gln	Val	Asp	Ile	Asp	Ser	Tyr	Phe	Trp	Thr
	115					120					125				
Gln	Lys	Lys	Leu	Arg	Leu	Tyr	Ser	Ala	Pro	Tyr	Val	Leu	Gly	Thr	Gln
	130					135					140				
Thr	Ile	Pro	Ser	Ser	Phe	Leu	Phe	Ala	Gln	Lys	Val	His	Ala	Thr	Gln
145					150					155					160
Met	Ala	Gln	Thr	Asn	His	Gly	Thr	Tyr	Tyr	Leu	Ile	Asp	Asp	Lys	Gly
			165					170						175	
Trp	Ala	Ser	Gln	Glu	Asp	Leu	Val	Gln	Phe	Asp	Asn	Arg	Met	Leu	Lys
			180					185					190		
Val	Gln	Glu	Met	Leu	Leu	Gln	Lys	Tyr	Asn	Asn	Pro	Asn	Tyr	Ser	Ile
	195					200						205			
Phe	Val	Lys	Gln	Leu	Asn	Thr	Gln	Thr	Ser	Ala	Gly	Ile	Asn	Ala	Asp
	210					215					220				
Lys	Lys	Met	Tyr	Ala	Ala	Ser	Ile	Ser	Lys	Leu	Ala	Pro	Leu	Tyr	Ile
225					230					235				240	
Val	Gln	Lys	Gln	Leu	Gln	Lys	Lys	Lys	Leu	Ala	Glu	Asn	Lys	Thr	Leu
			245					250						255	
Thr	Tyr	Thr	Lys	Asp	Val	Asn	His	Phe	Tyr	Gly	Asp	Tyr	Asp	Pro	Leu
			260					265					270		
Gly	Ser	Gly	Lys	Ile	Ser	Lys	Ile	Ala	Asp	Asn	Lys	Asp	Tyr	Arg	Val
	275					280						285			
Glu	Asp	Leu	Leu	Lys	Ala	Val	Ala	Gln	Gln	Ser	Asp	Asn	Val	Ala	Thr
	290					295				300					
Asn	Ile	Leu	Gly	Tyr	Tyr	Leu	Cys	His	Gln	Tyr	Asp	Lys	Ala	Phe	Arg
305					310					315					320
Ser	Glu	Ile	Lys	Ala	Leu	Ser	Gly	Ile	Asp	Trp	Asp	Met	Glu	Gln	Arg
			325					330					335		
Leu	Leu	Thr	Ser	Arg	Ser	Ala	Ala	Asn	Met	Met	Glu	Ala	Ile	Tyr	His
			340					345					350		

Gln	Lys	Gly	Gln	Ile	Ile	Ser	Tyr	Leu	Ser	Asn	Thr	Glu	Phe	Asp	Gln
		355					360					365			
Gln	Arg	Ile	Thr	Lys	Asn	Ile	Thr	Val	Pro	Val	Ala	His	Lys	Ile	Gly
	370					375					380				
Asp	Ala	Tyr	Asp	Tyr	Lys	His	Asp	Val	Ala	Ile	Val	Tyr	Gly	Asn	Thr
385					390					395					400
Pro	Phe	Ile	Leu	Ser	Ile	Phe	Thr	Asn	Lys	Ser	Thr	Tyr	Glu	Asp	Ile
			405					410						415	
Thr	Ala	Ile	Ala	Asp	Asp	Val	Tyr	Gly	Ile	Leu	Lys				
			420					425							

<210> SEQ ID NO 603

<211> LENGTH: 2577

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 603

atgaaaaata	ataataaatg	gataattgct	ggacttgcta	gttttttgtt	ccctcttagt	60
attatattta	tcatccttct	atcgatgggc	atttattata	atagtataaa	aacaattcta	120
gctagtgatg	cttttcatca	gtatgttatt	tttgcgagc	actttcgtaa	catcatgcac	180
ggttctgata	gtttttttta	tacctttaca	agcggactag	ggataaattt	ttatgcttta	240
atgtgttatt	atcttggcag	tttcttttct	ccattacttt	tcttttttaa	tttaacctct	300
atgccagatg	ctatctatct	gtttaccttg	ataaaaattg	ggttaatagg	attagctgca	360
tgctattctt	ttcatagatt	atatccaaaa	atcagtgctt	tcttgatgat	ttccatctca	420
gttttttata	gcttaaatgag	cttcttgaca	agtcaaatgg	aactaaattc	ttgggttagat	480
gttttcatct	ttcttccact	tgttatactt	ggattaaata	aacttatcac	agaaaaataa	540
accagaactt	attatctttc	gatatcatta	ttattcattc	aaaattacta	ctttggctac	600
atgattgctc	ttttttgtat	tctttacgcc	ttagtttgct	ttttacgtct	caatgatttt	660
aacaaaatgt	ttatcgcttt	tgttaggttt	acagctgtgt	caatatgtgc	tgctttaaca	720
agtgtcttag	taatacttcc	tacctatcta	gatttgtcaa	cttatggaga	gaatctatcc	780
ccgataaaac	agttagttac	gaacaatgct	tggtttttgg	atatacctgc	taagctctca	840
ataggagtgt	acgatactac	caagtttaat	gctctgccta	tgatttacgt	aggattatct	900
cccctaattg	ttagtgttat	ttattttact	ttagaaagta	tccctttaaa	aataaaaatta	960
gccaatgcct	gcttggtaac	ttttattata	ataagttttt	acctacagcc	acttgatctt	1020
ttttggcagg	ggatgcactc	accaaataat	tttttgcata	gctacgcttg	gtctttttcc	1080
atagttatcc	tattactcgc	atgtgagact	ctctctcgac	taaaagaagt	gactcaaata	1140
aaagcagggt	ttgcttttat	tttcctcatt	atactgacat	ctcttcctta	tagcttttct	1200
caacaatata	attttctacc	tttaactctt	tttttactta	gtgttttttt	attattaggt	1260
tatactatct	cactattttc	gtttagaaat	tctcaaattc	catctacttt	tatttctgct	1320
ttcatactta	tctttagcct	tcttgaatca	gggttaaaca	cctactacca	gcttcaagga	1380
attaataagg	agtggggatt	cccatcacga	cagatatata	atagtcaatt	aaaggatatt	1440
aacaaccttg	tcaactctgt	gtcaaaaaat	agtcaacctt	tttttagaat	ggaaaggcta	1500
cttcccaaaa	cagggaacga	tagcatgaaa	tttaattatt	acggcatttc	acaattttcc	1560
tctgtaagaa	atagactatc	tagttcttta	ttggatcgat	tgggatttca	gtctaaaggc	1620
acaaatttaa	accttagata	ccaaaacaat	actattatta	tggacagtct	acttggtata	1680
aaatataatc	ttagcgaagg	acctccaaat	aaatttggat	ttacaaaact	aaaaactagc	1740
gggaataact	ctctttatca	aaatcactat	agtagccctt	tagctatatt	aacacgtaat	1800
gtttacaaaag	atgtcaacct	aaatgtcaat	acccttgata	accaaaccac	attacttaac	1860
caactaagtg	ggaaatcttt	aacctatttt	aacttacagc	cagctcaact	tatttctggt	1920
gctaataaat	ttaacggaca	aatatctgca	caagcttctg	attatcaaaa	ctccgttacc	1980
cttaattatc	aaattaacat	ccctaaacat	agtcaactct	atgttagcat	acccaatatt	2040
atatttttcaa	atcctgatgc	taaagagatg	cgtattcaga	cagataatca	taatttcata	2100
tatactacag	ataacgctta	ctcttttttt	gatttaggat	atttcgccga	tgccaaagtt	2160
gctacatttt	cgtttggttt	tccaaaaaat	aaacaaatta	gttttaagga	acctcatttt	2220
tatagtgtgt	ctattgaatc	ttaccttgaa	gcaattgaata	gcattaaaca	aaaaaatgtt	2280
catacttacy	ctaaaagtaa	tacggtaatc	actgattata	attcaaaaac	gaaaggttct	2340
cttatttttta	cacttcctta	cgataaaagg	tggtcagcac	aaaaagatgg	gaaaaatctt	2400
ccagtcaaaa	aagcacaagg	aggattttcta	tcagttacta	ttcctaaagg	aaagggacgt	2460

gttatccctta cctttattcc taatgggtttt aaattagggt tatctctatc ttgtgtagga 2520
 attatcgctt atatgctttt gtataagtac atagatataa agtctaaatt acttttag 2577

<210> SEQ ID NO 604
 <211> LENGTH: 858
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 604

Met	Lys	Asn	Asn	Asn	Lys	Trp	Ile	Ile	Ala	Gly	Leu	Ala	Ser	Phe	Leu
1			5						10					15	
Phe	Pro	Leu	Ser	Ile	Ile	Phe	Ile	Ile	Leu	Leu	Ser	Met	Gly	Ile	Tyr
		20						25					30		
Tyr	Asn	Ser	Asp	Lys	Thr	Ile	Leu	Ala	Ser	Asp	Ala	Phe	His	Gln	Tyr
		35					40					45			
Val	Ile	Phe	Ala	Gln	Asn	Phe	Arg	Asn	Ile	Met	His	Gly	Ser	Asp	Ser
	50					55				60					
Phe	Phe	Tyr	Thr	Phe	Thr	Ser	Gly	Leu	Gly	Ile	Asn	Phe	Tyr	Ala	Leu
65					70					75					80
Met	Cys	Tyr	Tyr	Leu	Gly	Ser	Phe	Phe	Ser	Pro	Leu	Leu	Phe	Phe	Phe
				85					90					95	
Asn	Leu	Thr	Ser	Met	Pro	Asp	Ala	Ile	Tyr	Leu	Phe	Thr	Leu	Ile	Lys
			100					105					110		
Phe	Gly	Leu	Ile	Gly	Leu	Ala	Ala	Cys	Tyr	Ser	Phe	His	Arg	Leu	Tyr
	115					120						125			
Pro	Lys	Ile	Ser	Ala	Phe	Leu	Met	Ile	Ser	Ile	Ser	Val	Phe	Tyr	Ser
	130					135					140				
Leu	Met	Ser	Phe	Leu	Thr	Ser	Gln	Met	Glu	Leu	Asn	Ser	Trp	Leu	Asp
145					150					155					160
Val	Phe	Ile	Leu	Leu	Pro	Leu	Val	Ile	Leu	Gly	Leu	Asn	Lys	Leu	Ile
			165						170					175	
Thr	Glu	Asn	Lys	Thr	Arg	Thr	Tyr	Tyr	Leu	Ser	Ile	Ser	Leu	Leu	Phe
			180					185					190		
Ile	Gln	Asn	Tyr	Tyr	Phe	Gly	Tyr	Met	Ile	Ala	Leu	Phe	Cys	Ile	Leu
	195					200						205			
Tyr	Ala	Leu	Val	Cys	Leu	Leu	Arg	Leu	Asn	Asp	Phe	Asn	Lys	Met	Phe
	210					215					220				
Ile	Ala	Phe	Val	Arg	Phe	Thr	Ala	Val	Ser	Ile	Cys	Ala	Ala	Leu	Thr
225					230					235					240
Ser	Ala	Leu	Val	Ile	Leu	Pro	Thr	Tyr	Leu	Asp	Leu	Ser	Thr	Tyr	Gly
			245						250					255	
Glu	Asn	Leu	Ser	Pro	Ile	Lys	Gln	Leu	Val	Thr	Asn	Asn	Ala	Trp	Phe
		260						265					270		
Leu	Asp	Ile	Pro	Ala	Lys	Leu	Ser	Ile	Gly	Val	Tyr	Asp	Thr	Thr	Lys
	275						280				285				
Phe	Asn	Ala	Leu	Pro	Met	Ile	Tyr	Val	Gly	Leu	Phe	Pro	Leu	Met	Leu
	290					295					300				
Ser	Val	Ile	Tyr	Phe	Thr	Leu	Glu	Ser	Ile	Pro	Leu	Lys	Ile	Lys	Leu
305					310					315					320
Ala	Asn	Ala	Cys	Leu	Leu	Thr	Phe	Ile	Ile	Ile	Ser	Phe	Tyr	Leu	Gln
			325						330					335	
Pro	Leu	Asp	Leu	Phe	Trp	Gln	Gly	Met	His	Ser	Pro	Asn	Met	Phe	Leu
		340					345						350		
His	Arg	Tyr	Ala	Trp	Ser	Phe	Ser	Ile	Val	Ile	Leu	Leu	Ala	Cys	
	355					360					365				
Glu	Thr	Leu	Ser	Arg	Leu	Lys	Glu	Val	Thr	Gln	Ile	Lys	Ala	Gly	Phe
	370					375					380				
Ala	Phe	Ile	Phe	Leu	Ile	Ile	Leu	Thr	Ser	Leu	Pro	Tyr	Ser	Phe	Ser

385					390					395					400
Gln	Gln	Tyr	Asn	Phe	Leu	Pro	Leu	Thr	Leu	Phe	Leu	Leu	Ser	Val	Phe
				405					410					415	
Leu	Leu	Leu	Gly	Tyr	Thr	Ile	Ser	Leu	Phe	Ser	Phe	Arg	Asn	Ser	Gln
			420					425					430		
Ile	Pro	Ser	Thr	Phe	Ile	Ser	Ala	Phe	Ile	Leu	Ile	Phe	Ser	Leu	Leu
		435					440					445			
Glu	Ser	Gly	Leu	Asn	Thr	Tyr	Tyr	Gln	Leu	Gln	Gly	Ile	Asn	Lys	Glu
	450					455				460					
Trp	Gly	Phe	Pro	Ser	Arg	Gln	Ile	Tyr	Asn	Ser	Gln	Leu	Lys	Asp	Ile
465					470					475				480	
Asn	Asn	Leu	Val	Asn	Ser	Val	Ser	Lys	Asn	Ser	Gln	Pro	Phe	Phe	Arg
				485					490					495	
Met	Glu	Arg	Leu	Pro	Gln	Thr	Gly	Asn	Asp	Ser	Met	Lys	Phe	Asn	
			500				505					510			
Tyr	Tyr	Gly	Ile	Ser	Gln	Phe	Ser	Ser	Val	Arg	Asn	Arg	Leu	Ser	Ser
		515					520					525			
Ser	Leu	Leu	Asp	Arg	Leu	Gly	Phe	Gln	Ser	Lys	Gly	Thr	Asn	Leu	Asn
	530					535					540				
Leu	Arg	Tyr	Gln	Asn	Asn	Thr	Ile	Ile	Met	Asp	Ser	Leu	Leu	Gly	Ile
545					550					555				560	
Lys	Tyr	Asn	Leu	Ser	Glu	Gly	Pro	Pro	Asn	Lys	Phe	Gly	Phe	Thr	Lys
				565					570					575	
Leu	Lys	Thr	Ser	Gly	Asn	Thr	Thr	Leu	Tyr	Gln	Asn	His	Tyr	Ser	Ser
			580					585					590		
Pro	Leu	Ala	Ile	Leu	Thr	Arg	Asn	Val	Tyr	Lys	Asp	Val	Asn	Leu	Asn
		595					600					605			
Val	Asn	Thr	Leu	Asp	Asn	Gln	Thr	Lys	Leu	Leu	Asn	Gln	Leu	Ser	Gly
	610					615					620				
Lys	Ser	Leu	Thr	Tyr	Phe	Asn	Leu	Gln	Pro	Ala	Gln	Leu	Ile	Ser	Gly
625					630					635				640	
Ala	Asn	Gln	Phe	Asn	Gly	Gln	Ile	Ser	Ala	Gln	Ala	Ser	Asp	Tyr	Gln
				645					650					655	
Asn	Ser	Val	Thr	Leu	Asn	Tyr	Gln	Ile	Asn	Ile	Pro	Lys	His	Ser	Gln
			660					665					670		
Leu	Tyr	Val	Ser	Ile	Pro	Asn	Ile	Ile	Phe	Ser	Asn	Pro	Asp	Ala	Lys
		675					680					685			
Glu	Met	Arg	Ile	Gln	Thr	Asp	Asn	His	Asn	Phe	Ile	Tyr	Thr	Thr	Asp
	690					695					700				
Asn	Ala	Tyr	Ser	Phe	Phe	Asp	Leu	Gly	Tyr	Phe	Ala	Asp	Ala	Lys	Val
705					710					715				720	
Ala	Thr	Phe	Ser	Phe	Val	Phe	Pro	Lys	Asn	Lys	Gln	Ile	Ser	Phe	Lys
				725					730					735	
Glu	Pro	His	Phe	Tyr	Ser	Leu	Ser	Ile	Glu	Ser	Tyr	Leu	Glu	Ala	Met
			740					745					750		
Asn	Ser	Ile	Lys	Gln	Lys	Asn	Val	His	Thr	Tyr	Ala	Lys	Ser	Asn	Thr
		755					760					765			
Val	Ile	Thr	Asp	Tyr	Asn	Ser	Lys	Thr	Lys	Gly	Ser	Leu	Ile	Phe	Thr
	770					775					780				
Leu	Pro	Tyr	Asp	Lys	Gly	Trp	Ser	Ala	Gln	Lys	Asp	Gly	Lys	Asn	Leu
785					790					795				800	
Pro	Val	Lys	Lys	Ala	Gln	Gly	Gly	Phe	Leu	Ser	Val	Thr	Ile	Pro	Lys
				805					810					815	
Gly	Lys	Gly	Arg	Val	Ile	Leu	Thr	Phe	Ile	Pro	Asn	Gly	Phe	Lys	Leu
			820					825					830		
Gly	Leu	Ser	Leu	Ser	Cys	Val	Gly	Ile	Ile	Ala	Tyr	Met	Leu	Leu	Tyr
		835					840					845			

Lys Tyr Ile Asp Ile Lys Ser Lys Leu Leu
850 855

<210> SEQ ID NO 605
<211> LENGTH: 864
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 605

ttggaaggta	ttttttatgc	acttattccc	atgtttacat	ggggaagcat	tggatttggt	60
agtaacaaaa	ttggaggaaa	accttcgcaa	caaactctag	gaatgacttt	tggggcttta	120
ttattttcat	tagctgtttg	gttaattggt	agacctgaga	tgacactgca	actttggctt	180
tttggaatat	tgggtggttt	tatctggtca	attggtcaaa	ctggtcaatt	tcatgccatg	240
caatacatgg	gagtctccgt	tgccaatcct	ttgtcaagtg	gctctcaact	tgttctggga	300
agtttgattg	gtgtcctcgt	ttttcatgaa	tggacaagac	ctatgcaatt	tgtagtagga	360
agtctagcac	tattacttct	gattgttggt	ttttactttt	ctagtaaaca	agatgatgct	420
aatgcacaag	tcaatcacct	tcataatttt	tcaaaaggat	ttagggcgct	cacttattca	480
acaattgggt	acgtgatgta	tgctgtatta	tttaataaca	tcatgaaatt	tgaagttttg	540
tcagtcattt	tacccatggc	agtaggtatg	gttttaggag	ctataacttt	catgtcattt	600
aaaattttcca	ttgaccagta	tgtgattaaa	aatagcggtg	ttggattact	ttggggcatt	660
gggaatatatt	ttatgctttt	agctgcatca	aaagcaggac	ttgctattgc	cttttagtttc	720
tcacaattag	gtgctatcat	ttcgattgtc	ggaggcattt	tattcctagg	cgaaaccaaa	780
accaaaaaag	aaatgcgttg	ggttgtcaca	ggaattattt	gttttatcgt	aggtgctatt	840
ttattagggtg	tgggtcaaattc	ttaa				864

<210> SEQ ID NO 606
<211> LENGTH: 287
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 606

Met	Glu	Gly	Ile	Phe	Tyr	Ala	Leu	Ile	Pro	Met	Phe	Thr	Trp	Gly	Ser
1			5					10						15	
Ile	Gly	Phe	Val	Ser	Asn	Lys	Ile	Gly	Gly	Lys	Pro	Ser	Gln	Gln	Thr
			20					25					30		
Leu	Gly	Met	Thr	Phe	Gly	Ala	Leu	Leu	Phe	Ser	Leu	Ala	Val	Trp	Leu
		35					40					45			
Ile	Val	Arg	Pro	Glu	Met	Thr	Leu	Gln	Leu	Trp	Leu	Phe	Gly	Ile	Leu
	50					55				60					
Gly	Gly	Phe	Ile	Trp	Ser	Ile	Gly	Gln	Thr	Gly	Gln	Phe	His	Ala	Met
65				70				75						80	
Gln	Tyr	Met	Gly	Val	Ser	Val	Ala	Asn	Pro	Leu	Ser	Ser	Gly	Ser	Gln
			85					90					95		
Leu	Val	Leu	Gly	Ser	Leu	Ile	Gly	Val	Leu	Val	Phe	His	Glu	Trp	Thr
		100					105					110			
Arg	Pro	Met	Gln	Phe	Val	Val	Gly	Ser	Leu	Ala	Leu	Leu	Leu	Leu	Ile
		115					120					125			
Val	Gly	Phe	Tyr	Phe	Ser	Ser	Lys	Gln	Asp	Asp	Ala	Asn	Ala	Gln	Val
	130					135				140					
Asn	His	Leu	His	Asn	Phe	Ser	Lys	Gly	Phe	Arg	Ala	Leu	Thr	Tyr	Ser
145				150				155						160	
Thr	Ile	Gly	Tyr	Val	Met	Tyr	Ala	Val	Leu	Phe	Asn	Asn	Ile	Met	Lys
			165					170					175		
Phe	Glu	Val	Leu	Ser	Val	Ile	Leu	Pro	Met	Ala	Val	Gly	Met	Val	Leu
		180					185					190			
Gly	Ala	Ile	Thr	Phe	Met	Ser	Phe	Lys	Ile	Ser	Ile	Asp	Gln	Tyr	Val
	195					200					205				
Ile	Lys	Asn	Ser	Val	Val	Gly	Leu	Leu	Trp	Gly	Ile	Gly	Asn	Ile	Phe
	210					215					220				

Met	Leu	Leu	Ala	Ala	Ser	Lys	Ala	Gly	Leu	Ala	Ile	Ala	Phe	Ser	Phe
225					230					235					240
Ser	Gln	Leu	Gly	Ala	Ile	Ile	Ser	Ile	Val	Gly	Gly	Ile	Leu	Phe	Leu
			245						250					255	
Gly	Glu	Thr	Lys	Thr	Lys	Lys	Glu	Met	Arg	Trp	Val	Val	Thr	Gly	Ile
			260				265						270		
Ile	Cys	Phe	Ile	Val	Gly	Ala	Ile	Leu	Leu	Gly	Val	Val	Lys	Ser	
	275						280						285		

<210> SEQ ID NO 607

<211> LENGTH: 915

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 607

atgaccaaag	tcagaaaagc	cattattcct	gctgcaggtc	taggaacacg	ttttttacct	60
gctaccaaag	ctcttgccaa	agagatgttg	cccatcgttg	ataaaccaac	catccagttt	120
atcgtcgaag	aagcgctaaa	atctggcatc	gaggaaatcc	ttgtggtgac	cggaaaagct	180
aaacgctcta	tcgaggacca	ttttgattca	aactttgaat	tagaatacaa	cctccaagct	240
aaggggaaaa	atgaactggt	gaaattagtg	gatgaaacca	ctgccattaa	ccttcatttt	300
atccgtcaaa	gccacccaag	agggtgggga	gatgctgtct	tacaagccaa	agcctttgtg	360
ggcaatgaac	cctttgtggt	catgcttgga	gatgacttaa	tggacattac	aaatgcatcc	420
gctaaacctc	tcaccaaaca	actcatggag	gactatgaca	agacgcatgc	atccactatc	480
gctgtgatga	aagttcctca	tgaagatgtg	tctagctatg	gggttatcgc	tcctcaaggc	540
aaggctgtca	agggccttta	cagtgtagac	acctttgttg	aaaaaccaca	accagaagat	600
gcgcctagtg	atttggttat	tattggtcgt	tacctcctaa	cccctgaaat	ttttggtatt	660
ttggaaaagac	agacccttgg	agcaggtaac	gaagtgcac	tcacagatgc	tatcgatacc	720
ctcaataaaaa	ctcagcgtgt	ctttgcacga	gaatttaaag	gcaatcggtta	cgatgttggg	780
gataaattttg	gattcatgaa	aacatctatc	gactatgcct	tagaacaccc	acaggtcaaa	840
gaggacttga	aaaattacat	tatcaaacta	ggaaaagctt	tggaaaaaag	taaagtacca	900
acacattcaa	agtaa					915

<210> SEQ ID NO 608

<211> LENGTH: 304

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 608

Met	Thr	Lys	Val	Arg	Lys	Ala	Ile	Ile	Pro	Ala	Ala	Gly	Leu	Gly	Thr
1			5					10					15		
Arg	Phe	Leu	Pro	Ala	Thr	Lys	Ala	Leu	Ala	Lys	Glu	Met	Leu	Pro	Ile
		20					25					30			
Val	Asp	Lys	Pro	Thr	Ile	Gln	Phe	Ile	Val	Glu	Glu	Ala	Leu	Lys	Ser
	35					40					45				
Gly	Ile	Glu	Glu	Ile	Leu	Val	Val	Thr	Gly	Lys	Ala	Lys	Arg	Ser	Ile
	50				55				60						
Glu	Asp	His	Phe	Asp	Ser	Asn	Phe	Glu	Leu	Glu	Tyr	Asn	Leu	Gln	Ala
65				70				75					80		
Lys	Gly	Lys	Asn	Glu	Leu	Leu	Lys	Leu	Val	Asp	Glu	Thr	Thr	Ala	Ile
		85					90					95			
Asn	Leu	His	Phe	Ile	Arg	Gln	Ser	His	Pro	Arg	Gly	Leu	Gly	Asp	Ala
	100						105					110			
Val	Leu	Gln	Ala	Lys	Ala	Phe	Val	Gly	Asn	Glu	Pro	Phe	Val	Val	Met
	115					120					125				
Leu	Gly	Asp	Asp	Leu	Met	Asp	Ile	Thr	Asn	Ala	Ser	Ala	Lys	Pro	Leu
	130				135					140					
Thr	Lys	Gln	Leu	Met	Glu	Asp	Tyr	Asp	Lys	Thr	His	Ala	Ser	Thr	Ile
145				150					155					160	
Ala	Val	Met	Lys	Val	Pro	His	Glu	Asp	Val	Ser	Ser	Tyr	Gly	Val	Ile

				165					170					175			
Ala	Pro	Gln	Gly	Lys	Ala	Val	Lys	Gly	Leu	Tyr	Ser	Val	Asp	Thr	Phe		
			180					185					190				
Val	Glu	Lys	Pro	Gln	Pro	Glu	Asp	Ala	Pro	Ser	Asp	Leu	Ala	Ile	Ile		
		195					200					205					
Gly	Arg	Tyr	Leu	Leu	Thr	Pro	Glu	Ile	Phe	Gly	Ile	Leu	Glu	Arg	Gln		
	210					215					220						
Thr	Pro	Gly	Ala	Gly	Asn	Glu	Val	Gln	Leu	Thr	Asp	Ala	Ile	Asp	Thr		
225					230					235				240			
Leu	Asn	Lys	Thr	Gln	Arg	Val	Phe	Ala	Arg	Glu	Phe	Lys	Gly	Asn	Arg		
			245					250					255				
Tyr	Asp	Val	Gly	Asp	Lys	Phe	Gly	Phe	Met	Lys	Thr	Ser	Ile	Asp	Tyr		
	260						265						270				
Ala	Leu	Glu	His	Pro	Gln	Val	Lys	Glu	Asp	Leu	Lys	Asn	Tyr	Ile	Ile		
	275					280						285					
Lys	Leu	Gly	Lys	Ala	Leu	Glu	Lys	Ser	Lys	Val	Pro	Thr	His	Ser	Lys		
	290					295					300						

<210> SEQ ID NO 609

<211> LENGTH: 1338

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 609

ttgacattac	cccttattta	tattagaata	tcgagggtccc	tgtctttcaa	ggaaattaaa	60
aaagaaagag	gtgtaattgt	gcctattttt	aaaaaaaaactt	taattgtttt	atccttttatt	120
tttttgatat	ctatcttgat	ttatctaaat	atgtatctat	ttggaacatc	aactgtagga	180
atztatggag	taatattaat	aacctatcta	gttattaaac	ttggattatc	tttcctttat	240
gagccattta	aaggaaagcc	acatgactat	aaagttgctg	ctgtaattcc	ttcttataat	300
gaagatgccg	agtcattatt	agaaactcct	aaaagtgtgt	tagcacagac	ctatccgtta	360
tcagaaattt	atattgttga	tgatgggagt	tcaaacacag	atgcaataca	attaattgaa	420
gagtatgtaa	atagagaagt	ggatatttgt	cgaaacgtaa	tcgttcaccg	ttcccttgtc	480
aataaaggaa	aacgccatgc	tcaagcgtgg	gcatttgaaa	gatctgacgc	tgacgttttt	540
ttaaccgtag	attcagatac	ttatatctat	ccaaatgcct	tagaagaact	cctaaaaagc	600
ttcaatgatg	agacagttta	tgctgcaaca	ggacatttga	atgctagaaa	cagacaaact	660
aatctattaa	cgcgacttac	agatatccgt	tacgataatg	cctttggggg	ggagcgtgct	720
gctcaatcat	taacaggtaa	tatttttagtt	tgctcaggac	cattgagtat	ttatcgacgt	780
gaagtgatta	ttcctaactt	agagcgctat	aaaaatcaaa	cattcctagg	tttacctggt	840
agcattgggg	atgatcgatg	tttaacaaat	tatgctattg	atttaggacg	cactgtctac	900
caatcaacag	ctagatgtga	tactgatgta	cctttccaat	taaaaagtta	tttaaagcaa	960
caaaatcgat	ggaataaatc	ttttttttaga	gaatctatta	tttctgttaa	aaaaattcct	1020
tctaatacca	tcggtgcctt	atggactatt	ttcgaaatcg	ttatgtttat	gatgttgatt	1080
gtcgcaattg	ggaatctttt	gtttaatcaa	gctattcaat	tagaccttat	taaacttttt	1140
gcctttttat	ccatcatctt	tatcgttgct	ttatgtcgta	atgttcatta	tatgatcaaa	1200
catcctgcta	gttttttggt	atctcctctg	tatggaatat	tacacttggt	tgtcttacag	1260
cccctaaaac	tttattcttt	atgcaccatt	aaaaatacgg	aatggggaac	acgtaaaaag	1320
gtcactattt	ttaaataa					1338

<210> SEQ ID NO 610

<211> LENGTH: 445

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 610

Met	Thr	Leu	Pro	Leu	Ile	Tyr	Ile	Arg	Ile	Ser	Arg	Ser	Leu	Ser	Phe
1			5					10					15		
Lys	Glu	Ile	Lys	Lys	Glu	Arg	Gly	Val	Ile	Val	Pro	Ile	Phe	Lys	Lys
			20				25				30				
Thr	Leu	Ile	Val	Leu	Ser	Phe	Ile	Phe	Leu	Ile	Ser	Ile	Leu	Ile	Tyr

	35					40					45				
Leu	Asn	Met	Tyr	Leu	Phe	Gly	Thr	Ser	Thr	Val	Gly	Ile	Tyr	Gly	Val
	50					55					60				
Ile	Leu	Ile	Thr	Tyr	Leu	Val	Ile	Lys	Leu	Gly	Leu	Ser	Phe	Leu	Tyr
65					70					75				80	
Glu	Pro	Phe	Lys	Gly	Lys	Pro	His	Asp	Tyr	Lys	Val	Ala	Ala	Val	Ile
			85					90						95	
Pro	Ser	Tyr	Asn	Glu	Asp	Ala	Glu	Ser	Leu	Leu	Glu	Thr	Leu	Lys	Ser
		100						105					110		
Val	Leu	Ala	Gln	Thr	Tyr	Pro	Leu	Ser	Glu	Ile	Tyr	Ile	Val	Asp	Asp
	115					120						125			
Gly	Ser	Ser	Asn	Thr	Asp	Ala	Ile	Gln	Leu	Ile	Glu	Glu	Tyr	Val	Asn
	130					135					140				
Arg	Glu	Val	Asp	Ile	Cys	Arg	Asn	Val	Ile	Val	His	Arg	Ser	Leu	Val
145				150						155				160	
Asn	Lys	Gly	Lys	Arg	His	Ala	Gln	Ala	Trp	Ala	Phe	Glu	Arg	Ser	Asp
			165					170						175	
Ala	Asp	Val	Phe	Leu	Thr	Val	Asp	Ser	Asp	Thr	Tyr	Ile	Tyr	Pro	Asn
		180					185						190		
Ala	Leu	Glu	Glu	Leu	Leu	Lys	Ser	Phe	Asn	Asp	Glu	Thr	Val	Tyr	Ala
	195					200					205				
Ala	Thr	Gly	His	Leu	Asn	Ala	Arg	Asn	Arg	Gln	Thr	Asn	Leu	Leu	Thr
	210					215					220				
Arg	Leu	Thr	Asp	Ile	Arg	Tyr	Asp	Asn	Ala	Phe	Gly	Val	Glu	Arg	Ala
225				230						235				240	
Ala	Gln	Ser	Leu	Thr	Gly	Asn	Ile	Leu	Val	Cys	Ser	Gly	Pro	Leu	Ser
			245					250						255	
Ile	Tyr	Arg	Arg	Glu	Val	Ile	Ile	Pro	Asn	Leu	Glu	Arg	Tyr	Lys	Asn
		260						265					270		
Gln	Thr	Phe	Leu	Gly	Leu	Pro	Val	Ser	Ile	Gly	Asp	Asp	Arg	Cys	Leu
	275					280						285			
Thr	Asn	Tyr	Ala	Ile	Asp	Leu	Gly	Arg	Thr	Val	Tyr	Gln	Ser	Thr	Ala
	290					295					300				
Arg	Cys	Asp	Thr	Asp	Val	Pro	Phe	Gln	Leu	Lys	Ser	Tyr	Leu	Lys	Gln
305				310						315				320	
Gln	Asn	Arg	Trp	Asn	Lys	Ser	Phe	Phe	Arg	Glu	Ser	Ile	Ile	Ser	Val
			325					330						335	
Lys	Lys	Ile	Leu	Ser	Asn	Pro	Ile	Val	Ala	Leu	Trp	Thr	Ile	Phe	Glu
		340						345					350		
Ile	Val	Met	Phe	Met	Met	Leu	Ile	Val	Ala	Ile	Gly	Asn	Leu	Leu	Phe
	355					360						365			
Asn	Gln	Ala	Ile	Gln	Leu	Asp	Leu	Ile	Lys	Leu	Phe	Ala	Phe	Leu	Ser
	370					375					380				
Ile	Ile	Phe	Ile	Val	Ala	Leu	Cys	Arg	Asn	Val	His	Tyr	Met	Ile	Lys
385				390						395				400	
His	Pro	Ala	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Tyr	Gly	Ile	Leu	His	Leu
			405					410						415	
Phe	Val	Leu	Gln	Pro	Leu	Lys	Leu	Tyr	Ser	Leu	Cys	Thr	Ile	Lys	Asn
		420						425					430		
Thr	Glu	Trp	Gly	Thr	Arg	Lys	Lys	Val	Thr	Ile	Phe	Lys			
	435					440						445			

<210> SEQ ID NO 611

<211> LENGTH: 543

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 611

```

atgataaaaa aagaaaatat tcctaatacta ttaactcttg ttcgaatcgc aatgattcct      60
ttctttcttt ttattacttc ctcataataat aagggtggggg ggcataatttt tgcagctgtg    120
atTTTTgcaa ttgccagttt taccgattat ctagatgggt atcttgcgcg taagtggcat      180
gtagccagta atTTTtgaaa gtttgccgat cctctagcag ataagatgct tgtcatgagt      240
gcctttatca tgttagttgg acttggttta gttcctgcgt ggggtgtcagc tgttattatt      300
tgccgagaat tggcagtaac tggctcttca ttactacttg ttgaaaccgg aggaaaggct      360
cttgccagctg ctatgccggg aaaaatcaaaa acagcgacac aaatgttgctc tattattttta    420
ttactttgcc attggatatt cctaggaaac gtcttactct atattgctct ttttttcact      480
atTTattctg gatatgatta ttttaaagga gcaagctttc tttttaagga tacgtttaaa      540
taa                                                                    543

```

<210> SEQ ID NO 612
 <211> LENGTH: 180
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 612

```

Met Ile Lys Lys Glu Asn Ile Pro Asn Leu Leu Thr Leu Val Arg Ile
1           5           10           15
Ala Met Ile Pro Phe Phe Leu Phe Ile Thr Ser Ser Ser Asn Lys Val
20          25          30
Gly Trp His Ile Phe Ala Ala Val Ile Phe Ala Ile Ala Ser Phe Thr
35          40          45
Asp Tyr Leu Asp Gly Tyr Leu Ala Arg Lys Trp His Val Ala Ser Asn
50          55          60
Phe Gly Lys Phe Ala Asp Pro Leu Ala Asp Lys Met Leu Val Met Ser
65          70          75          80
Ala Phe Ile Met Leu Val Gly Leu Gly Leu Val Pro Ala Trp Val Ser
85          90          95
Ala Val Ile Ile Cys Arg Glu Leu Ala Val Thr Gly Leu Arg Leu Leu
100         105         110
Leu Val Glu Thr Gly Gly Lys Val Leu Ala Ala Ala Met Pro Gly Lys
115         120         125
Ile Lys Thr Ala Thr Gln Met Leu Ser Ile Ile Leu Leu Leu Cys His
130         135         140
Trp Ile Phe Leu Gly Asn Val Leu Leu Tyr Ile Ala Leu Phe Phe Thr
145         150         155         160
Ile Tyr Ser Gly Tyr Asp Tyr Phe Lys Gly Ala Ser Phe Leu Phe Lys
165         170         175
Asp Thr Phe Lys
180

```

<210> SEQ ID NO 613
 <211> LENGTH: 921
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 613

```

ttgctctttt tttcactatt tattctggat atgattattt taaaggagca agctttcttt      60
ttaaggatac gtttaaataa catgtcagct attattgaac ttaaaaaagt tacatttaat    120
taccataaaag accaagaaaa accaacatta gatggcgtat cgtttcatgt gaaacaagg      180
gagtggctgt ctatcattgg ccataatgga tctggtaaat caacgactat tcggttaatt      240
gatggattat tggaaccaga atcagggctc attattgttg atggagatct actaaccata      300
actaatgttt gggaaattcg tcataaaatt ggtatggtct ttcaaaaccc tgataatcag      360
tttgttggag caactgttga agatgatgtt gcttttgggc ttgaaaataa aggtattgca      420
catgaagata taaaagagag ggtaaatcat gcttttagagt tagtcggcat gcagaacttt      480
aaagaaaaaag aaccagcccg tttatctggt ggccaaaaac agcgcgtagc tattgcaggt      540
gcagtttgcta tgaagcctaa aattattatt ttagatgaag ctactagtat gcttgaccct      600
aaaggacgat tagagttaat caaaactata aaaaacatcc gtgacgacta ccagctgact      660

```

gttattttcca ttactcatga cttagatgaa gttgctctta gtgatagagt tttagtgatg	720
aaagatgggtc aagtggaatc aacatcaaca ccagaacaat tatttgcaag aggggatgaa	780
ctactccaat taggtcttga tatccctttt acaacatctg ttgtacagat gcttcaagaa	840
gaaggttatc ctgttgacta tggatatctc acagaaaagg aattagaaaa tcagttatgt	900
caattaatct ccaaaatgta a	921

<210> SEQ ID NO 614
 <211> LENGTH: 306
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 614

Met Leu Phe Phe Ser Leu Phe Ile Leu Asp Met Ile Ile Leu Lys Glu	
1 5 10 15	
Gln Ala Phe Phe Leu Arg Ile Arg Leu Asn Asn Met Ser Ala Ile Ile	
20 25 30	
Glu Leu Lys Lys Val Thr Phe Asn Tyr His Lys Asp Gln Glu Lys Pro	
35 40 45	
Thr Leu Asp Gly Val Ser Phe His Val Lys Gln Gly Glu Trp Leu Ser	
50 55 60	
Ile Ile Gly His Asn Gly Ser Gly Lys Ser Thr Thr Ile Arg Leu Ile	
65 70 75 80	
Asp Gly Leu Leu Glu Pro Glu Ser Gly Ser Ile Ile Val Asp Gly Asp	
85 90 95	
Leu Leu Thr Ile Thr Asn Val Trp Glu Ile Arg His Lys Ile Gly Met	
100 105 110	
Val Phe Gln Asn Pro Asp Asn Gln Phe Val Gly Ala Thr Val Glu Asp	
115 120 125	
Asp Val Ala Phe Gly Leu Glu Asn Lys Gly Ile Ala His Glu Asp Ile	
130 135 140	
Lys Glu Arg Val Asn His Ala Leu Glu Leu Val Gly Met Gln Asn Phe	
145 150 155 160	
Lys Glu Lys Glu Pro Ala Arg Leu Ser Gly Gly Gln Lys Gln Arg Val	
165 170 175	
Ala Ile Ala Gly Ala Val Ala Met Lys Pro Lys Ile Ile Ile Leu Asp	
180 185 190	
Glu Ala Thr Ser Met Leu Asp Pro Lys Gly Arg Leu Glu Leu Ile Lys	
195 200 205	
Thr Ile Lys Asn Ile Arg Asp Asp Tyr Gln Leu Thr Val Ile Ser Ile	
210 215 220	
Thr His Asp Leu Asp Glu Val Ala Leu Ser Asp Arg Val Leu Val Met	
225 230 235 240	
Lys Asp Gly Gln Val Glu Ser Thr Ser Thr Pro Glu Gln Leu Phe Ala	
245 250 255	
Arg Gly Asp Glu Leu Leu Gln Leu Gly Leu Asp Ile Pro Phe Thr Thr	
260 265 270	
Ser Val Val Gln Met Leu Gln Glu Glu Gly Tyr Pro Val Asp Tyr Gly	
275 280 285	
Tyr Leu Thr Glu Lys Glu Leu Glu Asn Gln Leu Cys Gln Leu Ile Ser	
290 295 300	
Lys Met	
305	

<210> SEQ ID NO 615
 <211> LENGTH: 615
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 615

```

atgtttaaga aagaaaattht aaaacaacgt tattttaatt ttggattagt agcgtagct      60
ctaacaatat tagccatcat ttttgccctt tcaagtaaaa atgctgatac taagtcttat      120
gctaagaagt cagaaagtaa aatggtaaca atcgacaagg ctccaaaaaa taatcatgct      180
attactaaag aagaaagcaa agaaaaagca aagagcattg cttcggagcc tattcccaca      240
gtagaaaact ctgtagctcc gacagtaaca gaggaagtac cggttgttca gcaagaagtg      300
actcaaactg ttcagcaggt atcttcagta gcctataatc caaacaatgt ggtactttcc      360
aatggaaata ctgctggtat thtaggaagt caagcggcgg cacagatggc agcagcaaca      420
ggtgttccac aatcaacttg ggaacatata attgcgcgtg aatctaattg aaatcctaac      480
gcagctaatt cttctggggc atcaggggtt ttccagacaa tgccagggtg gggttctaca      540
gcaacgggtt aagatcaagt caatgcagcc ttgaaagcct atagtgcaca aggtttatca      600
gcttgggggt actaa                                           615

```

<210> SEQ ID NO 616
 <211> LENGTH: 204
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 616

```

Met Phe Lys Lys Glu Asn Leu Lys Gln Arg Tyr Phe Asn Phe Gly Leu
1           5           10           15
Val Ala Leu Ala Leu Thr Ile Leu Ala Ile Ile Phe Ala Phe Ser Ser
          20           25           30
Lys Asn Ala Asp Thr Lys Ser Tyr Ala Lys Lys Ser Glu Ser Lys Met
          35           40           45
Val Thr Ile Asp Lys Ala Pro Lys Asn Asn His Ala Ile Thr Lys Glu
          50           55           60
Glu Ser Lys Glu Lys Ala Lys Ser Ile Ala Ser Glu Pro Ile Pro Thr
65           70           75           80
Val Glu Asn Ser Val Ala Pro Thr Val Thr Glu Glu Val Pro Val Val
          85           90           95
Gln Gln Glu Val Thr Gln Thr Val Gln Gln Val Ser Ser Val Ala Tyr
          100          105          110
Asn Pro Asn Asn Val Val Leu Ser Asn Gly Asn Thr Ala Gly Ile Val
          115          120          125
Gly Ser Gln Ala Ala Ala Gln Met Ala Ala Ala Thr Gly Val Pro Gln
          130          135          140
Ser Thr Trp Glu His Ile Ile Ala Arg Glu Ser Asn Gly Asn Pro Asn
145          150          155          160
Ala Ala Asn Ala Ser Gly Ala Ser Gly Leu Phe Gln Thr Met Pro Gly
          165          170          175
Trp Gly Ser Thr Ala Thr Val Glu Asp Gln Val Asn Ala Ala Leu Lys
          180          185          190
Ala Tyr Ser Ala Gln Gly Leu Ser Ala Trp Gly Tyr
          195          200

```

<210> SEQ ID NO 617
 <211> LENGTH: 1977
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 617

```

atgaaaaaat ttcgttttga aaccattcat ttgattatga tgggattgat tttatttggga      60
ctgctggcac tttgtgtcag tattatgcaa tcaaaaatat taatattatt agctattttt      120
ctcgttttgc tatttgttgt tgctctttta tggatatcaa aagaagctta tcaattatca      180
gacttagctc atattgagct cttaaataaa caaacagaag ataacctaaa aacgctactt      240
gataatatgc ctgttgaggt agttcaattt gatcaagaga ccaacgctgt agaatgggat      300
aatccttatg cagaattaat ttttacaact gaagagggtt ttatacaaaa cggtttgatt      360
cagcaaatga ttacggaaaa acgtcgtgaa gatatttttc aaacatttga agtttctggt      420
aataaataca cttcttatat tgatgtatca tcaggaattt tttatttttt tgatagcttt      480

```

```

gtgggaaaca ggcaattagc tgatgctagt atgttaagac cggttgttgg cattatttcg 540
gttgataatt atgatgatat cactgatgat ttatcagatg cagataacctc aaaaattaat 600
tcatttgtag ctaacttcat tgatgagttt atggagtcaa aacggattttt ttaccgtcgt 660
gttaatatgg atcgctacta tttctttaca gacttttaaaa cattaaatga tttgatggat 720
aataaatttt ctgtcttaga agagtttcgt aaagaagctc aagatgctca gcgcccttta 780
acactcagca taggaatttc ttttggtgaa gaaaatcata gccagattgg acaggtagct 840
cttgagaatc ttaatatgtc gcttgttcgt ggtggtgatc agattgtcat tcgtgaaaat 900
gcggatcata cgaatccaat ttatttcggg ggagggctctg tttctacagt taaacgttca 960
agaacacgta cccgtgctat gatgacagct atttcagatc gaatcaagat ggtggacaat 1020
gtttttattg ttggacatag gaaacttgat atggatgcac taggttcagc tgttggtatg 1080
caatttttcg caggtaacat tattgaaaat agttttgccg tttacaatcc agatgagatg 1140
agtccagata ttgaaagggc tattgagcga ttgcaggctg acggaaagac tcgtctaate 1200
agtgtttctc aagcaatggg tttagtgtact ccaagatcac ttttagtaat ggttgaccat 1260
tctaagatat cttaacact ttctaaagaa ttttatgaac agtttcaaaa tgttattgta 1320
gttgatcatc acagaagaga tgatgatttt cctgataatg ctatcttaac ttttattgaa 1380
agtggagcaa gtagtgctgc ggagctcgtc cctgagttaa ttcaatttca aaatgctaaa 1440
aaatgtttta ataagatcca agccagtgtt ttaatggcag gtattatgct tgatactaaa 1500
aatttttcta cgcgagtgc aagtcgtacc tttgatgtcg ctagtactt aagaagcaaa 1560
ggaagtgata gtgttgaaat tcaaaatata tccgcaacag attttgaaga atataagcaa 1620
ataaatgaaa ttattttaca aggagaacgt cttggtgaca gtatcattgt agctgcagga 1680
gaaaaaaatc atctttatag caatgttatt gctagtaaag ctgcagatac gatactgtca 1740
atggctcacg ttgaggctag ctttgtatta gttgaaacag cttctcataa gattgctatt 1800
tcagctagaa gtcgtagtaa aatcaatgtt caacgtgtga tggaaaaatt aggtggagga 1860
ggccacttta atcttgctgc ctgtcagtta acggatatca gtcttcccca agcgaagtac 1920
ttattattga aaactattaa tatgacaatg aaagaaacag gagaagtaga atcatga 1977

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```

<210> SEQ ID NO 618
<211> LENGTH: 658
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 618

```

```

Met Lys Lys Phe Arg Phe Glu Thr Ile His Leu Ile Met Met Gly Leu
1          5          10          15
Ile Leu Phe Gly Leu Leu Ala Leu Cys Val Ser Ile Met Gln Ser Lys
20          25          30
Ile Leu Ile Leu Leu Ala Ile Phe Leu Val Leu Leu Phe Val Val Ala
35          40          45
Leu Leu Trp Tyr Gln Lys Glu Ala Tyr Gln Leu Ser Asp Leu Ala His
50          55          60
Ile Glu Leu Leu Asn Glu Gln Thr Glu Asp Asn Leu Lys Thr Leu Leu
65          70          75          80
Asp Asn Met Pro Val Gly Val Val Gln Phe Asp Gln Glu Thr Asn Ala
85          90          95
Val Glu Trp Tyr Asn Pro Tyr Ala Glu Leu Ile Phe Thr Thr Glu Glu
100         105         110
Gly Phe Ile Gln Asn Gly Leu Ile Gln Gln Ile Ile Thr Glu Lys Arg
115         120         125
Arg Glu Asp Ile Ser Gln Thr Phe Glu Val Ser Gly Asn Lys Tyr Thr
130         135         140
Ser Tyr Ile Asp Val Ser Ser Gly Ile Phe Tyr Phe Phe Asp Ser Phe
145         150         155         160
Val Gly Asn Arg Gln Leu Ala Asp Ala Ser Met Leu Arg Pro Val Val
165         170         175
Gly Ile Ile Ser Val Asp Asn Tyr Asp Asp Ile Thr Asp Asp Leu Ser
180         185         190
Asp Ala Asp Thr Ser Lys Ile Asn Ser Phe Val Ala Asn Phe Ile Asp
195         200         205

```

Glu	Phe	Met	Glu	Ser	Lys	Arg	Ile	Phe	Tyr	Arg	Arg	Val	Asn	Met	Asp
210						215				220					
Arg	Tyr	Tyr	Phe	Phe	Thr	Asp	Phe	Lys	Thr	Leu	Asn	Asp	Leu	Met	Asp
225					230					235					240
Asn	Lys	Phe	Ser	Val	Leu	Glu	Glu	Phe	Arg	Lys	Glu	Ala	Gln	Asp	Ala
				245					250					255	
Gln	Arg	Pro	Leu	Thr	Leu	Ser	Ile	Gly	Ile	Ser	Phe	Gly	Glu	Glu	Asn
			260					265					270		
His	Ser	Gln	Ile	Gly	Gln	Val	Ala	Leu	Glu	Asn	Leu	Asn	Ile	Ala	Leu
		275					280					285			
Val	Arg	Gly	Gly	Asp	Gln	Ile	Val	Ile	Arg	Glu	Asn	Ala	Asp	His	Thr
	290					295				300					
Asn	Pro	Ile	Tyr	Phe	Gly	Gly	Ser	Val	Ser	Thr	Val	Lys	Arg	Ser	
305					310				315					320	
Arg	Thr	Arg	Thr	Arg	Ala	Met	Met	Thr	Ala	Ile	Ser	Asp	Arg	Ile	Lys
				325					330					335	
Met	Val	Asp	Asn	Val	Phe	Ile	Val	Gly	His	Arg	Lys	Leu	Asp	Met	Asp
			340					345					350		
Ala	Leu	Gly	Ser	Ala	Val	Gly	Met	Gln	Phe	Phe	Ala	Gly	Asn	Ile	Ile
		355					360					365			
Glu	Asn	Ser	Phe	Ala	Val	Tyr	Asn	Pro	Asp	Glu	Met	Ser	Pro	Asp	Ile
	370					375				380					
Glu	Arg	Ala	Ile	Glu	Arg	Leu	Gln	Ala	Asp	Gly	Lys	Thr	Arg	Leu	Ile
385					390					395				400	
Ser	Val	Ser	Gln	Ala	Met	Gly	Leu	Val	Thr	Pro	Arg	Ser	Leu	Leu	Val
				405					410					415	
Met	Val	Asp	His	Ser	Lys	Ile	Ser	Leu	Thr	Leu	Ser	Lys	Glu	Phe	Tyr
			420					425					430		
Glu	Gln	Phe	Gln	Asn	Val	Ile	Val	Val	Asp	His	His	Arg	Arg	Asp	Asp
		435					440					445			
Asp	Phe	Pro	Asp	Asn	Ala	Ile	Leu	Thr	Phe	Ile	Glu	Ser	Gly	Ala	Ser
	450					455				460					
Ser	Ala	Ala	Glu	Leu	Val	Thr	Glu	Leu	Ile	Gln	Phe	Gln	Asn	Ala	Lys
465					470					475				480	
Lys	Cys	Leu	Asn	Lys	Ile	Gln	Ala	Ser	Val	Leu	Met	Ala	Gly	Ile	Met
				485					490					495	
Leu	Asp	Thr	Lys	Asn	Phe	Ser	Thr	Arg	Val	Thr	Ser	Arg	Thr	Phe	Asp
			500					505					510		
Val	Ala	Ser	Tyr	Leu	Arg	Ser	Lys	Gly	Ser	Asp	Ser	Val	Glu	Ile	Gln
		515					520					525			
Asn	Ile	Ser	Ala	Thr	Asp	Phe	Glu	Glu	Tyr	Lys	Gln	Ile	Asn	Glu	Ile
	530					535				540					
Ile	Leu	Gln	Gly	Glu	Arg	Leu	Gly	Asp	Ser	Ile	Ile	Val	Ala	Ala	Gly
545					550					555					560
Glu	Lys	Asn													

<210> SEQ ID NO 619
 <211> LENGTH: 2304
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 619

```

ttgaacagta tgtccatttt aggagaaaaat atgttagaag aattgaaaac acttattaaa      60
aatccaaaat taatgattac aatgattggt gtggccctag tgctgcctt atataattta      120
tcctttctag gctcaatgtg ggatccttat ggtcgggtca atgaccttcc cattgctggt      180
gttaatcatg ataagcctgc aaagagagct gataagtcac tgacaattgg gaatgatatg      240
gtggacaaga tgtctaaaag taaagattta gagtatcatt ttgtctcagc taagcaagct      300
caagagggac ttaaagaagg tgattattat atggttatta ctttaccgga agatctttct      360
caacgggcag caaccttatt aaatcccga ccccaaaaat taactatccg ttaccaaacy      420
agtaaaggac atggaatggt cgctgctaag atgggggaaa cagcgatggc taagctgaaa      480
gagtcctgtt cgcaaaacat tacgaagact tatacctcag cagtttttag cagtatgaca      540
gacctccaat caggattaaa agaagcctca gctggaagtc aagcacttgc ttcaggagcg      600
aagactgctc aggcggggag tcaaacactt tcgacgaact tagcagcctt aacgggtgct      660
agccaacagt ttcaacaagg tactggctga ttgacatcag gtttgactac ctatacagat      720
ggtgtcaacc aagtcaagaa tgggttagga acattatcaa cggacatccc caattatctg      780
aatggggttt ctaggttatc ccaggagct tctcagctta atcagggtct ttcacagttg      840
acacaagcaa caacactttc tgacgagaaa gctaagggaa ttcaatcctt aattgtagga      900
ctaccagtc taaatcaagg cattcagcaa ctaaatacag agctatcaac attgcaaccc      960
cctaacctta atgctgatga gttaggtaat agcttaggag ctatcgctca agctgccaaa     1020
caagtcattg ctgaagagac tgccgctcag aatgaagaat tatcggctct ccaagctact     1080
agcgtttacc aatcattaac tgctgaacaa caaggagagt tagctgcggc cctcagtcaa     1140
tctgataaaa gtcagaccgt atctgcagcc caaactatth taagttctgt tcaaactttg     1200
tcaacaagtt tacagtctct ctctcaagaa gatcagtcac aacagttgga gcaacttaag     1260
gaagctgttg cacagattgc taatcaatcc aatcaagctt tgccgggagc aagttctgct     1320
ttaactgaat tatcaacggg attagcaaaag gtaaatggta gcttaaatca acaagttcta     1380
ccaggaagta atcaattgac aacaggatta gcacaattaa acaggtataa tactgccatt     1440
ggttctgggg taataaaact ctcagaagggt gccaatgcct tgctatccaa gtccggagaa     1500
ttactagatg gtagccatca attatcagaa ggtgctacta aactagctga tggtagttct     1560
caattgagtc aggggtggtc tcaattaacg agcggattga ctgaattatc aacaggattg     1620
tcaaccttaa atggttcctt agccaaagcc tctcagcagt tatcgcttgt tctgtgact     1680
gataaaaaatg ctaaaagctgt cgcaaaacct cttgtgttaa atgagaaaga caaagatggg     1740
gttaagacga atgggatcgg gatggcacct tatatgattg ctgtttctct aatggttgtg     1800
gccctttcaa ccaacgtcat ttttgcta atctttatctg gtcgtccggg caaagataaa     1860
tgggattggg ctaaaacaaa atttgttatt aatggtttta tttcgactat gggatccatt     1920
gttctctact tagctattca attattaggg tttgaagccc gttatgggat ggaaacctta     1980
ggatttatta tgctaagtgg ttggacgttt atggctcttg tcacagcttt ggtcggttgg     2040
gatgatcgat atggctcttt tgcttctttg gtcattgttat tgcttcaggt tggctcttca     2100
ggtggctctt accccattga gttaagtggg gcattcttcc aaaagttaca tcctttctta     2160
ccaatgactt atgtggtatc tggtttacga caaaccttt cattatcagg tcatattgga     2220
gtagaagtga aagtcttaac tggtttctta ctggcattta tggatttagc actactcatt     2280
tatcgthcca agaaaacagt ctaa                                     2304
  
```

<210> SEQ ID NO 620
 <211> LENGTH: 767
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 620

```

Met Asn Ser Met Ser Ile Leu Gly Glu Asn Met Leu Glu Glu Leu Lys
1              5              10              15
Thr Leu Ile Lys Asn Pro Lys Leu Met Ile Thr Met Ile Gly Val Ala
              20              25              30
Leu Val Pro Ala Leu Tyr Asn Leu Ser Phe Leu Gly Ser Met Trp Asp
              35              40              45
  
```


Pro	Tyr	Gly	Arg	Val	Asn	Asp	Leu	Pro	Ile	Ala	Val	Val	Asn	His	Asp
50						55					60				
Lys	Pro	Ala	Lys	Arg	Ala	Asp	Lys	Ser	Leu	Thr	Ile	Gly	Asn	Asp	Met
65					70					75					80
Val	Asp	Lys	Met	Ser	Lys	Ser	Lys	Asp	Leu	Glu	Tyr	His	Phe	Val	Ser
			85						90					95	
Ala	Lys	Gln	Ala	Gln	Glu	Gly	Leu	Lys	Glu	Gly	Asp	Tyr	Tyr	Met	Val
			100					105					110		
Ile	Thr	Leu	Pro	Glu	Asp	Leu	Ser	Gln	Arg	Ala	Ala	Thr	Leu	Leu	Asn
		115					120					125			
Pro	Glu	Pro	Gln	Lys	Leu	Thr	Ile	Arg	Tyr	Gln	Thr	Ser	Lys	Gly	His
130						135					140				
Gly	Met	Val	Ala	Ala	Lys	Met	Gly	Glu	Thr	Ala	Met	Ala	Lys	Leu	Lys
145					150					155					160
Glu	Ser	Val	Ser	Gln	Asn	Ile	Thr	Lys	Thr	Tyr	Thr	Ser	Ala	Val	Phe
				165					170					175	
Ser	Ser	Met	Thr	Asp	Leu	Gln	Ser	Gly	Leu	Lys	Glu	Ala	Ser	Ala	Gly
			180					185					190		
Ser	Gln	Ala	Leu	Ala	Ser	Gly	Ala	Lys	Thr	Ala	Gln	Ala	Gly	Ser	Gln
		195					200					205			
Thr	Leu	Ser	Thr	Asn	Leu	Ala	Ala	Leu	Thr	Gly	Ala	Ser	Gln	Gln	Phe
	210					215					220				
Gln	Gln	Gly	Thr	Gly	Arg	Leu	Thr	Ser	Gly	Leu	Thr	Thr	Tyr	Thr	Asp
225					230					235					240
Gly	Val	Asn	Gln	Val	Lys	Asn	Gly	Leu	Gly	Thr	Leu	Ser	Thr	Asp	Ile
				245					250					255	
Pro	Asn	Tyr	Leu	Asn	Gly	Val	Ser	Arg	Leu	Ser	Gln	Gly	Ala	Ser	Gln
			260					265					270		
Leu	Asn	Gln	Gly	Leu	Ser	Gln	Leu	Thr	Gln	Ala	Thr	Thr	Leu	Ser	Asp
		275					280					285			
Glu	Lys	Ala	Lys	Gly	Ile	Gln	Ser	Leu	Ile	Val	Gly	Leu	Pro	Val	Leu
290						295					300				
Asn	Gln	Gly	Ile	Gln	Gln	Leu	Asn	Thr	Glu	Leu	Ser	Thr	Leu	Gln	Pro
305					310					315					320
Pro	Asn	Leu	Asn	Ala	Asp	Glu	Leu	Gly	Asn	Ser	Leu	Gly	Ala	Ile	Ala
				325					330					335	
Gln	Ala	Ala	Lys	Gln	Val	Ile	Ala	Glu	Glu	Thr	Ala	Ala	Gln	Asn	Glu
			340					345					350		
Glu	Leu	Ser	Ala	Leu	Gln	Ala	Thr	Ser	Val	Tyr	Gln	Ser	Leu	Thr	Ala
		355					360					365			
Glu	Gln	Gln	Gly	Glu	Leu	Ala	Ala	Ala	Leu	Ser	Gln	Ser	Asp	Lys	Ser
370						375					380				
Gln	Thr	Val	Ser	Ala	Ala	Gln	Thr	Ile	Leu	Ser	Ser	Val	Gln	Thr	Leu
385					390					395					400
Ser	Thr	Ser	Leu	Gln	Ser	Leu	Ser	Gln	Glu	Asp	Gln	Ser	Lys	Gln	Leu
				405					410					415	
Glu	Gln	Leu	Lys	Glu	Ala	Val	Ala	Gln	Ile	Ala	Asn	Gln	Ser	Asn	Gln
			420					425					430		
Ala	Leu	Pro	Gly	Ala	Ser	Ser	Ala	Leu	Thr	Glu	Leu	Ser	Thr	Gly	Leu
		435					440					445			
Ala	Lys	Val	Asn	Gly	Ser	Leu	Asn	Gln	Gln	Val	Leu	Pro	Gly	Ser	Asn
450						455					460				
Gln	Leu	Thr	Thr	Gly	Leu	Ala	Gln	Leu	Asn	Arg	Tyr	Asn	Thr	Ala	Ile
465					470					475					480
Gly	Ser	Gly	Val	Ile	Lys	Leu	Ser	Glu	Gly	Ala	Asn	Ala	Leu	Ser	Ser
				485					490					495	
Lys	Ser	Gly	Glu	Leu	Leu	Asp	Gly	Ser	His	Gln	Leu	Ser	Glu	Gly	Ala

			500					505					510				
Thr	Lys	Leu	Ala	Asp	Gly	Ser	Ser	Gln	Leu	Ser	Gln	Gly	Gly	His	Gln		
		515					520					525					
Leu	Thr	Ser	Gly	Leu	Thr	Glu	Leu	Ser	Thr	Gly	Leu	Ser	Thr	Leu	Asn		
	530					535					540						
Gly	Ser	Leu	Ala	Lys	Ala	Ser	Gln	Gln	Leu	Ser	Leu	Val	Ser	Val	Thr		
545				550					555						560		
Asp	Lys	Asn	Ala	Lys	Ala	Val	Ala	Lys	Pro	Leu	Val	Leu	Asn	Glu	Lys		
		565						570					575				
Asp	Lys	Asp	Gly	Val	Lys	Thr	Asn	Gly	Ile	Gly	Met	Ala	Pro	Tyr	Met		
	580						585						590				
Ile	Ala	Val	Ser	Leu	Met	Val	Val	Ala	Leu	Ser	Thr	Asn	Val	Ile	Phe		
	595					600						605					
Ala	Asn	Ser	Leu	Ser	Gly	Arg	Pro	Val	Lys	Asp	Lys	Trp	Asp	Trp	Ala		
	610				615						620						
Lys	Gln	Lys	Phe	Val	Ile	Asn	Gly	Phe	Ile	Ser	Thr	Met	Gly	Ser	Ile		
625				630					635						640		
Val	Leu	Tyr	Leu	Ala	Ile	Gln	Leu	Leu	Gly	Phe	Glu	Ala	Arg	Tyr	Gly		
		645				650							655				
Met	Glu	Thr	Leu	Gly	Phe	Ile	Met	Leu	Ser	Gly	Trp	Thr	Phe	Met	Ala		
	660					665						670					
Leu	Val	Thr	Ala	Leu	Val	Gly	Trp	Asp	Asp	Arg	Tyr	Gly	Ser	Phe	Ala		
	675					680						685					
Ser	Leu	Val	Met	Leu	Leu	Leu	Gln	Val	Gly	Ser	Ser	Gly	Gly	Ser	Tyr		
	690				695						700						
Pro	Ile	Glu	Leu	Ser	Gly	Ala	Phe	Phe	Gln	Lys	Leu	His	Pro	Phe	Leu		
705				710					715						720		
Pro	Met	Thr	Tyr	Val	Val	Ser	Gly	Leu	Arg	Gln	Thr	Ile	Ser	Leu	Ser		
		725					730						735				
Gly	His	Ile	Gly	Val	Glu	Val	Lys	Val	Leu	Thr	Gly	Phe	Leu	Leu	Ala		
	740						745					750					
Phe	Met	Val	Leu	Ala	Leu	Leu	Ile	Tyr	Arg	Pro	Lys	Lys	Thr	Val			
	755					760						765					

<210> SEQ ID NO 621

<211> LENGTH: 843

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 621

atggtttcat	ttattttcaag	agttttttaa	ggcatgatta	ttgcactagg	ttttatttta	60
cctggtgtat	ccggtggtgt	tctcgcagcc	atttttaggaa	tctatgagcg	aatgatttcc	120
tttttagctc	atatgaggga	taactttatt	gaaaatgtct	tatttttctt	accagtagga	180
attggtggta	tttttaggtat	tgctctcttt	tctttccccg	ttgagttttt	gcttaagcac	240
tatcaagtta	gcgtcttatg	gggatttgct	ggcgctattg	tcggcactat	tcctagtctg	300
attaaggagt	caaccaagca	gtctcaaaga	gacaaagctg	actggctatg	gctagtcctt	360
acctttgtta	tttcaggact	aggtctttac	ttcttaaagt	acttaatcgg	taccttacca	420
gctaactttt	taacctttat	tttagcaggt	gccttaattg	ctttaggagt	actggtcctt	480
ggactaagcc	cgtcaaactc	cttacttatc	ttaggactct	atggtcctat	gttaataggg	540
ttcaaactct	tggatttatt	agggactttc	ttacctattg	ctatcggagg	agtcctagcc	600
atcttggtct	tttctaaaag	tatggattat	gctttacagc	accatcattc	aaaagtttac	660
cactttatca	ttggtattgt	attatccagc	acgctattaa	ttcttattcc	aaatagtagt	720
agtcccgaat	ccatttccta	cagtcatgca	ggtatcttaa	cctggcttat	ggcctttgtg	780
ttatttgctc	ttggtatttg	gctcggactt	tggatgagtc	aattagaaga	aaaatacaaa	840
taa						843

<210> SEQ ID NO 622

<211> LENGTH: 280

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 622

```
Met Val Ser Phe Ile Ser Arg Val Phe Lys Gly Met Ile Ile Ala Leu
1      5      10      15
Gly Phe Ile Leu Pro Gly Val Ser Gly Gly Val Leu Ala Ala Ile Leu
20      25      30
Gly Ile Tyr Glu Arg Met Ile Ser Phe Leu Ala His Met Arg Asp Asn
35      40      45
Phe Ile Glu Asn Val Leu Phe Phe Leu Pro Val Gly Ile Gly Gly Ile
50      55      60
Leu Gly Ile Ala Leu Phe Ser Phe Pro Val Glu Phe Leu Leu Lys His
65      70      75      80
Tyr Gln Val Ser Val Leu Trp Gly Phe Ala Gly Ala Ile Val Gly Thr
85      90      95
Ile Pro Ser Leu Ile Lys Glu Ser Thr Lys Gln Ser Gln Arg Asp Lys
100     105     110
Ala Asp Trp Leu Trp Leu Val Leu Thr Phe Val Ile Ser Gly Leu Gly
115     120     125
Leu Tyr Phe Leu Asn Asp Leu Ile Gly Thr Leu Pro Ala Asn Phe Leu
130     135     140
Thr Phe Ile Leu Ala Gly Ala Leu Ile Ala Leu Gly Val Leu Val Pro
145     150     155     160
Gly Leu Ser Pro Ser Asn Leu Leu Leu Ile Leu Gly Leu Tyr Gly Pro
165     170     175
Met Leu Ile Gly Phe Lys Ser Leu Asp Leu Leu Gly Thr Phe Leu Pro
180     185     190
Ile Ala Ile Gly Gly Val Leu Ala Ile Leu Ala Phe Ser Lys Ser Met
195     200     205
Asp Tyr Ala Leu Gln His His His Ser Lys Val Tyr His Phe Ile Ile
210     215     220
Gly Ile Val Leu Ser Ser Thr Leu Leu Ile Leu Ile Pro Asn Ser Ser
225     230     235     240
Ser Pro Glu Ser Ile Ser Tyr Ser His Ala Gly Ile Leu Thr Trp Leu
245     250     255
Met Ala Phe Val Leu Phe Ala Leu Gly Ile Trp Leu Gly Leu Trp Met
260     265     270
Ser Gln Leu Glu Glu Lys Tyr Lys
275     280
```

<210> SEQ ID NO 623

<211> LENGTH: 942

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 623

```
atgattaaga aaacaaccta taagaaaaaa gttaaatatg tcattagtag aggggccaaag      60
aaagttaggcc tactccacgc tctaagaagt atttcaagag aaaaatatgc agagaagatt      120
tcggcttctc tgctttatgg cattctctct agtattgctg tgaatttttt cttccagcct      180
gggcatgttt attcaagtgg agcaactggt ctagcacagg ttttttcagc tcttagtcat      240
cgtcttttag gctatgattt tcccatcgcc tttgcgtttt atttgattaa tattcctttg      300
cttatttttag cttggtataa aattgggcat caatttacca tttttacctt tatcacagtc      360
agcatgagtt ctttctttat tcaaatcatg cctcaagtga cgctgacgac tgatcctctt      420
atcaatgcta tttttggtgg tttggttatg ggaatgggaa ttggtacagg tctcaaatca      480
cgtatctcta gtggggggac tgatattgtc agtttgacc ttaggaaacg aacaggcaag      540
gatgtgggca gtctctcatt gatggttaat ggtgcaattt tagcctttgc agggatttta      600
tttggtggc agtacgccct ttattctatg gtctctatct ttgtatcaag tcgtgttacg      660
gatgccattt tcaccaagca aaagaaaatg caggcaacta ttgttaccag ccatccagag      720
```

cgtgtgattc	atatgatcca	taaacgtctg	catcgcggag	tgaccagtat	caacgacgca	780
gaagggactt	acaagcatga	acaaaaagca	gttttgatta	ccattttgac	atgtgaagaa	840
tacccagaat	tcaaattggct	gatgttaaaa	acagacccac	aagcctttgt	ttcagtggct	900
gagaatgtta	gaattatcgg	tcgttttgtg	gaagatgatt	aa		942

<210> SEQ ID NO 624
 <211> LENGTH: 313
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 624

Met	Ile	Lys	Lys	Thr	Tyr	Lys	Lys	Lys	Val	Lys	Tyr	Val	Ile	Ser
1			5					10					15	
Arg	Gly	Ala	Lys	Val	Gly	Leu	Leu	His	Ala	Leu	Arg	Ser	Ile	Ser
			20				25					30		
Arg	Glu	Lys	Tyr	Ala	Glu	Lys	Ile	Ser	Ala	Ser	Leu	Leu	Tyr	Gly
		35				40					45			Ile
Leu	Ser	Ser	Ile	Ala	Val	Asn	Phe	Phe	Phe	Gln	Pro	Gly	His	Val
	50					55				60				Tyr
Ser	Ser	Gly	Ala	Thr	Gly	Leu	Ala	Gln	Val	Phe	Ser	Ala	Leu	Ser
65					70				75					80
Arg	Leu	Leu	Gly	Tyr	Asp	Phe	Pro	Ile	Ala	Phe	Ala	Phe	Tyr	Leu
				85					90					95
Asn	Ile	Pro	Leu	Leu	Ile	Leu	Ala	Trp	Tyr	Lys	Ile	Gly	His	Gln
			100					105					110	Phe
Thr	Ile	Phe	Thr	Phe	Ile	Thr	Val	Ser	Met	Ser	Ser	Phe	Phe	Ile
		115					120					125		Gln
Ile	Met	Pro	Gln	Val	Thr	Leu	Thr	Thr	Asp	Pro	Leu	Ile	Asn	Ala
	130					135					140			Ile
Phe	Gly	Gly	Leu	Val	Met	Gly	Met	Gly	Ile	Gly	Thr	Gly	Leu	Lys
145					150				155					160
Arg	Ile	Ser	Ser	Gly	Gly	Thr	Asp	Ile	Val	Ser	Leu	Thr	Leu	Arg
				165					170					175
Arg	Thr	Gly	Lys	Asp	Val	Gly	Ser	Leu	Ser	Leu	Met	Val	Asn	Gly
			180				185						190	Ala
Ile	Leu	Ala	Phe	Ala	Gly	Ile	Leu	Phe	Gly	Trp	Gln	Tyr	Ala	Leu
	195					200						205		Tyr
Ser	Met	Val	Ser	Ile	Phe	Val	Ser	Ser	Arg	Val	Thr	Asp	Ala	Ile
	210					215					220			Phe
Thr	Lys	Gln	Lys	Lys	Met	Gln	Ala	Thr	Ile	Val	Thr	Ser	His	Pro
225					230				235					240
Arg	Val	Ile	His	Met	Ile	His	Lys	Arg	Leu	His	Arg	Gly	Val	Thr
				245					250					255
Ile	Asn	Asp	Ala	Glu	Gly	Thr	Tyr	Lys	His	Glu	Gln	Lys	Ala	Val
			260					265					270	Leu
Ile	Thr	Ile	Leu	Thr	Cys	Glu	Glu	Tyr	Pro	Glu	Phe	Lys	Trp	Leu
		275				280						285		Met
Leu	Lys	Thr	Asp	Pro	Gln	Ala	Phe	Val	Ser	Val	Ala	Glu	Asn	Val
	290					295					300			Arg
Ile	Ile	Gly	Arg	Phe	Val	Glu	Asp	Asp						
305					310									

<210> SEQ ID NO 625
 <211> LENGTH: 873
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 625

atggcacatc	acgataaatt	gactaaacta	ctaaaactgt	ttttgattgc	cctaggtgta	60
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```

gccatttata ccttcggttt tgtaatttt aacatggcta atgctttggc tgaaggtggt 120
gtggcaggaa taaccttgat tttacacgcg cattttggga ttaatcctgc ttactcttct 180
ctcttattta atcttcact ttttatttta ggggcaaaga tttttgggaa gcgttctttg 240
gctctaacca tctatggaac agttctgatg tccgctttta tctggatgtg gcaaaaagtt 300
cctatcgaac ttggcttgga aaatgacatg atgttggtgg ctgtagtggc aggtctcttt 360
tcagggattg ggagtggcat tgtttttcgc tatggtgcaa ccacaggtgg aacggatatt 420
attggtcgca ttgcagaaga aaaatttgga gctaagctag gtcaaacttt gcttttggtg 480
gatgctcttg tattgacagc ttcgttgact tatgtggatt taaaacacat gctttacact 540
ttggtggcaa gctttgtttt tagccaaatg attagtgtgg ttcaaaatgg tggttacact 600
atccgtggaa tgattattat taccaagcat tcagaggctg ccgctcaagc tatcctaacc 660
gaaatcaatc gtggagtgc ttacttgaaa ggtcaaggag cttactctgg taatgattac 720
aatatcatgt atgtgacctt gaacccaact gaagttcggg aagtcaaacg tatttttagct 780
ggtttggtgc cagatgcctt tatctccatt attgatgtgg acgaagttaa tagctctgat 840
tttaaaattc gccgaagaaa ttatgataaa taa 873

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<210> SEQ ID NO 626

<211> LENGTH: 290

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 626

```

Met Ala His His Asp Lys Leu Thr Lys Leu Leu Lys Leu Phe Leu Ile
1          5          10          15
Ala Leu Gly Val Ala Ile Tyr Thr Phe Gly Phe Val Asn Phe Asn Met
20          25          30
Ala Asn Ala Leu Ala Glu Gly Gly Val Ala Gly Ile Thr Leu Ile Leu
35          40          45
His Ala His Phe Gly Ile Asn Pro Ala Tyr Ser Ser Leu Leu Phe Asn
50          55          60
Leu Pro Leu Phe Ile Leu Gly Ala Lys Ile Phe Gly Lys Arg Ser Leu
65          70          75          80
Ala Leu Thr Ile Tyr Gly Thr Val Leu Met Ser Ala Phe Ile Trp Met
85          90          95
Trp Gln Lys Val Pro Ile Glu Leu Gly Leu Glu Asn Asp Met Met Leu
100         105         110
Val Ala Val Val Ala Gly Leu Phe Ser Gly Ile Gly Ser Gly Ile Val
115         120         125
Phe Arg Tyr Gly Ala Thr Thr Gly Gly Thr Asp Ile Ile Gly Arg Ile
130         135         140
Ala Glu Glu Lys Phe Gly Ala Lys Leu Gly Gln Thr Leu Leu Leu Val
145         150         155         160
Asp Ala Leu Val Leu Thr Ala Ser Leu Thr Tyr Val Asp Leu Lys His
165         170         175
Met Leu Tyr Thr Leu Val Ala Ser Phe Val Phe Ser Gln Met Ile Ser
180         185         190
Val Val Gln Asn Gly Gly Tyr Thr Ile Arg Gly Met Ile Ile Ile Thr
195         200         205
Lys His Ser Glu Ala Ala Ala Gln Ala Ile Leu Thr Glu Ile Asn Arg
210         215         220
Gly Val Thr Tyr Leu Lys Gly Gln Gly Ala Tyr Ser Gly Asn Asp Tyr
225         230         235         240
Asn Ile Met Tyr Val Thr Leu Asn Pro Thr Glu Val Arg Glu Val Lys
245         250         255
Arg Ile Leu Ala Gly Leu Asp Pro Asp Ala Phe Ile Ser Ile Ile Asp
260         265         270
Val Asp Glu Val Ile Ser Ser Asp Phe Lys Ile Arg Arg Arg Asn Tyr
275         280         285
Asp Lys

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<210> SEQ ID NO 627
 <211> LENGTH: 576
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 627

```

ttgatattta attttaagga gaatatagtg aaaaagaaat tagttttagc taccttatgt      60
ctatcaatgg gtgctgtgag tgtagagcg gaaagtgatt ttgggaatgc taatgaaatc      120
gggctaggtt tttatggtag tgatgactat actaaccaac ctgctttaac aggagaccaa      180
gcgaaaatag gcttcagaaa cgattggaaa gatgctagag attttggagt aaaaccaata      240
aatctgggag atagtaaaat cgaagtaaaa acaaatccgg gagctcttgt aagagtttcc      300
ttgacaacgg gtgaaacaac caatagtata tgggagttaa caagtgtatc ttcctcaatg      360
agtaacggta tctacactaa cacttataaa ataaagccaa ctattgcaaa ttcctcagga      420
attgcaacgt tcgatttagc gaactcagga aaatacgaca aggaaaaaag tgaaattata      480
aagagtactg agagtaatgc aaagaaaggt gatacttact cagttactac aagtatagat      540
ggatggacaa taggttatgg agaatggact gtgtga                                576

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<210> SEQ ID NO 628
 <211> LENGTH: 191
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 628

```

Met Ile Phe Asn Phe Lys Glu Asn Ile Val Lys Lys Lys Leu Val Leu
1           5           10           15
Ala Thr Leu Cys Leu Ser Met Gly Ala Val Ser Val Arg Ala Glu Ser
20           25           30
Asp Phe Gly Asn Ala Asn Glu Ile Gly Leu Gly Phe Tyr Gly Ser Asp
35           40           45
Asp Tyr Thr Asn Gln Pro Ala Leu Thr Gly Asp Gln Ala Lys Ile Gly
50           55           60
Phe Arg Asn Asp Trp Lys Asp Ala Arg Asp Phe Gly Val Lys Pro Ile
65           70           75           80
Asn Leu Gly Asp Ser Lys Ile Glu Val Lys Thr Asn Pro Gly Ala Leu
85           90           95
Val Arg Val Ser Leu Thr Thr Gly Glu Thr Thr Asn Ser Ile Trp Glu
100          105          110
Leu Thr Ser Val Ser Ser Ser Met Ser Asn Gly Ile Tyr Thr Asn Thr
115          120          125
Tyr Lys Ile Lys Pro Thr Ile Ala Asn Ser Ser Gly Ile Ala Thr Phe
130          135          140
Asp Leu Ala Asn Ser Gly Lys Tyr Asp Lys Glu Lys Ser Glu Ile Ile
145          150          155          160
Lys Ser Thr Glu Ser Asn Ala Lys Lys Gly Asp Thr Tyr Ser Val Thr
165          170          175
Thr Ser Ile Asp Gly Trp Thr Ile Gly Tyr Gly Glu Trp Thr Val
180          185          190

```

<210> SEQ ID NO 629
 <211> LENGTH: 1221
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 629

```

atgcaagagt ttttaaacct tcctaagcag attcagctga ggcaactggg acgctttgtg      60
accattacct taggcagtag tatctttccc tttatggcca tgtattatac gacttacttt      120
gggtacgtttt ggacaggcct cttaatgatg attaccagtt tgatgggatt tgttggaact      180
ttatacgggtg ggcatctgtc agatgctctt ggtcgcaaaa aagtcattat gattgggtca      240

```

gtaggaacaa	cactaggctg	gtttctgact	attttagcta	atttgcctaa	tgccgctatt	300
ccttggttaa	cctttgcggg	tattttattg	gtagagattg	cttctagttt	ttatggtcct	360
gcctatgaag	ctatgttgat	tgatttgact	gatgagagta	atcgtcgatt	tgtttacacc	420
atcaattatt	ggtttatcaa	tattgccgtc	atgtttgggtg	cagggctatc	tgggcttttt	480
tatgaccatc	attttttagc	cttgtagta	gccttattac	tcgtcaatgt	actttgtttt	540
ggcgttgctt	actactgttt	tgatgaaact	agaccagaaa	cacacgcttt	tgaccatggg	600
aaaggattac	tggcgagttt	tcagaactac	cgtcagggtg	ttcatgatcg	tgcccttgct	660
ttgtttacct	taggtgccat	cttttctggg	agtatctgga	tgcatgatgga	taactatgtg	720
ccagtccatt	tgaaactgta	ttttcagcca	acggctgtat	taggtttcca	agtaactagt	780
tctaaaatgt	tatcattaat	ggttttaact	aatacattgc	tgattgtcct	tttcatgaca	840
gtagtaaata	aattaacgga	aaaatggaaa	ctattacctc	agcttgtggg	tggttcttta	900
ctatttactc	tagggatgct	cttgatcatt	acctttacgc	agttctatgc	tatctgggta	960
tcagttgttt	tgtaactttt	tggggaaatg	ataaatgttt	ctgctagtca	agtcctacgt	1020
gctgatatga	tggatcattc	ccaaatagga	tcttatacag	gttttgtgtc	aatggcacaa	1080
cccctagggtg	ctattttggc	tagtctacta	gtatctgtca	gccattttac	aggttcttta	1140
ggcgtgcaat	gcttatttgc	agtcattgct	ttgctaggga	tttattttac	ggttgtttct	1200
gcaaaaatga	aaaagggtgta	a				1221

<210> SEQ ID NO 630

<211> LENGTH: 406

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 630

Met	Gln	Glu	Phe	Leu	Asn	Leu	Pro	Lys	Gln	Ile	Gln	Leu	Arg	Gln	Leu
1				5				10				15			
Val	Arg	Phe	Val	Thr	Ile	Thr	Leu	Gly	Ser	Ser	Ile	Phe	Pro	Phe	Met
			20					25				30			
Ala	Met	Tyr	Tyr	Thr	Thr	Tyr	Phe	Gly	Thr	Phe	Trp	Thr	Gly	Leu	Leu
		35					40				45				
Met	Met	Ile	Thr	Ser	Leu	Met	Gly	Phe	Val	Gly	Thr	Leu	Tyr	Gly	Gly
	50					55				60					
His	Leu	Ser	Asp	Ala	Leu	Gly	Arg	Lys	Lys	Val	Ile	Met	Ile	Gly	Ser
65					70					75				80	
Val	Gly	Thr	Thr	Leu	Gly	Trp	Phe	Leu	Thr	Ile	Leu	Ala	Asn	Leu	Pro
				85					90					95	
Asn	Ala	Ala	Ile	Pro	Trp	Leu	Thr	Phe	Ala	Gly	Ile	Leu	Leu	Val	Glu
			100					105						110	
Ile	Ala	Ser	Ser	Phe	Tyr	Gly	Pro	Ala	Tyr	Glu	Ala	Met	Leu	Ile	Asp
		115					120					125			
Leu	Thr	Asp	Glu	Ser	Asn	Arg	Arg	Phe	Val	Tyr	Thr	Ile	Asn	Tyr	Trp
	130					135					140				
Phe	Ile	Asn	Ile	Ala	Val	Met	Phe	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Phe
145					150					155				160	
Tyr	Asp	His	His	Phe	Leu	Ala	Leu	Leu	Val	Ala	Leu	Leu	Leu	Val	Asn
				165					170					175	
Val	Leu	Cys	Phe	Gly	Val	Ala	Tyr	Tyr	Cys	Phe	Asp	Glu	Thr	Arg	Pro
			180					185					190		
Glu	Thr	His	Ala	Phe	Asp	His	Gly	Lys	Gly	Leu	Leu	Ala	Ser	Phe	Gln
	195						200					205			
Asn	Tyr	Arg	Gln	Val	Phe	His	Asp	Arg	Ala	Phe	Val	Leu	Phe	Thr	Leu
	210					215					220				
Gly	Ala	Ile	Phe	Ser	Gly	Ser	Ile	Trp	Met	Gln	Met	Asp	Asn	Tyr	Val
225					230					235				240	
Pro	Val	His	Leu	Lys	Leu	Tyr	Phe	Gln	Pro	Thr	Ala	Val	Leu	Gly	Phe
				245					250					255	
Gln	Val	Thr	Ser	Ser	Lys	Met	Leu	Ser	Leu	Met	Val	Leu	Thr	Asn	Thr
			260					265						270	

Leu	Leu	Ile	Val	Leu	Phe	Met	Thr	Val	Val	Asn	Lys	Leu	Thr	Glu	Lys
		275					280				285				
Trp	Lys	Leu	Leu	Pro	Gln	Leu	Val	Val	Gly	Ser	Leu	Leu	Phe	Thr	Leu
	290					295					300				
Gly	Met	Leu	Leu	Ser	Phe	Thr	Phe	Thr	Gln	Phe	Tyr	Ala	Ile	Trp	Leu
305					310					315					320
Ser	Val	Val	Leu	Leu	Thr	Phe	Gly	Glu	Met	Ile	Asn	Val	Ser	Ala	Ser
					325					330				335	
Gln	Val	Leu	Arg	Ala	Asp	Met	Met	Asp	His	Ser	Gln	Ile	Gly	Ser	Tyr
			340					345					350		
Thr	Gly	Phe	Val	Ser	Met	Ala	Gln	Pro	Leu	Gly	Ala	Ile	Leu	Ala	Ser
		355					360					365			
Leu	Leu	Val	Ser	Val	Ser	His	Phe	Thr	Gly	Pro	Leu	Gly	Val	Gln	Cys
	370					375					380				
Leu	Phe	Ala	Val	Ile	Ala	Leu	Leu	Gly	Ile	Tyr	Phe	Thr	Val	Val	Ser
385					390					395					400
Ala	Lys	Met	Lys	Lys	Val										
					405										

<210> SEQ ID NO 631

<211> LENGTH: 2025

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 631

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gcaaatgtca	aagagattga	aaaaatctct	gtagttaaag	ggacatttac	caatgctggg	180
cagtttcagg	taatcattgg	taatgatgtt	ccagtttttt	ataatgactt	tacagctggt	240
tctagtattg	aaggggtgtc	taaagaagct	gccaaatcag	cagctaaaaa	taatcaaaat	300
gccttacaac	gggtgatgac	catgtttggc	gagattttca	cacctattat	tccggcgatt	360
attgttgggg	ggcttatttt	aggtttccgt	aatatatttg	agagtgtgcc	ttttgaattt	420
cttgggcagc	aggtcgaaaa	agggaaatta	gtttttgatg	cagctgggga	tcctgtttgg	480
aatacgattg	tgagggtatc	tcctttctgg	tcaggggtta	accatttctt	gtggttacca	540
ggggaagcta	ttttccactt	cttaccagtt	gggattactt	ggtctgtgac	gcgtaagatg	600
ggaaccactc	aaattttagg	gattgtcctt	ggtatctgtt	tggtgtcacc	acaattattg	660
aatgcctatg	cgggtggcagg	aacgcctgct	gtcgagattg	ccaaaaactg	ggtttgggat	720
tttggtttct	ttaccattaa	tcgtattggg	tatcaggcac	aggttattcc	agccctttta	780
gctggtctgt	cccttgctta	tcttgaaatt	ttctggcgta	aacggattcc	agaagtgggt	840
tcaatgattt	ttgtgccatt	cctttctttg	attccagctt	tgatttttagc	gcatacggta	900
ttggggccaa	tcggttgac	tatttgtaaa	gggatttcct	ttgttgtgtt	agctggattg	960
actggtcctg	ttaaatggct	attcggtgct	atcctttggtg	ccttgtatgc	tccgctagtt	1020
attactgggt	tacatcacat	gacaaatgcc	attgataccc	aattaattgc	tgatactgca	1080
actcgtacaa	ctgggtttgtg	gccaatgatt	gctctttcaa	atatcgctca	agggtcagcc	1140
gtttttgctt	actatttaat	gaatcgtcat	gaagaacgtg	aggctgaaat	atcgcttcct	1200
gcagcaattt	ctgcttacct	tggggtaact	gagcctgcct	tatttggggg	taatgttaaa	1260
tacgtttatc	cctttgtagc	cggaatgatt	ggctcaggta	ttgcgggtct	cttatcaaca	1320
acctttaatg	ttcaggcaaa	ttctattggg	gttgggtggt	taccaggttt	catggctatc	1380
aatgtgaagt	acatgattcc	attcttcac	tgtatggcag	tagccattgt	ggtgccgatg	1440
tttttaacct	tctttttccg	taaatcacat	atcatgacta	agacagaaga	tgaagctaaa	1500
ctacctgaga	cacccgtttc	ggatgctcct	gtagcaactg	ctccacataa	gactatgcaa	1560
ggaacagtta	tcactttaac	aagcccttta	acgggtgaag	ttaaagcggt	gtctgaagct	1620
gttgatcctg	tctttgcaca	gggagttatg	ggccaagggtg	ctcttcttca	accgacagaa	1680
gggggtgttag	tagcgccttg	tgatgctgaa	gtatcggtct	tgttcccaac	taaacacgct	1740
atttgttttg	tgacgactga	aggtttggaa	ttattgatgc	atattggcat	ggatacgggt	1800
aacttagatg	gtcaaggatt	tgaagctttg	gtgaagcaag	gtgatcaggt	taaggctgga	1860
caaacattga	ttcaatttga	tatagcagca	atttctgaag	ctggatacgc	actgaaaacg	1920
cctcttgtgg	tgactaatca	agatgttttt	acggtaactg	ttgaaggtag	tttaccgcgt	1980

cagattaagg ttaatgataa gtttagcagta gcggtgaaaa agtag

2025

<210> SEQ ID NO 632

<211> LENGTH: 674

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 632

Met	Gly	Lys	Phe	Glu	Gln	Asp	Ala	Lys	Ser	Leu	Leu	Thr	Ala	Ile	Gly
1				5					10					15	
Gly	Lys	Glu	Asn	Ile	Lys	Val	Val	Thr	His	Cys	Ala	Thr	Arg	Met	Arg
			20					25					30		
Phe	Val	Leu	Asn	Asp	Asn	Asn	Lys	Ala	Asn	Val	Lys	Glu	Ile	Glu	Lys
		35					40					45			
Ile	Ser	Val	Val	Lys	Gly	Thr	Phe	Thr	Asn	Ala	Gly	Gln	Phe	Gln	Val
	50					55					60				
Ile	Ile	Gly	Asn	Asp	Val	Pro	Val	Phe	Tyr	Asn	Asp	Phe	Thr	Ala	Val
65				70					75					80	
Ser	Ser	Ile	Glu	Gly	Val	Ser	Lys	Glu	Ala	Ala	Lys	Ser	Ala	Ala	Lys
			85					90					95		
Ser	Asn	Gln	Asn	Ala	Leu	Gln	Arg	Val	Met	Thr	Met	Leu	Ala	Glu	Ile
			100					105					110		
Phe	Thr	Pro	Ile	Ile	Pro	Ala	Ile	Ile	Val	Gly	Gly	Leu	Ile	Leu	Gly
		115				120						125			
Phe	Arg	Asn	Ile	Leu	Glu	Ser	Val	Pro	Phe	Glu	Phe	Leu	Gly	Gln	Gln
	130					135					140				
Val	Glu	Lys	Gly	Lys	Leu	Val	Phe	Asp	Ala	Ala	Gly	Asp	Pro	Val	Trp
145				150					155					160	
Asn	Thr	Ile	Val	Arg	Val	Ser	Pro	Phe	Trp	Ser	Gly	Val	Asn	His	Phe
			165					170					175		
Leu	Trp	Leu	Pro	Gly	Glu	Ala	Ile	Phe	His	Phe	Leu	Pro	Val	Gly	Ile
		180					185						190		
Thr	Trp	Ser	Val	Thr	Arg	Lys	Met	Gly	Thr	Thr	Gln	Ile	Leu	Gly	Ile
		195				200						205			
Val	Leu	Gly	Ile	Cys	Leu	Val	Ser	Pro	Gln	Leu	Leu	Asn	Ala	Tyr	Ala
	210					215					220				
Val	Ala	Gly	Thr	Pro	Ala	Ala	Glu	Ile	Ala	Lys	Asn	Trp	Val	Trp	Asp
225				230					235					240	
Phe	Gly	Phe	Phe	Thr	Ile	Asn	Arg	Ile	Gly	Tyr	Gln	Ala	Gln	Val	Ile
			245					250					255		
Pro	Ala	Leu	Leu	Ala	Gly	Leu	Ser	Leu	Ala	Tyr	Leu	Glu	Ile	Phe	Trp
		260				265						270			
Arg	Lys	Arg	Ile	Pro	Glu	Val	Val	Ser	Met	Ile	Phe	Val	Pro	Phe	Leu
		275				280						285			
Ser	Leu	Ile	Pro	Ala	Leu	Ile	Leu	Ala	His	Thr	Val	Leu	Gly	Pro	Ile
	290					295					300				
Gly	Trp	Thr	Ile	Gly	Lys	Gly	Ile	Ser	Phe	Val	Val	Leu	Ala	Gly	Leu
305				310					315					320	
Thr	Gly	Pro	Val	Lys	Trp	Leu	Phe	Gly	Ala	Ile	Phe	Gly	Ala	Leu	Tyr
			325					330					335		
Ala	Pro	Leu	Val	Ile	Thr	Gly	Leu	His	His	Met	Thr	Asn	Ala	Ile	Asp
		340					345						350		
Thr	Gln	Leu	Ile	Ala	Asp	Thr	Ala	Thr	Arg	Thr	Thr	Gly	Leu	Trp	Pro
	355					360						365			
Met	Ile	Ala	Leu	Ser	Asn	Ile	Ala	Gln	Gly	Ser	Ala	Val	Phe	Ala	Tyr
	370				375						380				
Tyr	Leu	Met	Asn	Arg	His	Glu	Glu	Arg	Glu	Ala	Glu	Ile	Ser	Leu	Pro
385					390					395					400

Ala	Ala	Ile	Ser	Ala	Tyr	Leu	Gly	Val	Thr	Glu	Pro	Ala	Leu	Phe	Gly	
				405					410					415		
Val	Asn	Val	Lys	Tyr	Val	Tyr	Pro	Phe	Val	Ala	Gly	Met	Ile	Gly	Ser	
			420					425					430			
Gly	Ile	Ala	Gly	Leu	Leu	Ser	Thr	Thr	Phe	Asn	Val	Gln	Ala	Asn	Ser	
		435					440					445				
Ile	Gly	Val	Gly	Gly	Leu	Pro	Gly	Phe	Met	Ala	Ile	Asn	Val	Lys	Tyr	
	450					455					460					
Met	Ile	Pro	Phe	Phe	Ile	Cys	Met	Ala	Val	Ala	Ile	Val	Val	Pro	Met	
465					470					475					480	
Phe	Leu	Thr	Phe	Phe	Phe	Arg	Lys	Ser	His	Ile	Met	Thr	Lys	Thr	Glu	
			485						490						495	
Asp	Glu	Ala	Lys	Leu	Pro	Glu	Thr	Pro	Val	Ser	Asp	Ala	Pro	Val	Ala	
			500					505					510			
Thr	Ala	Pro	His	Lys	Thr	Met	Gln	Gly	Thr	Val	Ile	Thr	Leu	Thr	Ser	
		515					520					525				
Pro	Leu	Thr	Gly	Glu	Val	Lys	Ala	Leu	Ser	Glu	Ala	Val	Asp	Pro	Val	
	530					535					540					
Phe	Ala	Gln	Gly	Val	Met	Gly	Gln	Gly	Ala	Leu	Leu	Gln	Pro	Thr	Glu	
545					550				555						560	
Gly	Val	Leu	Val	Ala	Pro	Cys	Asp	Ala	Glu	Val	Ser	Val	Leu	Phe	Pro	
			565					570						575		
Thr	Lys	His	Ala	Ile	Cys	Leu	Val	Thr	Thr	Glu	Gly	Leu	Glu	Leu	Leu	
			580					585					590			
Met	His	Ile	Gly	Met	Asp	Thr	Val	Asn	Leu	Asp	Gly	Gln	Gly	Phe	Glu	
	595					600					605					
Ala	Leu	Val	Lys	Gln	Gly	Asp	Gln	Val	Lys	Ala	Gly	Gln	Thr	Leu	Ile	
	610				615						620					
Gln	Phe	Asp	Ile	Ala	Ala	Ile	Ser	Glu	Ala	Gly	Tyr	Ala	Thr	Glu	Thr	
625					630				635						640	
Pro	Leu	Val	Val	Thr	Asn	Gln	Asp	Val	Phe	Thr	Val	Thr	Val	Glu	Gly	
			645					650						655		
Ser	Leu	Pro	Arg	Gln	Ile	Lys	Val	Asn	Asp	Lys	Leu	Ala	Val	Ala	Val	
			660					665					670			
Lys	Lys															

<210> SEQ ID NO 633

<211> LENGTH: 2337

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 633

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aatgccaatc	atttggactc	atcagctacc	aaaaactcag	aacaagaccc	tgcaacagct	180
ctgcaacgca	gtagagccta	cgaaggaagc	cctaaaagtc	ggcccgttg	gttgcaaaag	240
ctggaagctg	ttttgccgtc	tcctcaacgt	ccaattcggc	gtttttggcg	ccgctatcac	300
atcggaaaac	tgctaattgat	tctgattgga	actcttgtct	tactcttagg	atcatacttg	360
ttttacttat	caaaaaacagc	taaagtatct	gatttacaag	atgccttgaa	ggctacaacg	420
gttattttatg	atcacaaaagg	agagtatgca	ggcagtttat	ctgggtcaaaa	agggagttat	480
gttgagctca	acgctatttc	agatgatctt	gagaatgctg	ttattgccac	tgaggatagg	540
actttttaca	gtaatagcgg	tattaatctt	aaacgcttct	tattggcggg	agttacggcg	600
ggccgctttg	gaggtggctc	aacgattaca	cagcaactgg	ctaaaaatgc	ttatctctca	660
caagatcaga	caattaaacg	aaaggcccga	gagttttttt	tggcgttaga	gttgaccaaa	720
aaatacagta	aaaaagatat	tcttactatg	taccttaaca	actcctactt	tggaaatgga	780
gtttggggag	ttgaagatgc	cagtcaaaaa	tattttggaa	ccacagctgc	taacttaaca	840
ctggatgaag	ctgccacatt	agcaggtatg	ctcaaaggac	ctgaaatata	taacccttac	900
cattctctaa	aaaatgctac	tcaccgtaga	gatactgttt	taggagcgat	ggttgatgcc	960

aaaaagatta	cccaaacaaa	agctcagcaa	gctagagcag	tagggctaaa	aaatcgctta	1020
gctgatactt	atggttgtaa	gacagatgac	tacaaatacc	catcctactt	tgatgctggt	1080
attagtgaag	caatagcaac	ttatggtctt	tcagaaaaag	acattgttaa	taatggatac	1140
aaagtttaca	ctgagctaga	tcaaaattac	caaactggca	tgcaagacgac	ttttaacaac	1200
gatgaactat	ttcctgtttc	agcttatgac	ggtagctctg	ctcaagcagc	tagtggtgct	1260
ttagatccta	aaacaggagg	tgttagaggt	ctgattggtc	gtgtgaatag	tagtgaaaat	1320
ccgactttca	gaagttttta	ctatgcgact	caagcaaaaac	gtagtcccg	atcaacaatc	1380
aaaccactcg	tggttttacgc	gccagccggt	gcttcaggat	ggtcaattga	aaaagaacta	1440
ccaaataccg	ttcaagattt	cgatggctat	cagccacata	attatggaaa	ttatgaatca	1500
gaagatgttc	ctatgtatca	agcattagca	aactcttata	atattccagc	agtttctaca	1560
ttgaaccgata	tcggaatcga	taaagccttt	acctatggta	aaacatttgg	gttagatatg	1620
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aatggaacag	cagtcaatgc	taacgtatat	ggctatacac	tagctggtaa	aacagggacg	1920
acagaaacca	acttcaatcc	cgacttagca	ggcgatcagt	gggttattgg	ttatacgcca	1980
gatgttgta	ttagtcaatg	ggtaggattt	aatcagaccg	atgaaaatca	ttatctaacg	2040
gattcaagtg	caggcacggc	ctcagctatt	tttagcactc	aggcatctta	cattttgcct	2100
tataccaagg	gcagccaatt	tcatgtagat	aatgcctacg	ctcaaaatgg	tatttcagct	2160
gtttatggag	tcaatgaaac	aggtaatcaa	tcaggagtgtg	atactcaatc	tattattgat	2220
ggtttaagaa	aatcagcaca	agaagcttcg	caatcactat	caaaagcagt	cgatcagtca	2280
gggttacgtg	ataaagccca	atctatttgg	aaagagattg	ttgactat	tagatag	2337

<210> SEQ ID NO 634

<211> LENGTH: 778

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 634

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Gln	Glu	Lys	Gln	Phe	Leu	Met	His	Gln	Lys	Thr	Arg	Leu	Thr	Pro	Gln
			20					25					30		
His	Asn	Gln	Lys	Gln	Tyr	Ser	Pro	Asn	Ala	Asn	His	Leu	Asp	Ser	Ser
			35				40					45			
Ala	Thr	Lys	Asn	Ser	Glu	Gln	Asp	Pro	Ala	Thr	Ala	Leu	Gln	Arg	Ser
	50					55				60					
Arg	Ala	Tyr	Glu	Gly	Ser	Pro	Lys	Ser	Arg	Pro	Ala	Trp	Leu	Gln	Lys
65				70					75					80	
Leu	Glu	Ala	Val	Leu	Pro	Ser	Pro	Gln	Arg	Pro	Ile	Arg	Arg	Phe	Trp
			85					90					95		
Arg	Arg	Tyr	His	Ile	Gly	Lys	Leu	Leu	Met	Ile	Leu	Ile	Gly	Thr	Leu
			100				105						110		
Val	Leu	Leu	Leu	Gly	Ser	Tyr	Leu	Phe	Tyr	Leu	Ser	Lys	Thr	Ala	Lys
	115						120					125			
Val	Ser	Asp	Leu	Gln	Asp	Ala	Leu	Lys	Ala	Thr	Thr	Val	Ile	Tyr	Asp
	130					135					140				
His	Lys	Gly	Glu	Tyr	Ala	Gly	Ser	Leu	Ser	Gly	Gln	Lys	Gly	Ser	Tyr
145				150					155					160	
Val	Glu	Leu	Asn	Ala	Ile	Ser	Asp	Asp	Leu	Glu	Asn	Ala	Val	Ile	Ala
			165					170					175		
Thr	Glu	Asp	Arg	Thr	Phe	Tyr	Ser	Asn	Ser	Gly	Ile	Asn	Leu	Lys	Arg
			180				185					190			
Phe	Leu	Leu	Ala	Val	Val	Thr	Ala	Gly	Arg	Phe	Gly	Gly	Gly	Ser	Thr
	195					200					205				
Ile	Thr	Gln	Gln	Leu	Ala	Lys	Asn	Ala	Tyr	Leu	Ser	Gln	Asp	Gln	Thr
	210					215					220				

Ile	Lys	Arg	Lys	Ala	Arg	Glu	Phe	Phe	Leu	Ala	Leu	Glu	Leu	Thr	Lys	225	230	235	240
Lys	Tyr	Ser	Lys	Lys	Asp	Ile	Leu	Thr	Met	Tyr	Leu	Asn	Asn	Ser	Tyr	245	250		255
Phe	Gly	Asn	Gly	Val	Trp	Gly	Val	Glu	Asp	Ala	Ser	Gln	Lys	Tyr	Phe	260	265		270
Gly	Thr	Thr	Ala	Ala	Asn	Leu	Thr	Leu	Asp	Glu	Ala	Ala	Thr	Leu	Ala	275	280		285
Gly	Met	Leu	Lys	Gly	Pro	Glu	Ile	Tyr	Asn	Pro	Tyr	His	Ser	Leu	Lys	290	295	300	
Asn	Ala	Thr	His	Arg	Arg	Asp	Thr	Val	Leu	Gly	Ala	Met	Val	Asp	Ala	305	310	315	320
Lys	Lys	Ile	Thr	Gln	Thr	Lys	Ala	Gln	Gln	Ala	Arg	Ala	Val	Gly	Leu	325	330		335
Lys	Asn	Arg	Leu	Ala	Asp	Thr	Tyr	Val	Gly	Lys	Thr	Asp	Asp	Tyr	Lys	340	345		350
Tyr	Pro	Ser	Tyr	Phe	Asp	Ala	Val	Ile	Ser	Glu	Ala	Ile	Ala	Thr	Tyr	355	360		365
Gly	Leu	Ser	Glu	Lys	Asp	Ile	Val	Asn	Asn	Gly	Tyr	Lys	Val	Tyr	Thr	370	375	380	
Glu	Leu	Asp	Gln	Asn	Tyr	Gln	Thr	Gly	Met	Gln	Thr	Thr	Phe	Asn	Asn	385	390	395	400
Asp	Glu	Leu	Phe	Pro	Val	Ser	Ala	Tyr	Asp	Gly	Ser	Ser	Ala	Gln	Ala	405	410		415
Ala	Ser	Val	Ala	Leu	Asp	Pro	Lys	Thr	Gly	Gly	Val	Arg	Gly	Leu	Ile	420	425		430
Gly	Arg	Val	Asn	Ser	Ser	Glu	Asn	Pro	Thr	Phe	Arg	Ser	Phe	Asn	Tyr	435	440		445
Ala	Thr	Gln	Ala	Lys	Arg	Ser	Pro	Ala	Ser	Thr	Ile	Lys	Pro	Leu	Val	450	455	460	
Val	Tyr	Ala	Pro	Ala	Val	Ala	Ser	Gly	Trp	Ser	Ile	Glu	Lys	Glu	Leu	465	470	475	480
Pro	Asn	Thr	Val	Gln	Asp	Phe	Asp	Gly	Tyr	Gln	Pro	His	Asn	Tyr	Gly	485	490		495
Asn	Tyr	Glu	Ser	Glu	Asp	Val	Pro	Met	Tyr	Gln	Ala	Leu	Ala	Asn	Ser	500	505		510
Tyr	Asn	Ile	Pro	Ala	Val	Ser	Thr	Leu	Asn	Asp	Ile	Gly	Ile	Asp	Lys	515	520		525
Ala	Phe	Thr	Tyr	Gly	Lys	Thr	Phe	Gly	Leu	Asp	Met	Ser	Ser	Ala	Lys	530	535	540	
Lys	Glu	Leu	Gly	Val	Ala	Leu	Gly	Gly	Ser	Val	Thr	Thr	Asn	Pro	Leu	545	550	555	560
Glu	Met	Ala	Gln	Ala	Tyr	Ala	Ala	Phe	Ala	Asn	Asn	Gly	Val	Ile	His	565	570		575
Pro	Ala	His	Leu	Ile	Asn	Arg	Ile	Glu	Asn	Ala	Arg	Gly	Glu	Val	Leu	580	585		590
Lys	Thr	Phe	Thr	Asp	Lys	Ala	Lys	Arg	Val	Val	Ser	Gln	Ser	Val	Ala	595	600		605
Asp	Lys	Met	Thr	Ala	Met	Met	Leu	Gly	Thr	Phe	Ser	Asn	Gly	Thr	Ala	610	615	620	
Val	Asn	Ala	Asn	Val	Tyr	Gly	Tyr	Thr	Leu	Ala	Gly	Lys	Thr	Gly	Thr	625	630	635	640
Thr	Glu	Thr	Asn	Phe	Asn	Pro	Asp	Leu	Ala	Gly	Asp	Gln	Trp	Val	Ile	645	650		655
Gly	Tyr	Thr	Pro	Asp	Val	Val	Ile	Ser	Gln	Trp	Val	Gly	Phe	Asn	Gln	660	665		670
Thr	Asp	Glu	Asn	His	Tyr	Leu	Thr	Asp	Ser	Ser	Ala	Gly	Thr	Ala	Ser				

ccagcagaag	gtgaagctat	tggagatgct	atcagtaagg	tttggtttgg	tggtcaaggg	420
attattggtg	ctattgtgat	tggtttaacg	gtcggagctg	tttacacaac	atztatccgt	480
cgtcatatcg	tcattaaaat	gccagatcaa	gtgccacaag	ccatcgccaa	acagtttgaa	540
gccatgattc	cagcctttgt	gatctttacc	ttgtcaatgc	ttgtgtatat	tattgccaag	600
tcagtaacag	gtggtggcac	ctttattgaa	atgatttatg	atgtcattca	ggtaccgctg	660
caaggggttaa	cgggttctct	ttatggcgca	ctaggtattg	ccttctttat	ttcctttctt	720
tggtggtttg	gcgtgcatgg	gcaatctgtg	gtcaatggaa	ttgtcactgc	tcttctctta	780
tcaaacttag	atgccaataa	ggccttgatg	gcagcagggtg	agttatccct	agacaagggg	840
gcccatattg	taacccaaca	attttttagac	tctttcttga	ttctatcagg	ttctggcatt	900
acctttgggt	tagtggtagc	tatgatcttt	gcggtctaaat	ccaaacaata	caaggcttta	960
ggcaagggtg	cagccttccc	agccctcttt	aatgttaatg	aaccagtcgt	ctttggtttt	1020
ccaattgtga	tgaatccagt	catgttcttg	ccatttatct	tggttccggg	cttggcagct	1080
ctcacagttt	atggcgccat	tgctattggt	ttcatgcagc	cctttgcagg	agtgaccctt	1140
ccgtgggtcaa	caccagccat	tatctcaggg	ttcatggttg	gtggctggca	aggagctatt	1200
gtgcaaattc	ttatactcat	catgtcaacg	ttggtgtact	tccattctt	taaaatccaa	1260
gataatatgg	cttatcaaaa	tgaacaagct	agtgaagagt	catga		1305

<210> SEQ ID NO 638

<211> LENGTH: 434

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 638

Met	Ala	Lys	Met	Asn	Met	Gln	Asn	Ile	Ile	Lys	Pro	Ile	Met	Thr	Phe
1				5				10					15		
Val	Asn	Met	Arg	Gly	Ile	Ile	Ala	Leu	Lys	Asp	Gly	Met	Leu	Ala	Ile
			20					25					30		
Leu	Pro	Leu	Thr	Val	Val	Gly	Ser	Leu	Phe	Leu	Ile	Ala	Gly	Gln	Ile
			35				40					45			
Pro	Phe	Gln	Gly	Val	Asn	Asp	Ala	Ile	Ala	Ser	Val	Phe	Gly	Ala	Asp
	50					55					60				
Trp	Thr	Glu	Pro	Phe	Met	Gln	Val	Tyr	His	Gly	Thr	Phe	Ala	Ile	Met
65					70					75				80	
Gly	Leu	Ile	Ser	Cys	Phe	Ala	Ile	Gly	Tyr	Ser	Tyr	Ala	Lys	Asn	Ser
				85				90						95	
Gly	Val	Glu	Pro	Leu	Pro	Ser	Gly	Val	Leu	Ser	Leu	Ser	Ala	Phe	Phe
			100					105					110		
Ile	Leu	Leu	Arg	Ser	Ser	Tyr	Val	Pro	Ala	Glu	Gly	Glu	Ala	Ile	Gly
			115				120					125			
Asp	Ala	Ile	Ser	Lys	Val	Trp	Phe	Gly	Gly	Gln	Gly	Ile	Ile	Gly	Ala
	130					135					140				
Ile	Val	Ile	Gly	Leu	Thr	Val	Gly	Ala	Val	Tyr	Thr	Thr	Phe	Ile	Arg
145					150					155				160	
Arg	His	Ile	Val	Ile	Lys	Met	Pro	Asp	Gln	Val	Pro	Gln	Ala	Ile	Ala
				165				170						175	
Lys	Gln	Phe	Glu	Ala	Met	Ile	Pro	Ala	Phe	Val	Ile	Phe	Thr	Leu	Ser
			180				185						190		
Met	Leu	Val	Tyr	Ile	Ile	Ala	Lys	Ser	Val	Thr	Gly	Gly	Gly	Thr	Phe
	195						200					205			
Ile	Glu	Met	Ile	Tyr	Asp	Val	Ile	Gln	Val	Pro	Leu	Gln	Gly	Leu	Thr
	210					215					220				
Gly	Ser	Leu	Tyr	Gly	Ala	Leu	Gly	Ile	Ala	Phe	Phe	Ile	Ser	Phe	Leu
225					230					235					240
Trp	Trp	Phe	Gly	Val	His	Gly	Gln	Ser	Val	Val	Asn	Gly	Ile	Val	Thr
				245				250						255	
Ala	Leu	Leu	Leu	Ser	Asn	Leu	Asp	Ala	Asn	Lys	Ala	Leu	Met	Ala	Ala
			260					265					270		
Gly	Glu	Leu	Ser	Leu	Asp	Lys	Gly	Ala	His	Ile	Val	Thr	Gln	Gln	Phe

	275					280					285								
Leu	Asp	Ser	Phe	Leu	Ile	Leu	Ser	Gly	Ser	Gly	Ile	Thr	Phe	Gly	Leu				
	290					295					300								
Val	Val	Ala	Met	Ile	Phe	Ala	Ala	Lys	Ser	Lys	Gln	Tyr	Lys	Ala	Leu				
305					310					315					320				
Gly	Lys	Val	Ala	Ala	Phe	Pro	Ala	Leu	Phe	Asn	Val	Asn	Glu	Pro	Val				
			325						330					335					
Val	Phe	Gly	Phe	Pro	Ile	Val	Met	Asn	Pro	Val	Met	Phe	Leu	Pro	Phe				
			340					345					350						
Ile	Leu	Val	Pro	Val	Leu	Ala	Ala	Leu	Thr	Val	Tyr	Gly	Ala	Ile	Ala				
	355					360					365								
Ile	Gly	Phe	Met	Gln	Pro	Phe	Ala	Gly	Val	Thr	Leu	Pro	Trp	Ser	Thr				
370					375						380								
Pro	Ala	Ile	Ile	Ser	Gly	Phe	Met	Val	Gly	Gly	Trp	Gln	Gly	Ala	Ile				
385				390					395						400				
Val	Gln	Ile	Leu	Ile	Leu	Ile	Met	Ser	Thr	Leu	Val	Tyr	Phe	Pro	Phe				
			405					410					415						
Phe	Lys	Ile	Gln	Asp	Asn	Met	Ala	Tyr	Gln	Asn	Glu	Gln	Ala	Ser	Glu				
			420					425					430						
Glu	Ser																		

<210> SEQ ID NO 639

<211> LENGTH: 846

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 639

gtgagcgaaa	ttagaaaaga	ggacaagcat	atgaatctac	ttggatcaag	acgggttttt	60
tctaaaaaat	gtcggctagt	aaaattttca	atggtagctc	ttgtatcagc	cacaatggct	120
gtaacaacag	tcacacttga	aaatactgca	ctggcacgac	aaacacaggt	ctcaaagtat	180
gttgttctaa	atgatggcgc	aagcaagtac	ctaaacgaag	cattagcttg	gacattcaat	240
gacagtccca	actattacaa	aaccttaggt	actagtcaga	tcaactccagc	actctttcct	300
aaagcaggag	atattctcta	tagcaaatta	gatgagttag	gaaggacgcg	tactgctaga	360
ggtacattga	cttatgccaa	tgttgaaggt	agctacgggtg	ttagacaatc	tttcggtaaa	420
aatcaaaaacc	ccgcaggctg	gactggaaac	cctaatacatg	tcaaatataa	aattgaatgg	480
ttaaattggtc	tatcttatgt	cggagatttc	tggaatagaa	gtcatctcat	tcagatagt	540
ctcgggtggag	atgcactcag	agtcaatgcc	gttacaggga	cacgtaccca	aaatgtagga	600
ggtcgtgacc	aaaaaaggcgg	catgcgctat	accgaacaaa	gagctcaaga	atgggttagaa	660
gcaaatcgtg	atggctatct	ttattatgaa	gctgctccaa	tctataacgc	agacgagttg	720
attccaagag	ctgctgtggt	atcaatgcaa	tcttctgata	ataccatcaa	cgagaaagta	780
ttagttttaca	acacagctaa	tggctacacc	attaactacc	ataacggtac	acctactcag	840
aaataa						846

<210> SEQ ID NO 640

<211> LENGTH: 281

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 640

Met	Ser	Glu	Ile	Arg	Lys	Glu	Asp	Lys	His	Met	Asn	Leu	Leu	Gly	Ser
1			5						10					15	
Arg	Arg	Val	Phe	Ser	Lys	Lys	Cys	Arg	Leu	Val	Lys	Phe	Ser	Met	Val
		20						25				30			
Ala	Leu	Val	Ser	Ala	Thr	Met	Ala	Val	Thr	Thr	Val	Thr	Leu	Glu	Asn
		35					40				45				
Thr	Ala	Leu	Ala	Arg	Gln	Thr	Gln	Val	Ser	Asn	Asp	Val	Val	Leu	Asn
	50				55					60					
Asp	Gly	Ala	Ser	Lys	Tyr	Leu	Asn	Glu	Ala	Leu	Ala	Trp	Thr	Phe	Asn
65					70				75						80

Asp	Ser	Pro	Asn	Tyr	Tyr	Lys	Thr	Leu	Gly	Thr	Ser	Gln	Ile	Thr	Pro	
				85					90					95		
Ala	Leu	Phe	Pro	Lys	Ala	Gly	Asp	Ile	Leu	Tyr	Ser	Lys	Leu	Asp	Glu	
			100					105					110			
Leu	Gly	Arg	Thr	Arg	Thr	Ala	Arg	Gly	Thr	Leu	Thr	Tyr	Ala	Asn	Val	
		115					120					125				
Glu	Gly	Ser	Tyr	Gly	Val	Arg	Gln	Ser	Phe	Gly	Lys	Asn	Gln	Asn	Pro	
	130					135					140					
Ala	Gly	Trp	Thr	Gly	Asn	Pro	Asn	His	Val	Lys	Tyr	Lys	Ile	Glu	Trp	
145					150					155					160	
Leu	Asn	Gly	Leu	Ser	Tyr	Val	Gly	Asp	Phe	Trp	Asn	Arg	Ser	His	Leu	
			165						170					175		
Ile	Ala	Asp	Ser	Leu	Gly	Gly	Asp	Ala	Leu	Arg	Val	Asn	Ala	Val	Thr	
		180						185					190			
Gly	Thr	Arg	Thr	Gln	Asn	Val	Gly	Gly	Arg	Asp	Gln	Lys	Gly	Gly	Met	
	195						200					205				
Arg	Tyr	Thr	Glu	Gln	Arg	Ala	Gln	Glu	Trp	Leu	Glu	Ala	Asn	Arg	Asp	
	210					215					220					
Gly	Tyr	Leu	Tyr	Tyr	Glu	Ala	Ala	Pro	Ile	Tyr	Asn	Ala	Asp	Glu	Leu	
225					230					235					240	
Ile	Pro	Arg	Ala	Val	Val	Val	Ser	Met	Gln	Ser	Ser	Asp	Asn	Thr	Ile	
			245						250				255			
Asn	Glu	Lys	Val	Leu	Val	Tyr	Asn	Thr	Ala	Asn	Gly	Tyr	Thr	Ile	Asn	
		260						265					270			
Tyr	His	Asn	Gly	Thr	Pro	Thr	Gln	Lys								
		275					280									

<210> SEQ ID NO 641

<211> LENGTH: 1197

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 641

atgaataaaa	agaaattagg	tgctcagatta	ttaagtcttt	tagcattagg	tggtattgtt	60
cttgctaacc	cagtatttgc	cgatcaaaac	tttgctcgta	acgaaaaaga	agcaaaagat	120
agcgctatca	catttatcca	aaaatcagca	gctatcaaag	caggtgcacg	aagcgcagaa	180
gatattaagc	ttgacaaaag	taacttaggt	ggagaacttt	ctggctctaa	tatgtatgtt	240
tacaatat	ctactggagg	atttggtatc	gtttcaggag	ataaacgttc	tccagaaatt	300
ctaggatact	ctaccagcgg	atcatttgac	gctaacggta	aagaaaacat	tgcttccttc	360
atggaaagtt	atgtcgaaca	aatcaaagaa	aacaaaaaat	tagacactac	ttatgctggt	420
accgctgaga	ttaaacaacc	agttgttaaa	tctctccttg	attcaaaagg	cattcattac	480
aatcaaggta	acccttacia	cctattgaca	cctgttattg	aaaaagtaaa	accaggtgaa	540
caatcttttg	taggtcaaca	tgacagctaca	ggatgtgttg	ctactgcaac	tgctcaaatt	600
atgaaatatc	ataattaccc	taacaaaggg	ttgaaagact	acacttacac	actaagctca	660
aataacccat	atttcaacca	tcctaagaac	ttgtttgcag	ctatctctac	tagacaatac	720
aactggaaca	acatcttacc	tacttatagc	ggaagagaat	ctaacgttca	aaaaatggcg	780
atttcagaat	tgatggctga	tgttggtatt	tcagtagaca	tggtattatg	tccatctagt	840
ggttctgcag	gtagctctcg	tgttcaaaga	gccttgaaag	aaaacttttg	ctacaaccaa	900
tctgttcacc	aaatcaaccg	tggcgacttt	agcaaacaag	attgggaagc	acaaattgac	960
aaagaattat	ctcaaaacca	accagtatac	taccaagggt	tcggtaaagt	aggcggacat	1020
gcctttgtta	tcgatggtgc	tgacggacgt	aacttctacc	atgttaactg	gggttggggg	1080
ggagtctctg	acggcttctt	ccgtcttgac	gcactaaacc	cttcagctct	tggtactggt	1140
ggcggcgcag	gcggcttcaa	cgtttaccaa	agtgtgtgtg	taggcatcaa	accttag	1197

<210> SEQ ID NO 642

<211> LENGTH: 398

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 642

Met	Asn	Lys	Lys	Lys	Leu	Gly	Val	Arg	Leu	Leu	Ser	Leu	Leu	Ala	Leu	
1				5					10					15		
Gly	Gly	Phe	Val	Leu	Ala	Asn	Pro	Val	Phe	Ala	Asp	Gln	Asn	Phe	Ala	
			20					25					30			
Arg	Asn	Glu	Lys	Glu	Ala	Lys	Asp	Ser	Ala	Ile	Thr	Phe	Ile	Gln	Lys	
		35					40					45				
Ser	Ala	Ala	Ile	Lys	Ala	Gly	Ala	Arg	Ser	Ala	Glu	Asp	Ile	Lys	Leu	
	50					55					60					
Asp	Lys	Val	Asn	Leu	Gly	Gly	Glu	Leu	Ser	Gly	Ser	Asn	Met	Tyr	Val	
65				70						75				80		
Tyr	Asn	Ile	Ser	Thr	Gly	Gly	Phe	Val	Ile	Val	Ser	Gly	Asp	Lys	Arg	
				85				90						95		
Ser	Pro	Glu	Ile	Leu	Gly	Tyr	Ser	Thr	Ser	Gly	Ser	Phe	Asp	Ala	Asn	
			100					105					110			
Gly	Lys	Glu	Asn	Ile	Ala	Ser	Phe	Met	Glu	Ser	Tyr	Val	Glu	Gln	Ile	
		115					120					125				
Lys	Glu	Asn	Lys	Lys	Leu	Asp	Thr	Thr	Tyr	Ala	Gly	Thr	Ala	Glu	Ile	
	130					135					140					
Lys	Gln	Pro	Val	Val	Lys	Ser	Leu	Leu	Asp	Ser	Lys	Gly	Ile	His	Tyr	
145					150				155					160		
Asn	Gln	Gly	Asn	Pro	Tyr	Asn	Leu	Leu	Thr	Pro	Val	Ile	Glu	Lys	Val	
				165					170					175		
Lys	Pro	Gly	Glu	Gln	Ser	Phe	Val	Gly	Gln	His	Ala	Ala	Thr	Gly	Cys	
			180					185					190			
Val	Ala	Thr	Ala	Thr	Ala	Gln	Ile	Met	Lys	Tyr	His	Asn	Tyr	Pro	Asn	
		195					200					205				
Lys	Gly	Leu	Lys	Asp	Tyr	Thr	Tyr	Thr	Leu	Ser	Ser	Asn	Asn	Pro	Tyr	
	210					215						220				
Phe	Asn	His	Pro	Lys	Asn	Leu	Phe	Ala	Ala	Ile	Ser	Thr	Arg	Gln	Tyr	
225					230					235				240		
Asn	Trp	Asn	Asn	Ile	Leu	Pro	Thr	Tyr	Ser	Gly	Arg	Glu	Ser	Asn	Val	
				245					250					255		
Gln	Lys	Met	Ala	Ile	Ser	Glu	Leu	Met	Ala	Asp	Val	Gly	Ile	Ser	Val	
			260					265					270			
Asp	Met	Asp	Tyr	Gly	Pro	Ser	Ser	Gly	Ser	Ala	Gly	Ser	Ser	Arg	Val	
	275						280					285				
Gln	Arg	Ala	Leu	Lys	Glu	Asn	Phe	Gly	Tyr	Asn	Gln	Ser	Val	His	Gln	
	290					295					300					
Ile	Asn	Arg	Gly	Asp	Phe	Ser	Lys	Gln	Asp	Trp	Glu	Ala	Gln	Ile	Asp	
305					310					315				320		
Lys	Glu	Leu	Ser	Gln	Asn	Gln	Pro	Val	Tyr	Tyr	Gln	Gly	Val	Gly	Lys	
				325					330					335		
Val	Gly	Gly	His	Ala	Phe	Val	Ile	Asp	Gly	Ala	Asp	Gly	Arg	Asn	Phe	
			340					345					350			
Tyr	His	Val	Asn	Trp	Gly	Trp	Gly	Gly	Val	Ser	Asp	Gly	Phe	Phe	Arg	
	355						360					365				
Leu	Asp	Ala	Leu	Asn	Pro	Ser	Ala	Leu	Gly	Thr	Gly	Gly	Gly	Ala	Gly	
	370					375					380					
Gly	Phe	Asn	Gly	Tyr	Gln	Ser	Ala	Val	Val	Gly	Ile	Lys	Pro			
385					390						395					

<210> SEQ ID NO 643

<211> LENGTH: 1389

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 643

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gtgagactaa tcaaaaaaac ctttttggtc atcaatggct taattattgt agtgggttacc      60
tctattttgt tagtgcttta ttttgcaatg ccaattttatt acaccaaagt caaagacaaa      120
gaagttaagt gtgaatttga ccaaacaagc aagcaaatca aaggcaaaac ggtaaccgag      180
attagagata tcctaacaaa aaaaatcaac aaagataata tttggtacag cttagtagac      240
agtgataacc aactgctcta tccttccttg cagctcctag acggcgctcag tgaaagcaaa      300
gacagtcaaa atgttaatat cgtcaccacc tttgacaact cttatttctaa tgtaagggtg      360
atgagtcaaa aagtaaccct acgcgatgga aaaaaaatga cattgcttgg gcaatcttca      420
cttcaacccg taacagatgc tagcaaaagt ctccttgacc tctaccgctc actattgatt      480
ttttcagtga ccgtagggag tattgtcgcc tacttatata gtaggacttc tagccggcgt      540
atccttagca tgtcacaaac cgccaaaaaa atgggtcaacc tagaaccaaa cttaacgtgt      600
accattcacg gcaaagatga aatagcaatg ttggctagtg atattaaccg tttgtatgcg      660
agtctttcaa cgagcatcaa atccttgcaa aaagagtatg aaaaagcttc tgattcagaa      720
agagagaaat ctgagttttt acgcatgaca tcgcacgagc taaagacacc aatcactagt      780
gttatcgga tgaattgatgg aatgctctat aatgttgggtg actttgcaga tcgtgacaaa      840
tatttgcgaa agtgccgaga cgtccttgaa gggcaagccc aactggttca atccatttta      900
tctttatcta agattgaaac cctagcttct caaaaatcaag aactgttttc actaaaaagc      960
agcctagaag aagaaatgga agtctttctc gtcttatcag aactaaaaca cctcaaagtg     1020
actatcaatc tcgaagaaca attcgtcaaa gccaaataaag tatacttact aaaggcgatt     1080
aaaaatatta ttgacaatgc ctttcactat accaaatcag gcggccaagt gatgattcaa     1140
ctaaaagaca accaactagt gattaaaaat gaagcagaga cattattgac acaacagcag     1200
atgaaacagt tattccaacc gttttatcga ccagattata gtcgtaacag gaaagacggt     1260
ggtacaggat tggggctggt tatcaccac cagattcttg atcagcatca tctggcttat     1320
cgctttgttg ttcttgatca aagatggatg gtatttacga ttgattttcc atcccatcat     1380
gacgattga                                     1389

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<210> SEQ ID NO 644
<211> LENGTH: 462
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 644

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Met Arg Leu Ile Lys Lys Thr Phe Leu Val Ile Asn Gly Leu Ile Ile
1          5          10          15
Val Val Val Thr Ser Ile Leu Leu Val Leu Tyr Phe Ala Met Pro Ile
20          25          30
Tyr Tyr Thr Lys Val Lys Asp Lys Glu Val Lys Cys Glu Phe Asp Gln
35          40          45
Thr Ser Lys Gln Ile Lys Gly Lys Thr Val Thr Glu Ile Arg Asp Ile
50          55          60
Leu Thr Lys Lys Ile Asn Lys Asp Asn Ile Trp Tyr Ser Leu Val Asp
65          70          75          80
Ser Asp Asn Gln Leu Leu Tyr Pro Ser Leu Gln Leu Leu Asp Gly Val
85          90          95
Ser Glu Ser Lys Asp Ser Gln Asn Val Asn Ile Val Thr Thr Phe Asp
100         105         110
Asn Ser Tyr Ser Asn Val Lys Val Met Ser Gln Lys Val Thr Leu Arg
115         120         125
Asp Gly Lys Lys Met Thr Leu Leu Gly Gln Ser Ser Leu Gln Pro Val
130         135         140
Thr Asp Ala Ser Lys Val Leu Leu Asp Leu Tyr Pro Ser Leu Leu Ile
145         150         155         160
Phe Ser Val Thr Val Gly Ser Ile Val Ala Tyr Leu Tyr Ser Arg Thr
165         170         175
Ser Ser Arg Arg Ile Leu Ser Met Ser Gln Thr Ala Lys Lys Met Val
180         185         190
Asn Leu Glu Pro Asn Leu Thr Cys Thr Ile His Gly Lys Asp Glu Ile
195         200         205
Ala Met Leu Ala Ser Asp Ile Asn Arg Leu Tyr Ala Ser Leu Ser Thr

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210		215		220
Ser Ile Lys Ser Leu Gln Lys Glu Tyr Glu Lys Ala Ser Asp Ser Glu				
225		230		240
Arg Glu Lys Ser Glu Phe Leu Arg Met Thr Ser His Glu Leu Lys Thr				
	245		250	255
Pro Ile Thr Ser Val Ile Gly Met Ile Asp Gly Met Leu Tyr Asn Val				
	260		265	270
Gly Asp Phe Ala Asp Arg Asp Lys Tyr Leu Arg Lys Cys Arg Asp Val				
	275		280	285
Leu Glu Gly Gln Ala Gln Leu Val Gln Ser Ile Leu Ser Leu Ser Lys				
	290		295	300
Ile Glu Thr Leu Ala Ser Gln Asn Gln Glu Leu Phe Ser Leu Lys Ser				
305		310		320
Ser Leu Glu Glu Glu Met Glu Val Phe Leu Val Leu Ser Glu Leu Lys				
	325		330	335
His Leu Lys Val Thr Ile Asn Leu Glu Glu Gln Phe Val Lys Ala Asn				
	340		345	350
Lys Val Tyr Leu Leu Lys Ala Ile Lys Asn Ile Ile Asp Asn Ala Phe				
	355		360	365
His Tyr Thr Lys Ser Gly Gly Gln Val Met Ile Gln Leu Lys Asp Asn				
	370		375	380
Gln Leu Val Ile Lys Asn Glu Ala Glu Thr Leu Leu Thr Gln Gln Gln				
385		390		400
Met Lys Gln Leu Phe Gln Pro Phe Tyr Arg Pro Asp Tyr Ser Arg Asn				
	405		410	415
Arg Lys Asp Gly Gly Thr Gly Leu Gly Leu Phe Ile Thr His Gln Ile				
	420		425	430
Leu Asp Gln His His Leu Ala Tyr Arg Phe Val Val Leu Asp Gln Arg				
	435		440	445
Trp Met Val Phe Thr Ile Asp Phe Pro Ser His His Asp Asp				
	450		455	460

<210> SEQ ID NO 645

<211> LENGTH: 1626

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 645

atgaagaaaa	ggaaattggt	agcagtaaca	ctattaagta	ccataactctt	aaacagtgca	60
gtgccattag	ttgttgctga	tacctccttg	cgtaatagca	catcatccac	tgatcagcct	120
actacagcag	atactgatac	ggatgacgag	agtgaacac	caaaaaaaga	caaaaaaagc	180
aaggaaacag	cgtcgcagca	cgacacccaa	aaagaccata	agccatcaca	cactcaccca	240
acccccctt	caaatgatac	taagcagacc	gatcaggcat	catctgaagc	tactgacaaa	300
ccaaataaag	acaaaaacga	caccaagcaa	ccagacagca	gtgatcaatc	caccccatct	360
cccaaagacc	agtcgtctca	aaaagagtca	caaaacaaag	acggccgacc	taccccatca	420
cctgatcagc	aaaaagatca	gacacctgat	aaaacaccag	aaaaatcagc	tgataaaacc	480
cctgaaaaag	gaccagaaaa	agcaactgat	aaaacaccag	agccaaatcg	tgacgctcca	540
aaacccatcc	aacctccttt	agcagctgct	cctgtcttta	taccttgagg	agaaagtgc	600
aaagacctga	gcaagctaaa	accaagcagt	cgctcatcag	cggcttacgt	gagacactgg	660
acagggtgact	ctgcctacac	tcacaacctg	ttgtcacgcc	gttatgggat	tactgctgaa	720
cagctagatg	gttttttgaa	cagtctaggt	attcactatg	ataaagaacg	cttaaaccga	780
aagcgtttat	tagaatggga	aaaactaaca	ggactagacg	ttcgagctat	cgtagctatt	840
gcaatggcag	aaagctcact	aggtactcag	ggagttgcta	aagaaaaagg	agccaatatg	900
tttggttatg	gcgcccttga	cttcaaccca	aacaatgcc	aaaaatacag	cgatgaggtt	960
gctattcgtc	acatggtaga	agacaccatc	attgccaa	aaaaccaa	ctttgaaaga	1020
caagacctca	aagcaaaaaa	atggctcacta	ggccagttgg	ataccttgat	tgatggtggg	1080
gtttacttta	cagatacaag	tggcagtg	caagacagag	cagatatcat	gaccaaacta	1140
gaccaatgga	tagatgatca	tggaagcaca	cctgagattc	cagaacatct	caagataact	1200

tccgggacac aatttagcga agtgcccgta ggttataaaa gaagtcagcc acaaaacggt	1260
ttgacctaca agtcagagac ctacagcttt ggccaatgca cttggtacgc ctataatcgt	1320
gtcaaagagc taggttatca agtcgacagg tacatgggta acggtggcga ctggcagcgc	1380
aagccagggt ttgtgaccac ccataaacct aaagtgggct atgtcgtctc atttgcacca	1440
ggccaagcag gagcagatgc aacctatggg cactgtgctg ttgtagagca aatcaaagaa	1500
gatgggttcta tcttaatttc agagtcaaat gttatgggac taggcaccat ttcctatcgg	1560
acgttcacag ctgagcaggc tagtttgttg acctatgtcg taggggacaa actccaaga	1620
ccataa	1626

<210> SEQ ID NO 646

<211> LENGTH: 541

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 646

Met	Lys	Lys	Arg	Lys	Leu	Leu	Ala	Val	Thr	Leu	Leu	Ser	Thr	Ile	Leu
1				5					10					15	
Leu	Asn	Ser	Ala	Val	Pro	Leu	Val	Val	Ala	Asp	Thr	Ser	Leu	Arg	Asn
			20					25					30		
Ser	Thr	Ser	Ser	Thr	Asp	Gln	Pro	Thr	Thr	Ala	Asp	Thr	Asp	Thr	Asp
		35				40						45			
Asp	Glu	Ser	Glu	Thr	Pro	Lys	Lys	Asp	Lys	Lys	Ser	Lys	Glu	Thr	Ala
	50					55					60				
Ser	Gln	His	Asp	Thr	Gln	Lys	Asp	His	Lys	Pro	Ser	His	Thr	His	Pro
65					70					75					80
Thr	Pro	Pro	Ser	Asn	Asp	Thr	Lys	Gln	Thr	Asp	Gln	Ala	Ser	Ser	Glu
				85					90					95	
Ala	Thr	Asp	Lys	Pro	Asn	Lys	Asp	Lys	Asn	Asp	Thr	Lys	Gln	Pro	Asp
			100					105					110		
Ser	Ser	Asp	Gln	Ser	Thr	Pro	Ser	Pro	Lys	Asp	Gln	Ser	Ser	Gln	Lys
		115					120					125			
Glu	Ser	Gln	Asn	Lys	Asp	Gly	Arg	Pro	Thr	Pro	Ser	Pro	Asp	Gln	Gln
	130					135					140				
Lys	Asp	Gln	Thr	Pro	Asp	Lys	Thr	Pro	Glu	Lys	Ser	Ala	Asp	Lys	Thr
145					150					155					160
Pro	Glu	Lys	Gly	Pro	Glu	Lys	Ala	Thr	Asp	Lys	Thr	Pro	Glu	Pro	Asn
			165						170					175	
Arg	Asp	Ala	Pro	Lys	Pro	Ile	Gln	Pro	Pro	Leu	Ala	Ala	Ala	Pro	Val
		180						185					190		
Phe	Ile	Pro	Trp	Arg	Glu	Ser	Asp	Lys	Asp	Leu	Ser	Lys	Leu	Lys	Pro
	195						200					205			
Ser	Ser	Arg	Ser	Ser	Ala	Ala	Tyr	Val	Arg	His	Trp	Thr	Gly	Asp	Ser
	210				215						220				
Ala	Tyr	Thr	His	Asn	Leu	Leu	Ser	Arg	Arg	Tyr	Gly	Ile	Thr	Ala	Glu
225				230						235					240
Gln	Leu	Asp	Gly	Phe	Leu	Asn	Ser	Leu	Gly	Ile	His	Tyr	Asp	Lys	Glu
			245						250					255	
Arg	Leu	Asn	Gly	Lys	Arg	Leu	Leu	Glu	Trp	Glu	Lys	Leu	Thr	Gly	Leu
		260						265					270		
Asp	Val	Arg	Ala	Ile	Val	Ala	Ile	Ala	Met	Ala	Glu	Ser	Ser	Leu	Gly
	275						280					285			
Thr	Gln	Gly	Val	Ala	Lys	Glu	Lys	Gly	Ala	Asn	Met	Phe	Gly	Tyr	Gly
	290				295						300				
Ala	Phe	Asp	Phe	Asn	Pro	Asn	Asn	Ala	Lys	Lys	Tyr	Ser	Asp	Glu	Val
305				310						315					320
Ala	Ile	Arg	His	Met	Val	Glu	Asp	Thr	Ile	Ile	Ala	Asn	Lys	Asn	Gln
			325						330					335	
Thr	Phe	Glu	Arg	Gln	Asp	Leu	Lys	Ala	Lys	Lys	Trp	Ser	Leu	Gly	Gln

			340					345					350				
Leu	Asp	Thr	Leu	Ile	Asp	Gly	Gly	Val	Tyr	Phe	Thr	Asp	Thr	Ser	Gly		
			355				360					365					
Ser	Gly	Gln	Arg	Arg	Ala	Asp	Ile	Met	Thr	Lys	Leu	Asp	Gln	Trp	Ile		
			370				375					380					
Asp	Asp	His	Gly	Ser	Thr	Pro	Glu	Ile	Pro	Glu	His	Leu	Lys	Ile	Thr		
385					390					395					400		
Ser	Gly	Thr	Gln	Phe	Ser	Glu	Val	Pro	Val	Gly	Tyr	Lys	Arg	Ser	Gln		
				405					410					415			
Pro	Gln	Asn	Val	Leu	Thr	Tyr	Lys	Ser	Glu	Thr	Tyr	Ser	Phe	Gly	Gln		
			420					425					430				
Cys	Thr	Trp	Tyr	Ala	Tyr	Asn	Arg	Val	Lys	Glu	Leu	Gly	Tyr	Gln	Val		
		435					440					445					
Asp	Arg	Tyr	Met	Gly	Asn	Gly	Gly	Asp	Trp	Gln	Arg	Lys	Pro	Gly	Phe		
450					455					460							
Val	Thr	Thr	His	Lys	Pro	Lys	Val	Gly	Tyr	Val	Val	Ser	Phe	Ala	Pro		
465				470					475						480		
Gly	Gln	Ala	Gly	Ala	Asp	Ala	Thr	Tyr	Gly	His	Val	Ala	Val	Val	Glu		
				485				490						495			
Gln	Ile	Lys	Glu	Asp	Gly	Ser	Ile	Leu	Ile	Ser	Glu	Ser	Asn	Val	Met		
			500					505					510				
Gly	Leu	Gly	Thr	Ile	Ser	Tyr	Arg	Thr	Phe	Thr	Ala	Glu	Gln	Ala	Ser		
		515					520					525					
Leu	Leu	Thr	Tyr	Val	Val	Gly	Asp	Lys	Leu	Pro	Arg	Pro					
		530				535					540						

<210> SEQ ID NO 647

<211> LENGTH: 927

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 647

atgaatatta	gaaataagat	tgaaaatagt	aaaacactac	tatttacatc	ccttgtagcc	60
gtggctctac	taggagctac	acaaccagtt	tcagccgaaa	cgtatacatc	acgcaatttt	120
gactgggtctg	gagatgactg	gtctggagat	gactggcctg	aagatgactg	gtctggagat	180
ggtttggtcta	aatatgaccg	gtctggagtt	ggtttggtctc	aatatggctg	gtctaaatat	240
ggctgggtcta	gcgataaaga	agaatggcct	gaagattggc	ctgaagatga	ctgggtctagc	300
gataaaaaaag	atgagacaga	agataaaacg	agaccacat	atggagaagc	attaggtaca	360
gggtatgaaa	aacgtgatga	ttggggagga	cctggtagcg	tggcaactga	cccttacact	420
ccaccatatg	gaggagcatt	aggtacaggg	tatgaaaaac	gtgatgattg	gggaggacct	480
ggtagcgttg	caactgaccc	ttacactcca	ccatatggag	gagcattagg	tacagggtat	540
gaaaaacgtg	atgattggag	aggacctgga	catattccta	aacctgagaa	cgaacaatca	600
ccaaaccac	ttcatattcc	tgaacctcct	cagattgagt	ggcctcagt	gaatggcttt	660
gatggattat	catttggccc	ctctgattgg	ggccaatctg	aggacacccc	tccaagtga	720
cctcgtgtgc	cagaaaaacc	gcaacatact	cctcaaaaaa	atccacaaga	atcagatttt	780
gatagagggg	tttcagctgg	cttgaaagca	aaaaactcag	gtagagggtat	tgattttgaa	840
ggtttccagt	atggtggctg	gtcagacgaa	tataaaaaag	gttacatgca	agccttcggt	900
acaccatata	caccatcagc	aacgtaa				927

<210> SEQ ID NO 648

<211> LENGTH: 308

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 648

Met	Asn	Ile	Arg	Asn	Lys	Ile	Glu	Asn	Ser	Lys	Thr	Leu	Leu	Phe	Thr
1				5					10					15	
Ser	Leu	Val	Ala	Val	Ala	Leu	Leu	Gly	Ala	Thr	Gln	Pro	Val	Ser	Ala
			20					25					30		

Glu	Thr	Tyr	Thr	Ser	Arg	Asn	Phe	Asp	Trp	Ser	Gly	Asp	Asp	Trp	Ser		
		35					40					45					
Gly	Asp	Asp	Trp	Pro	Glu	Asp	Asp	Trp	Ser	Gly	Asp	Gly	Leu	Ser	Lys		
	50					55				60							
Tyr	Asp	Arg	Ser	Gly	Val	Gly	Leu	Ser	Gln	Tyr	Gly	Trp	Ser	Lys	Tyr		
65				70					75					80			
Gly	Trp	Ser	Ser	Asp	Lys	Glu	Glu	Trp	Pro	Glu	Asp	Trp	Pro	Glu	Asp		
			85					90					95				
Asp	Trp	Ser	Ser	Asp	Lys	Lys	Asp	Glu	Thr	Glu	Asp	Lys	Thr	Arg	Pro		
		100						105					110				
Pro	Tyr	Gly	Glu	Ala	Leu	Gly	Thr	Gly	Tyr	Glu	Lys	Arg	Asp	Asp	Trp		
	115					120						125					
Gly	Gly	Pro	Gly	Thr	Val	Ala	Thr	Asp	Pro	Tyr	Thr	Pro	Pro	Tyr	Gly		
	130				135						140						
Gly	Ala	Leu	Gly	Thr	Gly	Tyr	Glu	Lys	Arg	Asp	Asp	Trp	Gly	Gly	Pro		
145				150					155						160		
Gly	Thr	Val	Ala	Thr	Asp	Pro	Tyr	Thr	Pro	Pro	Tyr	Gly	Gly	Ala	Leu		
		165						170						175			
Gly	Thr	Gly	Tyr	Glu	Lys	Arg	Asp	Asp	Trp	Arg	Gly	Pro	Gly	His	Ile		
	180						185				190						
Pro	Lys	Pro	Glu	Asn	Glu	Gln	Ser	Pro	Asn	Pro	Leu	His	Ile	Pro	Glu		
	195					200			205								
Pro	Pro	Gln	Ile	Glu	Trp	Pro	Gln	Trp	Asn	Gly	Phe	Asp	Gly	Leu	Ser		
	210					215				220							
Phe	Gly	Pro	Ser	Asp	Trp	Gly	Gln	Ser	Glu	Asp	Thr	Pro	Pro	Ser	Glu		
225				230					235						240		
Pro	Arg	Val	Pro	Glu	Lys	Pro	Gln	His	Thr	Pro	Gln	Lys	Asn	Pro	Gln		
		245						250					255				
Glu	Ser	Asp	Phe	Asp	Arg	Gly	Phe	Ser	Ala	Gly	Leu	Lys	Ala	Lys	Asn		
	260					265			270								
Ser	Gly	Arg	Gly	Ile	Asp	Phe	Glu	Gly	Phe	Gln	Tyr	Gly	Gly	Trp	Ser		
	275					280					285						
Asp	Glu	Tyr	Lys	Lys	Gly	Tyr	Met	Gln	Ala	Phe	Gly	Thr	Pro	Tyr	Thr		
	290				295						300						
Pro	Ser	Ala	Thr														
305																	

<210> SEQ ID NO 649

<211> LENGTH: 822

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 649

atgatattga	aacgtcgaac	gatgggtttta	tggcaactgg	gtatcgccat	ttctctcatt	60
cttagtattc	tagccttaaa	cctttatttc	tataggacgc	ctttggaaac	caatgcagct	120
ttacgcaacc	tcgctccttc	cttaaaccat	ctttttggga	cagatgggtt	aggtagggat	180
atgtttgtca	gaacgattaa	agggctttat	ttctctttac	aagtcggctt	attaggcgcc	240
cttatgggag	tctttcttgc	gaccgttttt	ggagtgcctg	caggtctagg	aaatagcctt	300
attgataaaa	taatagcctg	gttggttgat	ttgtttattg	gtatgcctca	tttgattttt	360
atgattctca	tttcttttgt	tgttgggaaa	ggggctcaag	gggttatcat	tgcaacagct	420
gttaccatt	ggccctctct	agcaaggcct	atccgcaatg	aagtctatga	tctaaagaat	480
aaagcctttg	tccagctctc	taaaagcatg	ggaaaaacgc	cttattatat	tgtgaggcat	540
catatcctgc	ctttgattgc	ttctcaaatt	ttcattgggt	ttatcctctt	atttcgcac	600
gtcatcttgc	atgaagcatc	catgactttc	ttaggatttg	gcctttctgc	cgaacaacct	660
tcggttggtg	tcattttgtc	agaggcagct	aagcatatct	ctcttggtgaa	ttggtggttg	720
gtgatttttc	caggccttta	tcttattttg	gttgtcaatg	cctttgatac	tatcggagaa	780
tctttaaaga	aactctttta	ccctcaaacy	gatcattttt	ag		822

<210> SEQ ID NO 650
 <211> LENGTH: 273
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 650

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Met Ile Leu Lys Arg Arg Thr Met Val Leu Trp Gln Leu Gly Ile Ala
1      5      10      15
Ile Ser Leu Ile Leu Ser Ile Leu Ala Leu Asn Leu Tyr Phe Tyr Arg
      20      25      30
Thr Pro Leu Glu Thr Asn Ala Ala Leu Arg Asn Leu Ala Pro Ser Leu
      35      40      45
Asn His Leu Phe Gly Thr Asp Gly Leu Gly Arg Asp Met Phe Val Arg
      50      55      60
Thr Ile Lys Gly Leu Tyr Phe Ser Leu Gln Val Gly Leu Leu Gly Ala
65      70      75      80
Leu Met Gly Val Phe Leu Ala Thr Val Phe Gly Val Leu Ala Gly Leu
      85      90      95
Gly Asn Ser Leu Ile Asp Lys Ile Ile Ala Trp Leu Val Asp Leu Phe
      100     105     110
Ile Gly Met Pro His Leu Ile Phe Met Ile Leu Ile Ser Phe Val Val
      115     120     125
Gly Lys Gly Ala Gln Gly Val Ile Ile Ala Thr Ala Val Thr His Trp
      130     135     140
Pro Ser Leu Ala Arg Leu Ile Arg Asn Glu Val Tyr Asp Leu Lys Asn
145     150     155     160
Lys Ala Phe Val Gln Leu Ser Lys Ser Met Gly Lys Thr Pro Tyr Tyr
      165     170     175
Ile Val Arg His His Ile Leu Pro Leu Ile Ala Ser Gln Ile Phe Ile
      180     185     190
Gly Phe Ile Leu Leu Phe Pro His Val Ile Leu His Glu Ala Ser Met
      195     200     205
Thr Phe Leu Gly Phe Gly Leu Ser Ala Glu Gln Pro Ser Val Gly Ile
      210     215     220
Ile Leu Ser Glu Ala Ala Lys His Ile Ser Leu Gly Asn Trp Trp Leu
225     230     235     240
Val Ile Phe Pro Gly Leu Tyr Leu Ile Leu Val Val Asn Ala Phe Asp
      245     250     255
Thr Ile Gly Glu Ser Leu Lys Lys Leu Phe Tyr Pro Gln Thr Asp His
      260     265     270
Phe

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<210> SEQ ID NO 651
 <211> LENGTH: 978
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 651

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gtgaaacgta ctaccattat tatcatctgg aaaatcatca gatgtgtcac gcttattttt 60
ggggatatctg ttttgacctt cgttttggtt aaacaatctc cagtagatcc agtcatggca 120
agtgtcaatt atgacacatc actaaccctt gctcagtaca aagcgattgc tcaccactat 180
ggcttggata agccagctct agtccaatat tttatttggg tgaaaaatgt gatacaggga 240
gatttaggga cctcgctcgt ttatcggcaa cctggttagtg atattattag atcacgggca 300
gggtgcttctt tcatacttat gggactctct tggatcttat cgggtcttat tggatttatc 360
ttaggaacgt tatccgcttt ccatcaaggg aaattacttg accgagttgt caggtggttt 420
tcataccttc agatatcagt accaacgttt tggattggac tcattttttt attaatcttt 480
tctgtccagc tgggggtggtt cccgattggt atttcttccc cgataggcac tttgagtcaa 540
gatattacgt tagctgatcg agttaagcac cttatgtttac ctgttttcac gctaagtatt 600
ctaggcattg ccaatgtcac ccttcatacg agaactaaaa tgatgtcggg gcttttctagt 660

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gaatatgtct	tatttgccag	agcgcggtggg	gaaacacagt	ggcaaatttt	taaacatcat	720
tgcccttagaa	atgctatcgt	accagctatt	acactgcatt	tttcctattt	tgaggaaattg	780
tttggaggat	ctgttcttgc	tgagcaagtt	ttctcatatc	ctggccttagg	gtctaccctc	840
actgaagcag	gacttaaaag	tgatacacccg	ctccttctag	ctattgtgat	gatagggaca	900
ttatttgttt	ttgcgggcaa	tcttattgcg	gatattttta	atagcatcat	caatccacag	960
ttaaggagaa	aagtatga					978

<210> SEQ ID NO 652

<211> LENGTH: 325

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 652

Met	Lys	Arg	Thr	Thr	Ile	Ile	Ile	Ile	Trp	Lys	Ile	Ile	Arg	Cys	Val
1				5					10					15	
Thr	Leu	Ile	Phe	Gly	Val	Ser	Val	Leu	Thr	Phe	Val	Leu	Leu	Lys	Gln
			20					25					30		
Ser	Pro	Val	Asp	Pro	Val	Met	Ala	Ser	Val	Asn	Tyr	Asp	Thr	Ser	Leu
		35					40					45			
Thr	Pro	Ala	Gln	Tyr	Lys	Ala	Ile	Ala	His	His	Tyr	Gly	Leu	Asp	Lys
		50				55					60				
Pro	Ala	Leu	Val	Gln	Tyr	Phe	Ile	Trp	Leu	Lys	Asn	Val	Ile	Gln	Gly
65					70					75				80	
Asp	Leu	Gly	Thr	Ser	Leu	Val	Tyr	Arg	Gln	Pro	Val	Ser	Asp	Ile	Ile
				85					90					95	
Arg	Ser	Arg	Ala	Gly	Ala	Ser	Phe	Ile	Leu	Met	Gly	Leu	Ser	Trp	Ile
			100					105					110		
Leu	Ser	Gly	Leu	Ile	Gly	Phe	Ile	Leu	Gly	Thr	Leu	Ser	Ala	Phe	His
		115					120					125			
Gln	Gly	Lys	Leu	Leu	Asp	Arg	Val	Val	Arg	Trp	Phe	Ser	Tyr	Leu	Gln
		130				135					140				
Ile	Ser	Val	Pro	Thr	Phe	Trp	Ile	Gly	Leu	Ile	Phe	Leu	Leu	Ile	Phe
145					150					155					160
Ser	Val	Gln	Leu	Gly	Trp	Phe	Pro	Ile	Gly	Ile	Ser	Ser	Pro	Ile	Gly
				165					170					175	
Thr	Leu	Ser	Gln	Asp	Ile	Thr	Leu	Ala	Asp	Arg	Val	Lys	His	Leu	Met
			180					185					190		
Leu	Pro	Val	Phe	Thr	Leu	Ser	Ile	Leu	Gly	Ile	Ala	Asn	Val	Thr	Leu
		195					200					205			
His	Thr	Arg	Thr	Lys	Met	Met	Ser	Val	Leu	Ser	Ser	Glu	Tyr	Val	Leu
		210				215					220				
Phe	Ala	Arg	Ala	Arg	Gly	Glu	Thr	Gln	Trp	Gln	Ile	Phe	Lys	His	His
225					230					235					240
Cys	Leu	Arg	Asn	Ala	Ile	Val	Pro	Ala	Ile	Thr	Leu	His	Phe	Ser	Tyr
				245					250					255	
Phe	Gly	Glu	Leu	Phe	Gly	Gly	Ser	Val	Leu	Ala	Glu	Gln	Val	Phe	Ser
			260					265					270		
Tyr	Pro	Gly	Leu	Gly	Ser	Thr	Leu	Thr	Glu	Ala	Gly	Leu	Lys	Ser	Asp
		275					280					285			
Thr	Pro	Leu	Leu	Leu	Ala	Ile	Val	Met	Ile	Gly	Thr	Leu	Phe	Val	Phe
		290				295					300				
Ala	Gly	Asn	Leu	Ile	Ala	Asp	Ile	Leu	Asn	Ser	Ile	Ile	Asn	Pro	Gln
305					310					315					320
Leu	Arg	Arg	Lys	Val											
				325											

<210> SEQ ID NO 653

<211> LENGTH: 2187

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 653

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atgaaaacat cattcaagca actgtttcgt ttcgaatttt ggcaaaaatt tgggaaatgt      60
cttatggtcg ttattgctgt catgccagcg gctgggttaa tgatcagtat cggaaactct      120
attccaatga ttaaccacga ctacgcatTT ttggcatctc taggcaacat tatcgctcaa      180
attggttggg ctgttattgt taaccttcac ttgctatttg ccttggccat tgggtgtagt      240
tgggctaaag aaagagctgg aggggccttt gcctcagggc ttgcttttgt cttgatcaat      300
cggataacag gtgcttttta tggcgtgtct agtactatgc tagctgatcc agaagcaaaa      360
atcacaagcc tccttggcac tcaaatgatc gttaaaagatt atttcaccag tgccttgga      420
tctccagctt taaacacagg ggtttttgtt gggattattg cagggttcgt aggagcaacg      480
gcctataaca aatactataa ttaccgtaaa cttcctgaag ttttgacctt ctttaatggg      540
aagcgttttg taccatttgt cgttatttta cgttctattt ttgtagccct tattttgggt      600
gttggtttggc cgggtgatcca gtctgggatt aacagttttg ggatgtggat tgcctcttca      660
caagattcag ctccaatcct agccccattc ctatatggta ccttggaacg tctcttggtg      720
ccatttggtc ttcaccacat gttgacgatc ccaatgaact atacagctct tgggtggaact      780
tatgagggtca tgacagggtgc agcagcgggg acaaaaagtat ttggtcaaga ccctttgtgg      840
cttgcttggg taactgacct tgttcacctt aaaggatcag acgcttcagc ctatagtcac      900
ttaatggata gtgtgactcc agctcgtttc aaagtaggac aaatgattgg agctaccgga      960
acattgatgg gggttgcctt agccatgtac cgtaatgtgg atgccgataa aaaacacaca     1020
tacaaaatga tgttcatctc agcagcggca gcggtccttt tgacaggggt aactgagcca     1080
cttgagtacc tatttatgtt tgcagcaatg ccactttaca tcgtctatgc ccttgttcaa     1140
ggagcttcat ttgccatggc agacctgtg aatctccgtg ttcactcatt tggaaatata     1200
gagctactaa cccgcacccc tatggctctt aaagcaggcc taggcatgga tgtgattaac     1260
tttgtttggg tttctgtcct ctttgagtt atcatgtact ttattgcaga tatgatgatc     1320
aagaaaatgc atctcgcaac agctggccgt ttaggcaact acgatgccga tatactgggt     1380
gaccgtaaca ctcaacaag acctacccaa gtagcagata gcaactctca agtcgtgcaa     1440
atcgттаатс tccttgggtg ggcaggcaat attgatgatg ttgatgcttg tatgacgcgc     1500
ttacgagtga cgggtcaaaga ccccgctaag gttggtgctg aggacgattg gaaaaaagct     1560
ggcgctatag gcttgatcca aaaaggcaac ggcgttcaag cggctctatg ccctaaagca     1620
gatattttga aatcagatat tcaagatttg ctggactcag gtgctcttat tccagaagtc     1680
aatatgtcac agctcactag caaaccgact cccgcaaaag attttaaaca cgtgacagaa     1740
gagtgtctat cagtggcaga cgggatgggt ctccaatca caggtgtaaa agaccaggtg     1800
tttgcggtcta agatgatggg agatgggttt gcggttgaa caaccatgg taatatctat     1860
gcaccgtag ctggccttgt gaccagtgtc ttccgacca agcatgcctt tggtttactg     1920
acagataatg gtcttgaagt gctgggtgcac tggggacttg ataccgtcgc cttaaatggg     1980
gtgccttttt cagtcaaaagt ctcagaaggg caacgggttc atgcaggtga cctattagtc     2040
gtagcagatc ttgctgctat taaatcagca gagcgtgaaa caatcattgt tgttgctttt     2100
accaacacaa cagagatcca agatgtgacc ttgacatctt taggagctca gcctgctaag     2160
actaaagtag ctaccgtaga actttaaa                                     2187
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<210> SEQ ID NO 654

<211> LENGTH: 728

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 654

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1          5          10          15
Phe Gly Lys Cys Leu Met Val Val Ile Ala Val Met Pro Ala Ala Gly
          20          25          30
Leu Met Ile Ser Ile Gly Asn Ser Ile Pro Met Ile Asn His Asp Ser
          35          40          45
Ala Phe Leu Ala Ser Leu Gly Asn Ile Ile Ala Gln Ile Gly Trp Ala
          50          55          60
Val Ile Val Asn Leu His Leu Leu Phe Ala Leu Ala Ile Gly Gly Ser
65          70          75          80
Trp Ala Lys Glu Arg Ala Gly Gly Ala Phe Ala Ser Gly Leu Ala Phe
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				85					90				95				
Val	Leu	Ile	Asn	Arg	Ile	Thr	Gly	Ala	Phe	Tyr	Gly	Val	Ser	Ser	Thr		
			100					105					110				
Met	Leu	Ala	Asp	Pro	Glu	Ala	Lys	Ile	Thr	Ser	Leu	Leu	Gly	Thr	Gln		
		115					120					125					
Met	Ile	Val	Lys	Asp	Tyr	Phe	Thr	Ser	Val	Leu	Glu	Ser	Pro	Ala	Leu		
	130					135					140						
Asn	Thr	Gly	Val	Phe	Val	Gly	Ile	Ile	Ala	Gly	Phe	Val	Gly	Ala	Thr		
145					150					155					160		
Ala	Tyr	Asn	Lys	Tyr	Tyr	Asn	Tyr	Arg	Lys	Leu	Pro	Glu	Val	Leu	Thr		
			165						170					175			
Phe	Phe	Asn	Gly	Lys	Arg	Phe	Val	Pro	Phe	Val	Val	Ile	Leu	Arg	Ser		
		180					185						190				
Ile	Phe	Val	Ala	Leu	Ile	Leu	Val	Val	Val	Trp	Pro	Val	Ile	Gln	Ser		
	195						200					205					
Gly	Ile	Asn	Ser	Phe	Gly	Met	Trp	Ile	Ala	Ser	Ser	Gln	Asp	Ser	Ala		
210						215					220						
Pro	Ile	Leu	Ala	Pro	Phe	Leu	Tyr	Gly	Thr	Leu	Glu	Arg	Leu	Leu	Leu		
225					230					235					240		
Pro	Phe	Gly	Leu	His	His	Met	Leu	Thr	Ile	Pro	Met	Asn	Tyr	Thr	Ala		
			245						250					255			
Leu	Gly	Gly	Thr	Tyr	Glu	Val	Met	Thr	Gly	Ala	Ala	Ala	Gly	Thr	Lys		
		260						265					270				
Val	Phe	Gly	Gln	Asp	Pro	Leu	Trp	Leu	Ala	Trp	Val	Thr	Asp	Leu	Val		
	275						280					285					
His	Leu	Lys	Gly	Ser	Asp	Ala	Ser	Ala	Tyr	Ser	His	Leu	Met	Asp	Ser		
290						295					300						
Val	Thr	Pro	Ala	Arg	Phe	Lys	Val	Gly	Gln	Met	Ile	Gly	Ala	Thr	Gly		
305					310					315					320		
Thr	Leu	Met	Gly	Val	Ala	Leu	Ala	Met	Tyr	Arg	Asn	Val	Asp	Ala	Asp		
			325						330					335			
Lys	Lys	His	Thr	Tyr	Lys	Met	Met	Phe	Ile	Ser	Ala	Ala	Ala	Ala	Val		
		340						345					350				
Phe	Leu	Thr	Gly	Val	Thr	Glu	Pro	Leu	Glu	Tyr	Leu	Phe	Met	Phe	Ala		
	355						360					365					
Ala	Met	Pro	Leu	Tyr	Ile	Val	Tyr	Ala	Leu	Val	Gln	Gly	Ala	Ser	Phe		
370						375					380						
Ala	Met	Ala	Asp	Leu	Val	Asn	Leu	Arg	Val	His	Ser	Phe	Gly	Asn	Ile		
385					390					395					400		
Glu	Leu	Leu	Thr	Arg	Thr	Pro	Met	Ala	Leu	Lys	Ala	Gly	Leu	Gly	Met		
			405						410					415			
Asp	Val	Ile	Asn	Phe	Val	Trp	Val	Ser	Val	Leu	Phe	Ala	Val	Ile	Met		
		420						425					430				
Tyr	Phe	Ile	Ala	Asp	Met	Met	Ile	Lys	Lys	Met	His	Leu	Ala	Thr	Ala		
	435						440					445					
Gly	Arg	Leu	Gly	Asn	Tyr	Asp	Ala	Asp	Ile	Leu	Gly	Asp	Arg	Asn	Thr		
450						455					460						
Gln	Thr	Arg	Pro	Thr	Gln	Val	Ala	Asp	Ser	Asn	Ser	Gln	Val	Val	Gln		
465					470					475					480		
Ile	Val	Asn	Leu	Leu	Gly	Gly	Ala	Gly	Asn	Ile	Asp	Asp	Val	Asp	Ala		
			485						490					495			
Cys	Met	Thr	Arg	Leu	Arg	Val	Thr	Val	Lys	Asp	Pro	Ala	Lys	Val	Gly		
		500						505					510				
Ala	Glu	Asp	Asp	Trp	Lys	Lys	Ala	Gly	Ala	Ile	Gly	Leu	Ile	Gln	Lys		
	515						520					525					
Gly	Asn	Gly	Val	Gln	Ala	Val	Tyr	Gly	Pro	Lys	Ala	Asp	Ile	Leu	Lys		
530						535					540						

Ser	Asp	Ile	Gln	Asp	Leu	Leu	Asp	Ser	Gly	Ala	Leu	Ile	Pro	Glu	Val
545					550				555					560	
Asn	Met	Ser	Gln	Leu	Thr	Ser	Lys	Pro	Thr	Pro	Ala	Lys	Asp	Phe	Lys
			565						570					575	
His	Val	Thr	Glu	Asp	Val	Leu	Ser	Val	Ala	Asp	Gly	Met	Val	Leu	Pro
			580					585					590		
Ile	Thr	Gly	Val	Lys	Asp	Gln	Val	Phe	Ala	Ala	Lys	Met	Met	Gly	Asp
		595				600						605			
Gly	Phe	Ala	Val	Glu	Pro	Thr	His	Gly	Asn	Ile	Tyr	Ala	Pro	Val	Ala
	610					615					620				
Gly	Leu	Val	Thr	Ser	Val	Phe	Pro	Thr	Lys	His	Ala	Phe	Gly	Leu	Leu
625					630					635				640	
Thr	Asp	Asn	Gly	Leu	Glu	Val	Leu	Val	His	Val	Gly	Leu	Asp	Thr	Val
			645						650					655	
Ala	Leu	Asn	Gly	Val	Pro	Phe	Ser	Val	Lys	Val	Ser	Glu	Gly	Gln	Arg
			660					665					670		
Val	His	Ala	Gly	Asp	Leu	Leu	Val	Val	Ala	Asp	Leu	Ala	Ala	Ile	Lys
		675					680					685			
Ser	Ala	Glu	Arg	Glu	Thr	Ile	Ile	Val	Val	Ala	Phe	Thr	Asn	Thr	Thr
	690					695					700				
Glu	Ile	Gln	Asp	Val	Thr	Leu	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ala	Lys
705					710					715				720	
Thr	Lys	Val	Ala	Thr	Val	Glu	Leu								
					725										

<210> SEQ ID NO 655

<211> LENGTH: 417

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 655

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gctgctgtaa	agaatgggtt	ggcttgctca	ccagttgctg	gtagacgtct	gtggttgttg	120
gctacaggtg	tcttagccat	attgccattg	cggcgttctg	gcgtttgggt	agcttccttg	180
tcagcaggtt	tttctgcagc	tggagttacc	tctttgctct	tttctggagc	tttttcgcct	240
ggttggcctg	cttcgccttc	tgggctcttt	tctggagctt	tttcgcctgg	ttggcctgct	300
tcaccttggtg	ggcctgctgg	gccttgctca	cctggtttgc	ctgcctcacc	ttgtgggcct	360
gctgggcctt	gggcgcccgt	ttcacctttt	tcaccttggtg	ggcctactgg	acctga	417

<210> SEQ ID NO 656

<211> LENGTH: 138

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 656

Met	Phe	Ser	Leu	Arg	Phe	Val	Thr	Ala	Arg	Thr	Pro	Ala	Val	Val	Ile
1				5					10					15	
Thr	Ala	Thr	Ala	Ala	Ala	Val	Lys	Asn	Gly	Leu	Ala	Cys	Ser	Pro	Val
			20					25					30		
Ala	Gly	Arg	Arg	Leu	Trp	Leu	Leu	Ala	Thr	Gly	Val	Leu	Ala	Ile	Leu
		35				40						45			
Pro	Leu	Arg	Arg	Ser	Gly	Val	Trp	Leu	Ala	Ser	Leu	Ser	Ala	Gly	Phe
	50				55						60				
Ser	Ala	Ala	Gly	Val	Thr	Ser	Leu	Leu	Phe	Ser	Gly	Ala	Phe	Ser	Pro
65					70					75				80	
Gly	Trp	Pro	Ala	Ser	Pro	Ser	Gly	Leu	Phe	Ser	Gly	Ala	Phe	Ser	Pro
				85					90					95	
Gly	Trp	Pro	Ala	Ser	Pro	Cys	Gly	Pro	Ala	Gly	Pro	Cys	Ser	Pro	Gly
			100					105					110		

Leu Pro Ala Ser Pro Cys Gly Pro Ala Gly Pro Trp Ala Pro Val Ser
 115 120 125
 Pro Phe Ser Pro Cys Gly Pro Thr Gly Pro
 130 135

<210> SEQ ID NO 657
 <211> LENGTH: 1323
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 657

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gtcaagtcgg	tccaagctat	tgctgggtat	ggatggctac	cagaccgtcc	acctatcaat	120
aacagccagt	tagttgtag	tatggccgtg	atcgttgaag	gtaccgataa	aaaagttttt	180
ataaatTTTT	ttgaaatcga	tctaacaatca	caacctgctc	acggaggaaa	gacagagcag	240
ggcttaagtc	caaaatcaaaa	accattttgct	acagataatg	gcgcaatgcc	acataaaactt	300
gaaaaagctg	acttattaaa	agctattcaa	aaacagctga	tcgctaactg	tcacagtaac	360
gacggctact	ttgagggtcat	tgatttttgca	agcgatgcaa	ccattactga	tcgaaacggc	420
aaggtctact	ttgctgacaa	agatgggttcg	gtaaccttgc	cgacccaacc	tgtccaagaa	480
tttttggttaa	agggacatgt	gcgcgttaga	ccatataaaag	aaaaaccagt	acaaaatcaa	540
gcaaaatctg	ttgatgtaga	atatactgta	cagtttactc	ctttaaaccc	tgatgacgat	600
ttcagaccag	ggctcaaaga	tactaagcta	ttgaaaacac	tagctatcgg	tgacaccatc	660
acatctcaag	aattactagc	tcaagcacia	agcattttaa	acaaaaccca	cccaggctat	720
acgatttatg	aacgtgactc	ctcaatcgtc	actcatgaca	atgacatttt	ccgtacgatt	780
ttaccaatgg	atcaagagtt	tacttaccat	gtcaaaaatc	gggaacaagc	ttatgagatc	840
aatcctaaaa	caggtatttaa	agaaaaaacg	aacaacactg	atctgggtctc	tgagaaatat	900
tacgtcctta	aacaagggga	aaagccgtat	gatccctttg	atcgcgagtca	cttgaaactg	960
ttcaccatca	aatacgttga	tgtcaacacc	aacgaattgc	taaaaagcga	gcagctctta	1020
acagctagcg	aacgtaactt	agacttcaga	gatttatacg	atcctcgtga	taaggctaaa	1080
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gaggataatc	acgataagaa	taatcgtgtc	gttacagttt	atatgggcaa	gcgccctaaa	1200
ggggcaaagg	gtagctatca	tttagcttat	gataaagatc	tctataaccga	agaagaacga	1260
aaagcttaca	gctacctgcg	tgatacaggg	acacctatac	ctgataaacc	taaagacaaa	1320
taa						1323

<210> SEQ ID NO 658
 <211> LENGTH: 440
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 658

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1				5					10					15	
Thr	Phe	Gly	Thr	Val	Lys	Ser	Val	Gln	Ala	Ile	Ala	Gly	Tyr	Gly	Trp
			20					25					30		
Leu	Pro	Asp	Arg	Pro	Pro	Ile	Asn	Asn	Ser	Gln	Leu	Val	Val	Ser	Met
		35				40					45				
Ala	Gly	Ile	Val	Glu	Gly	Thr	Asp	Lys	Lys	Val	Phe	Ile	Asn	Phe	Phe
	50				55					60					
Glu	Ile	Asp	Leu	Thr	Ser	Gln	Pro	Ala	His	Gly	Gly	Lys	Thr	Glu	Gln
65				70					75					80	
Gly	Leu	Ser	Pro	Lys	Ser	Lys	Pro	Phe	Ala	Thr	Asp	Asn	Gly	Ala	Met
			85					90					95		
Pro	His	Lys	Leu	Glu	Lys	Ala	Asp	Leu	Leu	Lys	Ala	Ile	Gln	Lys	Gln
		100				105						110			
Leu	Ile	Ala	Asn	Val	His	Ser	Asn	Asp	Gly	Tyr	Phe	Glu	Val	Ile	Asp
	115				120						125				
Phe	Ala	Ser	Asp	Ala	Thr	Ile	Thr	Asp	Arg	Asn	Gly	Lys	Val	Tyr	Phe
	130				135						140				

tcacatcagc	gcttaaaaac	ggtggctgtg	aaaccacaaa	agcatgcaaa	gacatacacg	840
ataggagtta	aggcgagtct	gaaaacagga	tttaaggata	agctcttagg	cggtctagaa	900
ttagcttgga	gtagggcggt	tactattttg	aatgctttga	aaggattgat	cactggcttt	960
agtctcaata	aattaggtgg	acctgttgcc	atgtatgaca	tgtccaatca	ggctgctcaa	1020
aacggcttag	agtcagtctt	atctcttatg	gcaatgcttt	cgatcaattt	agggatcttt	1080
aacctgattc	cgattcctgc	acttgatggg	ggaaaaatct	tgatgaatat	cattgaagcc	1140
attcgtcgca	agcctatcaa	gcaagaaaca	gaggcctata	tcaccctagc	tggggttgct	1200
atcatggtcg	tattgatgat	tgctgtgaca	tggaatgata	tcatgcgcgt	ctttttctaa	1260

<210> SEQ ID NO 660

<211> LENGTH: 419

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 660

Met	Leu	Gly	Ile	Ile	Thr	Phe	Ile	Ile	Ile	Phe	Gly	Ile	Leu	Val	Ile	
1			5					10					15			
Val	His	Glu	Phe	Gly	His	Phe	Tyr	Phe	Ala	Lys	Lys	Ser	Gly	Ile	Leu	
			20					25					30			
Val	Arg	Glu	Phe	Ala	Ile	Gly	Met	Gly	Pro	Lys	Ile	Phe	Ser	His	Val	
			35				40					45				
Asp	Gln	Gly	Gly	Thr	Leu	Tyr	Thr	Leu	Arg	Met	Leu	Pro	Leu	Gly	Gly	
		50				55				60						
Tyr	Val	Arg	Met	Ala	Gly	Trp	Gly	Asp	Asp	Lys	Thr	Glu	Ile	Lys	Thr	
65				70				75						80		
Gly	Thr	Pro	Ala	Ser	Leu	Thr	Leu	Asn	Glu	Gln	Gly	Phe	Val	Lys	Arg	
			85					90					95			
Ile	Asn	Leu	Ser	Gln	Ser	Lys	Leu	Asp	Pro	Thr	Ser	Leu	Pro	Met	His	
			100					105					110			
Val	Thr	Gly	Tyr	Asp	Leu	Glu	Asp	Gln	Leu	Ser	Ile	Thr	Gly	Leu	Val	
		115				120						125				
Leu	Glu	Glu	Thr	Lys	Thr	Tyr	Lys	Val	Ala	His	Asp	Ala	Thr	Ile	Val	
		130				135					140					
Glu	Glu	Asp	Gly	Thr	Glu	Ile	Arg	Ile	Ala	Pro	Leu	Asp	Val	Gln	Tyr	
145				150						155				160		
Gln	Asn	Ala	Ser	Ile	Gly	Gly	Arg	Leu	Ile	Thr	Asn	Phe	Ala	Gly	Pro	
			165					170						175		
Met	Asn	Asn	Phe	Ile	Leu	Gly	Ile	Val	Val	Phe	Ile	Leu	Leu	Val	Phe	
			180					185					190			
Leu	Gln	Gly	Gly	Met	Pro	Asp	Phe	Ser	Ser	Asn	His	Val	Arg	Val	Gln	
		195				200					205					
Glu	Asn	Gly	Ala	Ala	Ala	Lys	Ala	Gly	Leu	Arg	Asp	Asn	Asp	Gln	Ile	
		210				215					220					
Val	Ala	Ile	Asn	Gly	Tyr	Lys	Val	Thr	Ser	Trp	Asn	Asp	Leu	Thr	Glu	
225				230						235				240		
Ala	Val	Asp	Leu	Ala	Thr	Arg	Asp	Leu	Gly	Pro	Ser	Gln	Thr	Ile	Lys	
			245						250				255			
Val	Thr	Tyr	Lys	Ser	His	Gln	Arg	Leu	Lys	Thr	Val	Ala	Val	Lys	Pro	
			260					265					270			
Gln	Lys	His	Ala	Lys	Thr	Tyr	Thr	Ile	Gly	Val	Lys	Ala	Ser	Leu	Lys	
		275				280					285					
Thr	Gly	Phe	Lys	Asp	Lys	Leu	Leu	Gly	Gly	Leu	Glu	Leu	Ala	Trp	Ser	
	290					295				300						
Arg	Ala	Phe	Thr	Ile	Leu	Asn	Ala	Leu	Lys	Gly	Leu	Ile	Thr	Gly	Phe	
305				310						315				320		
Ser	Leu	Asn	Lys	Leu	Gly	Gly	Pro	Val	Ala	Met	Tyr	Asp	Met	Ser	Asn	
			325					330					335			
Gln	Ala	Ala	Gln	Asn	Gly	Leu	Glu	Ser	Val	Leu	Ser	Leu	Met	Ala	Met	

			340					345					350				
Leu	Ser	Ile	Asn	Leu	Gly	Ile	Phe	Asn	Leu	Ile	Pro	Ile	Pro	Ala	Leu		
			355					360					365				
Asp	Gly	Gly	Lys	Ile	Leu	Met	Asn	Ile	Ile	Glu	Ala	Ile	Arg	Arg	Lys		
			370					375					380				
Pro	Ile	Lys	Gln	Glu	Thr	Glu	Ala	Tyr	Ile	Thr	Leu	Ala	Gly	Val	Ala		
			385					390					395			400	
Ile	Met	Val	Val	Leu	Met	Ile	Ala	Val	Thr	Trp	Asn	Asp	Ile	Met	Arg		
				405					410					415			
Val	Phe	Phe															

<210> SEQ ID NO 661
 <211> LENGTH: 2163
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 661

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gaaaacg	cctt	cattttat	ac	tgacatt	tata	ggaggaga	t	acatgct	atc	tcatgag	ctc	120
atcagaa	act	atcaact	cctt	ttctaaa	atat	aaaggac	att	cactggag	gc	atttga	atcc	180
attttaa	agg	caagcaa	acg	tcatata	ctg	gcagata	ttg	ctaaaat	caa	tgacacg	ttg	240
tcactct	atc	agttacc	cct	tattgct	ctg	gacaggc	cagc	tggtttat	cc	gccagac	cctt	300
actgaaa	agg	acttggt	gaa	tcgcatg	ccta	cctacct	tag	acgactat	ct	ctttca	agat	360
gagcgtc	tgg	atatgat	tat	catttac	atc	atgatgg	ccta	aagaattt	at	ctccatt	aac	420
cacttgg	aaa	gcttggt	acg	gctcagc	caga	aattctg	tta	ttgctg	attt	aaacttg	ggtg	480
cgtgatc	ggg	tacaagc	ttt	tcaggta	aact	ttagctt	aca	atcgccag	ga	tggttat	ttt	540
tttgaag	gag	aaccctt	agc	cttgccg	gct	ctcttaga	aat	cagcgg	tcag	ttctctt	ttg	600
caagtcac	at	ctggac	cctt	ggtgttc	cagt	tacttat	tgc	atgaact	ttg	tttgccc	gac	660
cagaaaa	agg	tgatggc	agc	aacggtt	ggag	gaactga	gca	gggaga	aacca	cttaact	ttt	720
atttcgg	aga	aattgag	gga	tttgatt	tat	ttttctg	ccc	ttctcgt	c	tcgacc	attt	780
tcacgga	acg	taagggt	ctga	agcagtg	gat	acttttc	cctt	tagcttc	gcc	agctgtt	gaa	840
acgatgg	tgg	accagtt	att	ggtcaac	ttc	cccagt	ctaa	ccgaaga	aaaa	atatttg	ggtt	900
caatcta	ggt	tacttgg	ttg	tatcca	agg	gacttag	agt	tagtctt	tca	gcaacct	att	960
tatgacac	ta	tgaggaa	aat	catcaat	tcg	gtggcgg	tta	acacggg	att	gtctat	cacc	1020
gatacccc	ag	aacttcg	tca	gaacct	tata	agtcac	ctt	tgccagc	tta	ttaccag	ctt	1080
tactacg	aca	ttaactt	gac	caatcct	ttt	aaggaac	aaa	tcaaaca	aga	ttatga	atct	1140
ctctttt	tact	tggtca	agcg	cagcctt	tct	cctctag	aaa	aacaatt	ggg	gaaatc	agtt	1200
aatgaag	atg	aggttg	ctta	ttttacc	att	cattttg	gga	gatgg	ttgca	ggccc	ctaag	1260
aagaggc	caa	gcaatc	agct	ggtagc	ctta	tctgttt	gcc	ctaattg	gcat	tagtte	ctct	1320
ctgatgt	tgg	aggcaac	cctt	gaagga	actt	tttccac	agc	tacagt	ttt	taggat	tcac	1380
cagctgg	aca	aaataa	agtt	gttggat	cca	gcac	ccttg	atttgat	ttt	ttcaac	agta	1440
gcttttg	act	gtgcta	aaacc	tgtttat	gtg	acgcaag	cctt	tgatggg	acc	tggtga	aaaaa	1500
atgatgt	tga	aaaagat	ggt	ctgtgat	gac	tttcat	cctt	ccttg	tcaga	gcaatt	cgt	1560
ttggatg	atc	tgttgag	tat	tattcata	aaa	catacc	acga	ttacta	aataa	agaagg	actt	1620
gttagtg	att	tatccc	gtta	cctgat	tgg	aaccatt	tta	cgattg	aaaa	aggagg	tcta	1680
ggactatt	gg	actgtta	aac	agcagat	ttt	attagg	cagg	ctgatg	ctgt	ttcgg	attgg	1740
caggaag	cga	ttcgttt	ggc	tgctcag	cct	ttactag	aac	accagat	gat	tgaaac	atct	1800
tatatcg	atg	gcatgat	tga	ttcgg	tcaat	gagctt	ggg	cctat	attgt	tttag	cccc	1860
aagg	tg	gctg	ctgc	ggcg	cctg	aaagga	acgc	ggcag	ttagg	catgt	ctctc	1920
ttacaac	taa	aagaac	ctgt	cagctt	t	ttgaag	caag	aagg	t	gatcc	agaca	1980
gtgca	attga	ttttt	gtttt	gtctg	ctgtg	gattct	agtt	cacatt	t	gaa	ggctt	2040
gaactg	tcgt	tgatttt	aga	tgatgat	gaa	catatt	gagc	aatta	attga	ggcta	agaat	2100
actgagg	aaa	taatgag	tct	gattag	ccat	atgatt	gaaa	aaggag	acga	atcac	atgat	2160
taa												2163

<210> SEQ ID NO 662
 <211> LENGTH: 720
 <212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 662

```
Met Ser Pro Ile Ala Val Lys Asn Asp Met Arg Gln Leu Asp Ser Ile
1          5          10          15
Tyr Leu Glu Asn Glu Asn Ala Ser Phe Tyr Thr Asp Ile Ile Gly Gly
20          25          30
Asp Asp Met Leu Ser His Glu Leu Ile Arg Asn Tyr Gln Leu Phe Ser
35          40          45
Lys Tyr Lys Gly His Ser Leu Glu Ala Phe Glu Ser Ile Leu Lys Ala
50          55          60
Ser Lys Arg His Ile Leu Ala Asp Ile Ala Lys Ile Asn Asp Thr Leu
65          70          75          80
Ser Leu Tyr Gln Leu Pro Leu Ile Ala Leu Asp Arg Gln Leu Val Tyr
85          90          95
Pro Pro Asp Leu Thr Glu Lys Asp Leu Leu Asn Arg Met Leu Pro Thr
100         105         110
Leu Asp Asp Tyr Leu Phe Gln Asp Glu Arg Leu Asp Met Ile Ile Ile
115         120         125
Tyr Ile Met Met Ala Lys Glu Phe Ile Ser Ile Asn His Leu Glu Ser
130         135         140
Leu Leu Arg Leu Ser Arg Asn Ser Val Ile Ala Asp Leu Asn Leu Val
145         150         155         160
Arg Asp Arg Val Gln Ala Phe Gln Val Thr Leu Ala Tyr Asn Arg Gln
165         170         175
Asp Gly Tyr Phe Phe Glu Gly Glu Pro Leu Ala Leu Arg Arg Leu Leu
180         185         190
Glu Ser Ala Val Ser Ser Leu Leu Gln Val Thr Ser Gly Pro Trp Val
195         200         205
Phe Ser Tyr Leu Leu His Glu Leu Gly Leu Pro Asp Gln Lys Lys Val
210         215         220
Met Ala Ala Thr Leu Glu Glu Leu Ser Arg Glu Asn His Leu Thr Phe
225         230         235         240
Ile Ser Glu Lys Leu Arg Asp Leu Ile Tyr Phe Phe Cys Leu Leu Ala
245         250         255
His Arg Pro Phe Ser Arg Asn Val Arg Ala Glu Ala Val Asp Thr Phe
260         265         270
Pro Leu Ala Ser Pro Ala Val Glu Thr Met Val Asp Gln Leu Leu Val
275         280         285
Asn Phe Pro Ser Leu Thr Glu Glu Lys Tyr Leu Val Gln Ser Arg Leu
290         295         300
Leu Gly Cys Ile Gln Gly Asp Leu Glu Leu Val Phe Gln Gln Pro Ile
305         310         315         320
Tyr Asp Ile Met Glu Glu Ile Ile Asn Ser Val Ala Val Asn Thr Gly
325         330         335
Leu Ser Ile Thr Asp Thr Pro Glu Leu Arg Gln Asn Leu Tyr Ser His
340         345         350
Leu Leu Pro Ala Tyr Tyr Arg Leu Tyr Tyr Asp Ile Asn Leu Thr Asn
355         360         365
Pro Leu Lys Glu Gln Ile Lys Gln Asp Tyr Glu Ser Leu Phe Tyr Leu
370         375         380
Val Lys Arg Ser Leu Ser Pro Leu Glu Lys Gln Leu Gly Lys Ser Val
385         390         395         400
Asn Glu Asp Glu Val Ala Tyr Phe Thr Ile His Phe Gly Arg Trp Leu
405         410         415
Gln Ala Pro Lys Lys Arg Pro Ser Asn Gln Leu Val Ala Leu Ser Val
420         425         430
Cys Pro Asn Gly Ile Ser Ser Ser Leu Met Leu Glu Ala Thr Leu Lys
```


<211> LENGTH: 265

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 664

```
Met Thr Thr Met Gln Lys Thr Ile Ser Leu Leu Ser Leu Ala Leu Leu
1      5      10      15
Ile Gly Leu Leu Gly Thr Ser Gly Lys Ala Ile Ser Val Tyr Ala Gln
      20      25      30
Asp Gln His Thr Asp Asn Val Ile Ala Glu Ser Thr Ile Ser Gln Val
      35      40      45
Ser Val Glu Ala Ser Met Arg Gly Thr Glu Pro Tyr Ile Asp Ala Thr
      50      55      60
Val Thr Thr Asp Gln Pro Val Arg Gln Pro Thr Gln Ala Thr Ile Thr
      65      70      75      80
Leu Lys Asp Ala Ser Asp Asn Thr Ile Asn Ser Trp Val Tyr Thr Met
      85      90      95
Ala Ala Gln Gln Arg Arg Phe Thr Ala Trp Phe Asp Leu Thr Gly Gln
      100     105     110
Lys Ser Gly Asp Tyr His Val Thr Val Thr Val His Thr Gln Glu Lys
      115     120     125
Ala Val Thr Gly Gln Ser Gly Thr Val His Phe Asp Gln Asn Lys Ala
      130     135     140
Arg Lys Thr Pro Thr Asn Met Gln Gln Lys Asp Thr Ser Lys Ala Met
      145     150     155     160
Thr Asn Ser Val Asp Val Asp Thr Lys Ala Gln Thr Asn Gln Ser Ala
      165     170     175
Asn Gln Glu Ile Asp Ser Thr Ser Asn Pro Phe Arg Ser Ala Thr Asn
      180     185     190
His Arg Ser Thr Ser Leu Lys Arg Ser Thr Lys Asn Glu Lys Leu Thr
      195     200     205
Pro Thr Ala Ser Asn Ser Gln Lys Asn Gly Ser Asn Lys Thr Lys Met
      210     215     220
Leu Val Asp Lys Glu Glu Val Lys Pro Thr Ser Lys Arg Gly Phe Pro
      225     230     235     240
Trp Val Leu Leu Gly Leu Val Val Ser Leu Ala Ala Gly Leu Phe Ile
      245     250     255
Ala Ile Gln Lys Val Ser Arg Arg Lys
      260     265
```

<210> SEQ ID NO 665

<211> LENGTH: 1908

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 665

```
atgatttgggt caattacaaa atctaacatt aaaaaaaatt tttcgttata tcgtatctat      60
tttctagcta cgattggttt attaagtatt tttatagctt ttctaaattt tatctcagat      120
aaaatcatta cagaaaaaat tggggatagt ggtcaagctc tagttatcgc taatgggtca      180
ttgattttttt tgattgtatt tttggtggta ttcttaattt acttcaataa tttctttgta      240
aaaaaacgta gtcaagagct tggagtcctta gcaatactag ggttttcaaa aagagaatta      300
acaaaattac taactttaga aaatcttggtt attctagttc tgagttactt ggtaagttta      360
ttgctgggac cgactttata ttttttagct gtactggcaa ttactcatct attgaattta      420
acaatggaag ttcagtgggtt tattacagtt aatgagatta tagagtcctt aggaatatta      480
gtcgtagttt ttctgattaa tgtcatcaca aatggactta tcattagtaa acagtcctttg      540
attgaatttg ttaatttctc aagaaaggct gagaaaaaaa ttaagataag aaaagtcaga      600
gctattattg ctatcactgc attgctattg tcatatatatt tatgtttggc gacagtgttt      660
tcatccacac gaaatatgct attaagcata gggatggtac cggtttctct attgataatt      720
gtcttagttg ttttaggaac agtgttcacc atcagatatg gattggcttt tgtagtttcg      780
```

ttgttaaaag	aaaataaaaa	aaggttatac	cgctcctctgt	ctaatatcat	ctatcccaaa	840
tttaactatc	gtattgcaac	aaaaaataaa	ttattaacag	tcttgggagg	tcttttaaca	900
gtaaccgttt	cagttgccgg	aatgatggta	atgctctatg	cttattctct	taatgggata	960
gagagggtga	ctccatctgc	catagaatat	aatgttgaat	cagaaaacgg	tcaagtcaat	1020
gttacaacta	ttttagagaa	cgaccaagtg	agcttggtg	atgtcggcct	gttgcgattg	1080
aatactatcc	cagagggtgac	tatcacagac	tctggggcaaa	caatacctta	ttttgatata	1140
attaactaca	gtgactacaa	agagttaatg	aaagctcaag	gcagaacaaa	ttctattgaa	1200
ggtagtaagt	cactcccat	gttaataaat	tattatccaa	cagaaattag	ccttggaana	1260
acctttaact	taggaaatgc	atatgatgtt	actgtaaaac	aagtatcaac	gaataatgtt	1320
tttagttttt	ctacaagtgt	cacgaccctg	gttgtttctg	ataaattata	tgctaaactt	1380
agttctcggt	ttccagagaa	agaaatgaca	attaggactt	ttaatggaac	ttcgattagg	1440
tcaagtgaag	cattttacaa	tcagtttagt	atgggtcctg	atgttatcag	tagttatagt	1500
aaggaacaca	cagtaaagac	tgctaataat	gcgacttata	tctttataac	tttcctatcc	1560
atactcttta	ttatttgtac	aggtagtatt	ctgtacttta	caagcctcat	cgaatcatg	1620
gaaaataaag	aagaatatgg	ctatctaagt	aagctagggt	atagtaaaaa	aatgattcat	1680
cggattcttc	gatataaaac	aggtataactt	ttccttattc	ctgtattcat	tgggattgta	1740
aatggtggta	tggtgcttat	ttactataaaa	tatttattca	tggatacatt	ggtagcaggc	1800
aatatcataa	tggtatcttt	attgctttgt	ctgcttttct	tcttgataat	atatggcaca	1860
ttttatgtat	tgacattgcg	gttagtgaca	tccataatca	aaaattaa		1908

<210> SEQ ID NO 666

<211> LENGTH: 635

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 666

Met	Ile	Trp	Ser	Ile	Thr	Lys	Ser	Asn	Ile	Lys	Lys	Asn	Phe	Ser	Leu
1				5					10					15	
Tyr	Arg	Ile	Tyr	Phe	Leu	Ala	Thr	Ile	Gly	Leu	Leu	Ser	Ile	Phe	Ile
			20					25					30		
Ala	Phe	Leu	Asn	Phe	Ile	Ser	Asp	Lys	Ile	Ile	Thr	Glu	Lys	Ile	Gly
		35					40					45			
Asp	Ser	Gly	Gln	Ala	Leu	Val	Ile	Ala	Asn	Gly	Ser	Leu	Ile	Phe	Leu
	50					55					60				
Ile	Val	Phe	Leu	Val	Val	Phe	Leu	Ile	Tyr	Phe	Asn	Asn	Phe	Phe	Val
65					70					75					80
Lys	Lys	Arg	Ser	Gln	Glu	Leu	Gly	Val	Leu	Ala	Ile	Leu	Gly	Phe	Ser
				85					90					95	
Lys	Arg	Glu	Leu	Thr	Lys	Leu	Leu	Thr	Leu	Glu	Asn	Leu	Val	Ile	Leu
			100					105					110		
Val	Leu	Ser	Tyr	Leu	Val	Ser	Leu	Leu	Leu	Gly	Pro	Thr	Leu	Tyr	Phe
	115					120						125			
Leu	Ala	Val	Leu	Ala	Ile	Thr	His	Leu	Leu	Asn	Leu	Thr	Met	Glu	Val
	130				135					140					
Gln	Trp	Phe	Ile	Thr	Val	Asn	Glu	Ile	Ile	Glu	Ser	Leu	Gly	Ile	Leu
145					150					155					160
Val	Val	Val	Phe	Leu	Ile	Asn	Val	Ile	Thr	Asn	Gly	Leu	Ile	Ile	Ser
			165					170						175	
Lys	Gln	Ser	Leu	Ile	Glu	Phe	Val	Asn	Phe	Ser	Arg	Lys	Ala	Glu	Lys
		180						185					190		
Lys	Ile	Lys	Ile	Arg	Lys	Val	Arg	Ala	Ile	Ile	Ala	Ile	Thr	Ala	Leu
	195					200					205				
Leu	Leu	Ser	Tyr	Ile	Leu	Cys	Leu	Ala	Thr	Val	Phe	Ser	Ser	Thr	Arg
	210					215					220				
Asn	Met	Leu	Leu	Ser	Ile	Gly	Met	Val	Pro	Val	Ser	Leu	Leu	Ile	Ile
225					230					235					240
Val	Leu	Val	Val	Leu	Gly	Thr	Val	Phe	Thr	Ile	Arg	Tyr	Gly	Leu	Ala
			245						250					255	

```
<210> SEQ ID NO 667
<211> LENGTH: 471
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 667
    atgcaaaaata gtaagatacg acaaatgagt ttaacagggg tattgacagc attggttggt      60
    gtttttaggaa gatttgatcat gctacctact ccaacaggtt ttttaacgct gttggatgca      120
    ggaatttatg ctgtcagctt ttccttttggg tcaagctcaag gagctattgt gggagggtta      180
```

tcagggttttt	taatcgattt	agtggcagga	taccctcagt	ggatgtttca	tagtttgatt	240
gctcacagtg	tccaagggtg	ttttgcggga	tggagagggc	gcaagcggtg	gcttgggtgt	300
gtgatagggt	cttttatcat	gatttttttg	tacttttttag	gctctcttat	gcttgggtat	360
ggccttttcg	gatcttttag	cggtatttgg	ggaaacgtca	tgcaaaatac	attagggtct	420
tttgttggtt	ttattatctt	taaggccata	ttaaggcaaa	aaaagagata	a	471

<210> SEQ ID NO 668
 <211> LENGTH: 156
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 668

Met	Gln	Asn	Ser	Lys	Ile	Arg	Gln	Met	Ser	Leu	Thr	Gly	Ile	Leu	Thr
1				5					10					15	
Ala	Leu	Val	Val	Val	Leu	Gly	Arg	Phe	Val	Met	Leu	Pro	Thr	Pro	Thr
			20					25					30		
Gly	Phe	Leu	Thr	Leu	Leu	Asp	Ala	Gly	Ile	Tyr	Ala	Val	Ser	Phe	Ser
	35						40					45			
Phe	Gly	Ser	Ala	Gln	Gly	Ala	Ile	Val	Gly	Gly	Leu	Ser	Gly	Phe	Leu
	50					55					60				
Ile	Asp	Leu	Val	Ala	Gly	Tyr	Pro	Gln	Trp	Met	Phe	His	Ser	Leu	Ile
65					70					75				80	
Ala	His	Ser	Val	Gln	Gly	Tyr	Phe	Ala	Gly	Trp	Arg	Gly	Arg	Lys	Arg
				85					90					95	
Trp	Leu	Gly	Val	Val	Ile	Gly	Ser	Phe	Ile	Met	Ile	Phe	Trp	Tyr	Phe
			100					105					110		
Leu	Gly	Ser	Leu	Met	Leu	Gly	Tyr	Gly	Leu	Ser	Gly	Ser	Leu	Ala	Gly
		115					120					125			
Ile	Trp	Gly	Asn	Val	Met	Gln	Asn	Thr	Leu	Gly	Leu	Phe	Val	Gly	Phe
	130					135					140				
Ile	Ile	Phe	Lys	Ala	Ile	Leu	Arg	Gln	Lys	Lys	Arg				
145					150					155					

<210> SEQ ID NO 669
 <211> LENGTH: 654
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 669

atggggaaaag	aaataaaaagt	gaaatgcttt	ttgcgtagat	cagctttttgg	attagttgcg	60
gtgtcagcat	cagtattagt	cggttcaaca	gtatctgctg	ttgactcacc	tatcgaacag	120
cctcgaatta	ttccaaatgg	cggaacctta	actaatcttc	ttggcaatgc	tccagaaaaa	180
ctggcattac	gtaatgaaga	aagagccatt	gatgaattaa	aaaaacaagc	tattgaggat	240
aaagaagcta	cgacagctat	agaagcagca	agttcagatg	ccttagaagc	attagcggat	300
caaacagacg	ctttacaatc	agaagaagct	gcggttggtta	aagcggataa	cgctgctagt	360
gacgccttag	aagcattggc	ggatcaaaca	gacgctttac	aatcagaaga	agctgaagta	420
gttcaatcag	ataacgctgc	tagtgacgcc	tgggaaaaag	cagcaactcc	aatcgcttta	480
gatgttaaga	aaactaaaga	tacaaaacct	gtagttaaaa	aagaagaaag	acaaaacgtt	540
aatacccttc	ctacaactgg	tgaagagtct	aaccatttct	ttacagctgc	tgcgcttgca	600
ataatggtaa	gtacagggtg	gttagttgta	agttcaaagt	gcaaagaaaa	ttag	654

<210> SEQ ID NO 670
 <211> LENGTH: 217
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes
 <400> SEQUENCE: 670

Met	Gly	Lys	Glu	Ile	Lys	Val	Lys	Cys	Phe	Leu	Arg	Arg	Ser	Ala	Phe
1				5					10					15	
Gly	Leu	Val	Ala	Val	Ser	Ala	Ser	Val	Leu	Val	Gly	Ser	Thr	Val	Ser

	20		25		30
Ala Val Asp Ser Pro Ile Glu Gln Pro Arg Ile Ile Pro Asn Gly Gly					
35		40		45	
Thr Leu Thr Asn Leu Leu Gly Asn Ala Pro Glu Lys Leu Ala Leu Arg					
50		55		60	
Asn Glu Glu Arg Ala Ile Asp Glu Leu Lys Lys Gln Ala Ile Glu Asp					
65		70		75	
Lys Glu Ala Thr Thr Ala Ile Glu Ala Ala Ser Ser Asp Ala Leu Glu					
85		90		95	
Ala Leu Ala Asp Gln Thr Asp Ala Leu Gln Ser Glu Glu Ala Ala Val					
100		105		110	
Val Lys Ala Asp Asn Ala Ala Ser Asp Ala Leu Glu Ala Leu Ala Asp					
115		120		125	
Gln Thr Asp Ala Leu Gln Ser Glu Glu Ala Glu Val Val Gln Ser Asp					
130		135		140	
Asn Ala Ala Ser Asp Ala Trp Glu Lys Ala Ala Thr Pro Ile Ala Leu					
145		150		155	
Asp Val Lys Lys Thr Lys Asp Thr Lys Pro Val Val Lys Lys Glu Glu					
165		170		175	
Arg Gln Asn Val Asn Thr Leu Pro Thr Thr Gly Glu Glu Ser Asn Pro					
180		185		190	
Phe Phe Thr Ala Ala Ala Leu Ala Ile Met Val Ser Thr Gly Val Leu					
195		200		205	
Val Val Ser Ser Lys Cys Lys Glu Asn					
210		215			

<210> SEQ ID NO 671

<211> LENGTH: 1662

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 671

atgccccccc	ctccacaact	tagacagcct	aactgtagca	actcaaaaac	agattcatca	60
ttaatagcat	ttaggtcaaa	aaggtggcaa	aagctaaaaa	agctggtctt	taccttttgg	120
cttttattat	ttacaataga	attattagag	ttaaaccctg	aaaatgaggg	tttcttccta	180
aaaaatgata	gcataaggag	cataaaaatg	gtagcggtag	ctttgactgt	tttaggggca	240
cttagaaaat	taaaaacagg	aacggcttca	gtagcggtag	ctttgactgt	tttaggggca	300
ggttttgCGA	atcaaacaga	ggttaaggct	aacggtgatg	gtaatcctag	ggaagttata	360
gaagatcttg	cagcaaaaca	tcccgcaata	caaaatatac	gtttacgtta	cgaaaacaag	420
gacttaaaaag	cgagattaga	gaatgcaatg	gaagttgcag	gaagagattt	taagagagct	480
gaagaacttg	aaaaagcaaa	acaagcctta	gaagaccagc	gtaaagattt	agaaactaaa	540
ttaaaagaac	tacaacaaga	ctatgactta	gcaaaggaat	caacaagttg	ggatagacaa	600
agacttgaaa	aagagttaga	agagaaaaag	gaagctcttg	aattagcgat	agaccaggca	660
agtcgggact	accatagagc	taccgcttta	gaaaaagagt	tagaagagaa	aaagaaagct	720
cttgaattag	cgatagacca	agcgagtcag	gactataata	gagctaacgt	cttagaaaaa	780
gagttagaaa	cgattactag	agaacaagag	attaatcgta	atcttttagg	caatgcaaaa	840
cttgaacttg	atcaactttc	atctgaaaaa	gagcagctaa	cgatcgaaaa	agcaaaaactt	900
gaggaagaaa	aacaaatctc	agacgcaagt	cgTcaaagcc	ttcgtcgtga	cttggacgca	960
tcacgtgaag	ctaagaaaca	ggttgaaaaa	gatttagcaa	acttgactgc	tgaacttgat	1020
aaggttaaaag	aagacaaaca	aatctcagac	gcaagccgtc	aaggccttcg	ccgtgacttg	1080
gacgcatcac	gtgaagctaa	gaaacagggt	gaaaaagatt	tagcaaactt	gactgctgaa	1140
cttgataagg	ttaaagaaga	aaaacaaatc	tcagacgcaa	gccgtcaagg	ccttcgccgt	1200
gacttggaag	catcacgtga	agctaagaaa	caagttgaaa	aagctttaga	agaagcaaac	1260
agcaaattag	ctgctcttga	aaaacttaac	aaagagcttg	aagaaaagca	gaaattaaca	1320
gaaaaagaaa	aagctgaact	acaagcaaaa	cttgaagcag	aagcaaaaagc	atccaaagaa	1380
caattagcga	aacaagctga	agaacttgca	aaactaagag	ctggaaaagc	atcagactca	1440
caaacccttg	atacaaaaacc	aggaaacaaa	gctgtttccag	gtaaaggtca	agcaccacaa	1500
gcagggtacaa	aacctaacca	aaacaaagca	ccaatgaagg	aaactaagag	acagttacca	1560

tcaacaggtg aaacagctaa cccattcttc acagcggcag cccttactgt tatggcaaca 1620
gctggagtag cagcagttgt aaaacgcaaa gaagaaaact aa 1662

<210> SEQ ID NO 672
<211> LENGTH: 553
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes
<400> SEQUENCE: 672

Met	Pro	Pro	Pro	Pro	Gln	Leu	Arg	Gln	Pro	Asn	Cys	Ser	Asn	Ser	Lys
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Thr	Asp	Ser	Ser	Leu	Ile	Ala	Phe	Arg	Ser	Lys	Arg	Trp	Gln	Lys	Leu
			20					25					30		
Lys	Lys	Leu	Val	Phe	Thr	Phe	Trp	Leu	Leu	Leu	Phe	Thr	Ile	Glu	Leu
			35				40					45			
Leu	Glu	Leu	Asn	Pro	Glu	Asn	Glu	Gly	Phe	Phe	Leu	Lys	Asn	Asp	Ser
			50			55					60				
Ile	Arg	Ser	Ile	Lys	Met	Ala	Lys	Asn	Asn	Thr	Asn	Arg	His	Tyr	Ser
65					70					75					80
Leu	Arg	Lys	Leu	Lys	Thr	Gly	Thr	Ala	Ser	Val	Ala	Val	Ala	Leu	Thr
				85					90					95	
Val	Leu	Gly	Ala	Gly	Phe	Ala	Asn	Gln	Thr	Glu	Val	Lys	Ala	Asn	Gly
			100					105					110		
Asp	Gly	Asn	Pro	Arg	Glu	Val	Ile	Glu	Asp	Leu	Ala	Ala	Asn	Asn	Pro
			115				120					125			
Ala	Ile	Gln	Asn	Ile	Arg	Leu	Arg	Tyr	Glu	Asn	Lys	Asp	Leu	Lys	Ala
			130			135					140				
Arg	Leu	Glu	Asn	Ala	Met	Glu	Val	Ala	Gly	Arg	Asp	Phe	Lys	Arg	Ala
145					150					155					160
Glu	Glu	Leu	Glu	Lys	Ala	Lys	Gln	Ala	Leu	Glu	Asp	Gln	Arg	Lys	Asp
				165					170					175	
Leu	Glu	Thr	Lys	Leu	Lys	Glu	Leu	Gln	Gln	Asp	Tyr	Asp	Leu	Ala	Lys
			180					185					190		
Glu	Ser	Thr	Ser	Trp	Asp	Arg	Gln	Arg	Leu	Glu	Lys	Glu	Leu	Glu	Glu
			195				200					205			
Lys	Lys	Glu	Ala	Leu	Glu	Leu	Ala	Ile	Asp	Gln	Ala	Ser	Arg	Asp	Tyr
			210			215					220				
His	Arg	Ala	Thr	Ala	Leu	Glu	Lys	Glu	Leu	Glu	Glu	Lys	Lys	Lys	Ala
225					230					235					240
Leu	Glu	Leu	Ala	Ile	Asp	Gln	Ala	Ser	Gln	Asp	Tyr	Asn	Arg	Ala	Asn
				245					250					255	
Val	Leu	Glu	Lys	Glu	Leu	Glu	Thr	Ile	Thr	Arg	Glu	Gln	Glu	Ile	Asn
			260					265					270		
Arg	Asn	Leu	Leu	Gly	Asn	Ala	Lys	Leu	Glu	Leu	Asp	Gln	Leu	Ser	Ser
			275				280					285			
Glu	Lys	Glu	Gln	Leu	Thr	Ile	Glu	Lys	Ala	Lys	Leu	Glu	Glu	Glu	Lys
			290			295					300				
Gln	Ile	Ser	Asp	Ala	Ser	Arg	Gln	Ser	Leu	Arg	Arg	Asp	Leu	Asp	Ala
305					310					315					320
Ser	Arg	Glu	Ala	Lys	Lys	Gln	Val	Glu	Lys	Asp	Leu	Ala	Asn	Leu	Thr
				325					330					335	
Ala	Glu	Leu	Asp	Lys	Val	Lys	Glu	Asp	Lys	Gln	Ile	Ser	Asp	Ala	Ser
			340					345					350		
Arg	Gln	Gly	Leu	Arg	Arg	Asp	Leu	Asp	Ala	Ser	Arg	Glu	Ala	Lys	Lys
			355				360					365			
Gln	Val	Glu	Lys	Asp	Leu	Ala	Asn	Leu	Thr	Ala	Glu	Leu	Asp	Lys	Val
			370			375					380				
Lys	Glu	Glu	Lys	Gln	Ile	Ser	Asp	Ala	Ser	Arg	Gln	Gly	Leu	Arg	Arg

385		390		395		400									
Asp	Leu	Asp	Ala	Ser	Arg	Glu	Ala	Lys	Lys	Gln	Val	Glu	Lys	Ala	Leu
		405						410						415	
Glu	Glu	Ala	Asn	Ser	Lys	Leu	Ala	Ala	Leu	Glu	Lys	Leu	Asn	Lys	Glu
		420						425						430	
Leu	Glu	Glu	Ser	Lys	Lys	Leu	Thr	Glu	Lys	Glu	Lys	Ala	Glu	Leu	Gln
		435						440						445	
Ala	Lys	Leu	Glu	Ala	Glu	Ala	Lys	Ala	Leu	Lys	Glu	Gln	Leu	Ala	Lys
		450						455						460	
Gln	Ala	Glu	Glu	Leu	Ala	Lys	Leu	Arg	Ala	Gly	Lys	Ala	Ser	Asp	Ser
465						470				475					480
Gln	Thr	Pro	Asp	Thr	Lys	Pro	Gly	Asn	Lys	Ala	Val	Pro	Gly	Lys	Gly
				485				490						495	
Gln	Ala	Pro	Gln	Ala	Gly	Thr	Lys	Pro	Asn	Gln	Asn	Lys	Ala	Pro	Met
		500						505						510	
Lys	Glu	Thr	Lys	Arg	Gln	Leu	Pro	Ser	Thr	Gly	Glu	Thr	Ala	Asn	Pro
		515						520						525	
Phe	Phe	Thr	Ala	Ala	Ala	Leu	Thr	Val	Met	Ala	Thr	Ala	Gly	Val	Ala
		530						535						540	
Ala	Val	Val	Lys	Arg	Lys	Glu	Glu	Asn							
545						550									

<210> SEQ ID NO 673

<211> LENGTH: 3546

<212> TYPE: DNA

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 673

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accgaacaag	ctgtagaaac	cccacaacca	acagcggttt	ctgaggaagc	accatcatca	180
aaggaaacca	aaacccca	aactcctgat	gacgcagaag	aaacaatagc	agatgacgct	240
aatgatctag	cccctcaagc	tcttgctaaa	actgctgata	caccagcaac	ctcaaaagcg	300
actattaggg	atttgaacga	cccttctcag	gtcaaaaccc	tgaggaaaa	agcaggcaaa	360
ggagctggga	ctgttggtgc	agtgattgat	gctgggtttg	ataaaaaatca	tgaagcgtgg	420
cgcttaacag	acaaaaccaa	agcacgttac	caatcaaaag	aagatcttga	aaaagctaaa	480
aaagagcacg	gtattaccta	tggcgagtgg	gtcaatgata	aggttgctta	ttaccacgac	540
tatagtaaa	atggtaaaac	cgctgtcgat	caagagcacg	gcacacacgt	gtcagggatc	600
ttgtcaggaa	atgctccatc	tgaaacgaaa	gaaccttacc	gcctagaagg	tgcatgcct	660
gaggctcaat	tgcttttgat	gcgtgtcgaa	attgtaaatg	gactagcaga	ctatgctcgt	720
aactacgctc	aagctatcat	agatgctgtc	aacttgggag	ctaagggtgat	taatatgagc	780
tttggtaatg	ctgcactagc	ctatgccaac	cttccagacg	aaacaaaaaa	agcctttgac	840
tatgccaaat	caaaagggtg	tagcattgtg	acctcagctg	gtaatgatag	tagctttggg	900
ggcaagaccc	gtctacctct	agcagatcat	cctgattatg	gggtgggttg	gacacctgca	960
gcggcagact	caacattgac	agttgcttct	tacagcccag	ataaacagct	cactgaaact	1020
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aagggtctcc	cgattgaatt	gccaaatgtt	gatcagatgc	ctgcggcctt	tatcagtcga	1320
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aagggtattgc	caacagcaag	tggcaccaaa	ctaagccgct	tctcaagctg	gggtctgaca	1440
gctacgggca	atattaagcc	agatattgca	gcacccggcc	aagatatttt	gtcatcagtg	1500
gctaacaaca	agtatgccaa	actttctgga	actagtatgt	ctgcgccatt	agtagcgggt	1560
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gaaaaagctt	atTTTTctcc	tcgccaacaa	ggagcaggag	cagtcgatgc	taaaaaagct	1740
tcagcagcaa	cgatgtatgt	gacagataag	gataatacct	caagcaaggt	tcacctgaac	1800

aatgtttctg	ataaatttga	agtaacagta	acagttcaca	acaaatctga	taaacctcaa	1860
gagttgtatt	accaagcaac	tgttcaaaca	gataaagtag	atggaaaact	ctttgccttg	1920
gctcctaaag	cattgtatga	gacatcatgg	caaaaaatca	caattccagc	caatagcagc	1980
aaacaagtca	ccattccaat	cgatgttagt	caatttagca	aggacttgct	tgccccaatg	2040
aaaaatggct	atttcttaga	aggttttggt	cgtttcaaac	aagatcctac	aaaagaagag	2100
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cttactacag	agtctaatac	atggacgatt	attaaagctg	tcaaagaagg	ggttgaaaaa	2340
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caagacgatg	atagccacta	ctatatccac	cgtcacgcta	atggcaagcc	atatgctgcg	2460
atctctccaa	atggggacgg	taacagagat	tatgtccaat	tccaaggtag	tttcttgctg	2520
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gaggtaaccg	agcaagttgt	taaaaactac	aacaatgact	tggcaagcac	acttggttca	2640
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tcaacagaag	atcgtcgttt	gacacttgca	tctaaaccaa	aaaccagcca	accggtttac	2880
cgtgagcgta	ttgcttacac	ttatatggat	gaggatctgc	caacaacaga	gtatatctct	2940
ccaaatgaag	atggtacctt	tactcttcct	gaagaggctg	aaacaatgga	aggcgctact	3000
gttccattga	aaatgtcaga	ctttacttat	gttggtgaag	atatggctgg	taacatcact	3060
tatacaccag	tgactaagct	attggaaggc	cactctaata	aaccagaaca	agacggttca	3120
gatcaagcac	cagacaaaaa	accagaaact	aaaccagaac	aagacggttc	aggtcaagca	3180
ccagataaaa	aaccagaaac	taaaccagaa	caagacggtt	caggtcaaac	accagacaaa	3240
aaaccagaaa	ctaaaccaga	acaagacggt	tcaggtcaaa	caccagataa	aaaaccagaa	3300
actaaaccag	aaaaagatag	ttcaggtcaa	acaccaggta	aaactcctca	aaaaggtcaa	3360
ccttctcgta	ctctagagaa	acgatcttct	aagcgtgctt	tagctacaaa	agcatcaaca	3420
aaagatcagt	taccaacgac	taatgacaag	gatacaaatc	gtttacatct	ccttaagtta	3480
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<210> SEQ ID NO 674

<211> LENGTH: 1181

<212> TYPE: PRT

<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 674

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1				5					10					15	
Met	Ser	Thr	Ser	Ile	Leu	Leu	Asn	Ala	Gln	Ser	Asp	Ile	Lys	Ala	Asn
			20					25					30		
Thr	Val	Thr	Glu	Asp	Thr	Pro	Ala	Thr	Glu	Gln	Ala	Val	Glu	Thr	Pro
			35				40					45			
Gln	Pro	Thr	Ala	Val	Ser	Glu	Glu	Ala	Pro	Ser	Ser	Lys	Glu	Thr	Lys
			50				55				60				
Thr	Pro	Gln	Thr	Pro	Asp	Asp	Ala	Glu	Glu	Thr	Ile	Ala	Asp	Asp	Ala
65					70					75				80	
Asn	Asp	Leu	Ala	Pro	Gln	Ala	Pro	Ala	Lys	Thr	Ala	Asp	Thr	Pro	Ala
				85					90					95	
Thr	Ser	Lys	Ala	Thr	Ile	Arg	Asp	Leu	Asn	Asp	Pro	Ser	Gln	Val	Lys
			100					105					110		
Thr	Leu	Gln	Glu	Lys	Ala	Gly	Lys	Gly	Ala	Gly	Thr	Val	Val	Ala	Val
			115				120					125			
Ile	Asp	Ala	Gly	Phe	Asp	Lys	Asn	His	Glu	Ala	Trp	Arg	Leu	Thr	Asp
			130				135				140				
Lys	Thr	Lys	Ala	Arg	Tyr	Gln	Ser	Lys	Glu	Asp	Leu	Glu	Lys	Ala	Lys
145					150					155					160
Lys	Glu	His	Gly	Ile	Thr	Tyr	Gly	Glu	Trp	Val	Asn	Asp	Lys	Val	Ala

				165					170				175			
Tyr	Tyr	His	Asp	Tyr	Ser	Lys	Asp	Gly	Lys	Thr	Ala	Val	Asp	Gln	Glu	
			180					185					190			
His	Gly	Thr	His	Val	Ser	Gly	Ile	Leu	Ser	Gly	Asn	Ala	Pro	Ser	Glu	
	195						200					205				
Thr	Lys	Glu	Pro	Tyr	Arg	Leu	Glu	Gly	Ala	Met	Pro	Glu	Ala	Gln	Leu	
	210					215					220					
Leu	Leu	Met	Arg	Val	Glu	Ile	Val	Asn	Gly	Leu	Ala	Asp	Tyr	Ala	Arg	
225					230				235						240	
Asn	Tyr	Ala	Gln	Ala	Ile	Ile	Asp	Ala	Val	Asn	Leu	Gly	Ala	Lys	Val	
			245					250						255		
Ile	Asn	Met	Ser	Phe	Gly	Asn	Ala	Ala	Leu	Ala	Tyr	Ala	Asn	Leu	Pro	
			260					265					270			
Asp	Glu	Thr	Lys	Lys	Ala	Phe	Asp	Tyr	Ala	Lys	Ser	Lys	Gly	Val	Ser	
	275						280					285				
Ile	Val	Thr	Ser	Ala	Gly	Asn	Asp	Ser	Ser	Phe	Gly	Gly	Lys	Thr	Arg	
	290					295					300					
Leu	Pro	Leu	Ala	Asp	His	Pro	Asp	Tyr	Gly	Val	Val	Gly	Thr	Pro	Ala	
305					310					315					320	
Ala	Ala	Asp	Ser	Thr	Leu	Thr	Val	Ala	Ser	Tyr	Ser	Pro	Asp	Lys	Gln	
			325					330					335			
Leu	Thr	Glu	Thr	Ala	Thr	Val	Lys	Thr	Ala	Asp	Gln	Gln	Asp	Lys	Glu	
			340					345				350				
Met	Pro	Val	Leu	Ser	Thr	Asn	Arg	Phe	Glu	Pro	Asn	Lys	Ala	Tyr	Asp	
	355					360					365					
Tyr	Ala	Tyr	Ala	Asn	Arg	Gly	Met	Lys	Glu	Asp	Asp	Phe	Lys	Asp	Val	
	370					375				380						
Lys	Gly	Lys	Ile	Ala	Leu	Ile	Glu	Arg	Gly	Asp	Ile	Asp	Phe	Lys	Asp	
385					390					395					400	
Lys	Ile	Ala	Asn	Ala	Lys	Lys	Ala	Gly	Ala	Val	Gly	Val	Leu	Ile	Tyr	
			405					410					415			
Asp	Asn	Gln	Asp	Lys	Gly	Phe	Pro	Ile	Glu	Leu	Pro	Asn	Val	Asp	Gln	
			420					425					430			
Met	Pro	Ala	Ala	Phe	Ile	Ser	Arg	Lys	Asp	Gly	Leu	Leu	Leu	Lys	Glu	
	435					440					445					
Asn	Pro	Gln	Lys	Thr	Ile	Thr	Phe	Asn	Ala	Thr	Pro	Lys	Val	Leu	Pro	
	450					455					460					
Thr	Ala	Ser	Gly	Thr	Lys	Leu	Ser	Arg	Phe	Ser	Ser	Trp	Gly	Leu	Thr	
465					470					475					480	
Ala	Asp	Gly	Asn	Ile	Lys	Pro	Asp	Ile	Ala	Ala	Pro	Gly	Gln	Asp	Ile	
			485					490					495			
Leu	Ser	Ser	Val	Ala	Asn	Asn	Lys	Tyr	Ala	Lys	Leu	Ser	Gly	Thr	Ser	
			500					505				510				
Met	Ser	Ala	Pro	Leu	Val	Ala	Gly	Ile	Met	Gly	Leu	Leu	Gln	Lys	Gln	
	515					520					525					
Tyr	Glu	Thr	Gln	Tyr	Pro	Asp	Met	Thr	Pro	Ser	Glu	Arg	Leu	Asp	Leu	
	530					535					540					
Ala	Lys	Lys	Val	Leu	Met	Ser	Ser	Ala	Thr	Ala	Leu	Tyr	Asp	Glu	Asp	
545					550					555					560	
Glu	Lys	Ala	Tyr	Phe	Ser	Pro	Arg	Gln	Gln	Gly	Ala	Gly	Ala	Val	Asp	
			565					570					575			
Ala	Lys	Lys	Ala	Ser	Ala	Ala	Thr	Met	Tyr	Val	Thr	Asp	Lys	Asp	Asn	
			580					585					590			
Thr	Ser	Ser	Lys	Val	His	Leu	Asn	Val	Ser	Asp	Lys	Phe	Glu	Val		
	595					600					605					
Thr	Val	Thr	Val	His	Asn	Lys	Ser	Asp	Lys	Pro	Gln	Glu	Leu	Tyr	Tyr	
	610					615					620					